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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"			
(57) Abstract <p>The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.</p>			

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

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Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

20

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

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In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

20 The invention is also directed to methods of identifying an ORFX polypeptide or nucleic acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

30 In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins; proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF_n according to the invention (wherein *n* is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2*n*-1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2*n*. For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected. Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of 7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoetin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form
10 of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in
15 hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a
20 membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent
25 cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_rna_bind	DNA/RNA binding protein/factor
	dna_rna_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase PIR	phosphorylase PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase potassium_channel prostaglandin protease proteaseinhib reductase ribosomalprot RTR	polymerase potassium channel protein prostaglandin protease protease inhibitor reductase ribosomal associated protein EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
10		
15	SIM SPTR	similar EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
20	struct sulfotransferase SWP	structural associated protein sulfotransferase SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN synthase tgf tgfreceptor thioesterase thiolase tm7	SWISS-PROT Update (release 11-NOV-98) synthase transforming growth factor transforming growth factor receptor thioesterase thiolase seven transmembrane domain G-protein coupled receptor
25		
30	tnf traffic tnfreceptor TRN	necrosis factor receptor tumor necrosis factor tumor trafficking associated protein EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor transferase transport tubulin ubiquitin unclassified	transcription factor transferase transport protein tubulin ubiquitin
40		Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

5 ORFX nucleic acids, and their encoded polypeptides, according to the invention are useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

10 ORFX nucleic acids and polypeptides according to the invention can also be used to identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2 n , wherein $n = 1$ to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2 n (wherein $n = 1$ to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), or a fragment thereof, any of whose bases may be changed from the
25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2 $n-1$ (wherein $n = 1$ to 3161), including fragments, derivatives,

analogs and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a
20 vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5 As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect. Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

10 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively, and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

20 Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);
5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be
10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides
15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX
20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4.

25 ORFX variants

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of
30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (*e.g.*, 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2*n*-1 for the corresponding *n*, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (*v*), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (*v*), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX -like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

5 An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than 10 about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium 15 represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the 20 language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

25 Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of 30 the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX
25 cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6 contiguous amino acids of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example, the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2*n* (wherein $n = 1$ to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)_2}$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein $n = 1$ to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab')₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab')₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the
5 nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as
10 described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY:
15 METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or
20 non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is
25 introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and
30 pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews--Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

5 The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, 10 antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human 15 serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

20 A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent 25 such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with 30 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired
5 therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of
10 routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the
15 complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

20 Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and
25 pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be
30 used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

 The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,
10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

 In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained
15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are
20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

 Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)
25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

 Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),
30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding
5 of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct
10 binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the
15 induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test
20 compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test
25 compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein
30 or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

5 In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also
10 likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene
15 encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor
20 are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

25 This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For
30 example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics"). Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs:___ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

10 Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

20 The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

5 Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

10 An exemplary method for detecting the presence or absence of ORFX in a biological sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

10 In other embodiments, genetic mutations in ORFX can be identified by hybridizing a sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that
5 cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest
10 mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

15 In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T
20 mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

25 In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments
30 of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163); Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models, in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include
5 *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

10 Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination);
15 benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate
20 (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of
25 apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Once a neurodegenerative disease or disorder has been shown to be amenable to treatment by modulation activity, that neurodegenerative disease or disorder can be treated or prevented by administration of a Therapeutic that modulates activity. Such diseases include all degenerative disorders involved with aging, especially osteoarthritis and neurodegenerative disorders.

Disorders related to organ transplantation

Some ORFX can be associated with disorders related to organ transplantation, in particular but not limited to organ rejection. Therapeutics of the invention, particularly those that modulate (or supply) activity, may be effective in treating or preventing diseases or disorders related to organ transplantation. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity of an aforementioned protein) can be assayed by any method known in the art for efficacy in treating or preventing such diseases and disorders related to organ transplantation. Such assays include *in vitro* assays for using cell culture models as described below, or *in vivo* assays using animal models of diseases and disorders related to organ transplantation, see *e.g.*, below. Potentially effective Therapeutics, for example but not by way of limitation, reduce immune rejection responses in animal models in comparison to controls.

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

Cardiovascular Disease

GENX has been implicated in cardiovascular disorders, including in atherosclerotic plaque formation. Diseases such as cardiovascular disease, including cerebral thrombosis or hemorrhage, ischemic heart or renal disease, peripheral vascular disease, or thrombosis of other major vessel, and other diseases, including diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage disease, systemic lupus erythematosus, homocysteinemia, and familial protein or lipid processing diseases, and the like, are either directly or indirectly associated with atherosclerosis. Accordingly, Therapeutics of the invention, particularly those that modulate (or supply) activity or formation may be effective in treating or preventing

atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

 Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (*e.g.*, B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J*
30 *Exp Med* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

 Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

 Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

 A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in 10 these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may 15 also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of 30 wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

5 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, 10 antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*, *J Immunol Methods* 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

25 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins 30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395[emb]CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gij2829506[sp]P71559[SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264689, 264638, 264567
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264805, 264636, 264691, 264907, 264692, 264629
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22279002, 264563
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415926[gib]AAD20157] - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 265009, 264910, 264595, 264596, 264758, 264603, 264604, 264760, 264762, 264683, 264766, 264767, 264689, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264486
8	56924278 (15, 16)	Novel Protein sim. GBank gij585562[sp]Q06458[NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT]		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264906
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145[emb]CAA99871] - (Z75543) similar to potassium channel protein [Caenorhabditis elegans]		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264564
14	95105114 (27, 28)	Novel Protein sim. GBank gij2832781[emb]CAA12645] - (AJ225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696286, 35696052, 264510, 35695917, 264691, 264628, 35696423, 264555, 264558, 264559, 83373044
15	20458307 (29, 30)	Novel Protein sim. GBank gij1710791[sp]Q10234[RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5]	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gi 174884 sp P44391 URE1_HAEIN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	264600	
18	80246804 (35, 36)	Novel Protein sim. GBank gi 2281102 (AC002333) - SF16 [isolat] [Arabidopsis thaliana]		29331827, 264555, 264557, 264638, 264558	
19	80076624 (37, 38)	Novel Protein sim. GBank gi 2508112 sp P43672 UUP_ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP	UNCLASSIFIED transport	22278996, 264907, 264910, 264600, 264693	
20	20724558 (39, 40)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21906764, 264691, 18108376, 264636, 18108387, 264486	
21	80417554 (41, 42)	Novel Protein sim. GBank gi 1730203 sp P50442 GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)	UNCLASSIFIED	22278995, 264906, 265008, 265010, 265011, 264602, 264605, 264766, 264688, 21906764, 264691, 18108376, 264636, 18108387, 264486	
22	11705858 (43, 44)	Novel Protein sim. GBank gi 1877329 emb CAB07077 - (Z92771) ladeE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
23	80419176 (45, 46)	Novel Protein sim. GBank gi 1877329 emb CAB07077 - (Z92771) ladeE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
24	20291697 (47, 48)	Novel Protein sim. GBank gi 1877329 emb CAB07077 - (Z92771) ladeE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
25	80253774 (49, 50)	Novel Protein sim. GBank gi 1877329 emb CAB07077 - (Z92771) ladeE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
26	80255394 (51, 52)	Novel Protein sim. GBank gi 1877329 emb CAB07077 - (Z92771) ladeE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	264685 264488, 264907, 264909, 264600, 264602, 264603, 264605, 264682, 264766, 32833986, 264636, 264486	
27	80235795 (53, 54)	Novel Protein sim. GBank gi 4808369 emb CAB42783.1 - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	Contains protein domain (PF00253) - Ribosomal protein S14p/S29e	22278996, 56182435, 265018, 264566 18108370, 35696423, 264635, 264555	
28	79483561 (55, 56)	Novel Protein sim. GBank gi 3122290 sp O08333 K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	UNCLASSIFIED kinase	264638 264601, 264762, 264766, 264769, 264636	
29	82448765 (57, 58)	Novel Protein sim. GBank gi 3122290 sp O08333 K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)	UNCLASSIFIED kinase	264638 264601, 264762, 264766, 264769, 264636	
30	79189333 (59, 60)	Novel Protein sim. GBank gi 3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
31	19948158 (61, 62)	Novel Protein sim. GBank gi 3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
32	82449495 (63, 64)	Novel Protein sim. GBank gi 3560504 (AF027770) - unknown [Mycobacterium smegmatis]	UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
33	79582628 (65, 66)	Novel Protein sim. GBank gi 2129003 pir G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
34	87467657 (67, 68)	Novel Protein sim. GBank gi 2129003 pir G64507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED	264908, 265019, 264687, 21906764, 21906766	
35	95005170 (69, 70)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	60432289, 264600, 264602, 264760, 18108357, 264769, 265020, 264691	
36	19642042 (71, 72)	Novel Protein sim. GBank gi 3287739 sp P73538 BIOB_SYN3 - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)	UNCLASSIFIED	264600, 264687, 264558, 264639	
37	20369215 (73, 74)	Novel Protein sim. GBank gi 2313134 gb AAD07126.1 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26695]	synthase dehydrogenase	264566 264603	

38	20466334 (75, 76)	Novel Protein sim. GBank gjl3805970[embjCAA06231] - (AJ004933) periplasmic nitrate reductase, large subunit [Rhodopseudomonas sp.]			reductase	264605
39	94300715 (77, 78)	Novel Protein sim. GBank gjl1929448 (L63543) - endodermin [Xenopus laevis]		Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	264905, 264908, 264907, 66712502, 264908, 264909, 264511, 265009, 264910, 55812038, 264758, 265011, 264762, 264682, 264763, 264784, 264766, 265022, 264693, 264628, 264631, 264634, 264635, 264555, 264638, 18108381, 264558, 18108385, 264482
40	20635625 (78, 80)				UNCLASSIFIED	264592
41	80023287 (81, 82)	Novel Protein sim. GBank gjl854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]				264591, 35695917
42	20724566 (83, 84)				UNCLASSIFIED	264602
43	20467069 (85, 86)	Novel Protein sim. GBank gjl3820584 (AF066781) - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]			synthase	264605
44	13085297 (87, 88)	Novel Protein sim. GBank gjl2494764[spjQ50729]GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	264769, 264636
45	39384711 (89, 90)	Novel Protein sim. GBank gjl1881738 (U89688) - myosin-I binding protein Acan125 [Acanthamoeba castellanii]			UNCLASSIFIED	264769, 264510, 264508
46	95003398 (91, 92)				ngl	264566
47	11698624 (93, 94)				UNCLASSIFIED	264689
48	79407218 (95, 96)					18108385, 264635, 264828
49	21659844 (97, 98)				UNCLASSIFIED	264603
50	80503996 (99, 100)					264508, 264603, 264769, 264689, 264636, 264558, 264486
51	80255569 (101, 102)	Novel Protein sim. GBank gjl3411177 (AF076240) - MocC [Rhizobium leguminosarum bv. viciae]			UNCLASSIFIED	264593, 18108387
52	79208528 (103, 104)	Novel Protein sim. GBank gjl3914992[spjQ26264]SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)			struct	264634
53	36996970 (105, 106)	Novel Protein sim. GBank gjl3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]			UNCLASSIFIED	264762
54	79570897 (107, 108)				UNCLASSIFIED	264630, 264909, 264766
55	80202703 (109, 110)	Novel Protein sim. GBank gjl1633572 (U52064) - Herpesvirus salmomi ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]				29331824, 264102, 265018, 18108376
56	8758408 (111, 112)	Novel Protein sim. GBank gjl4321580[gbjAAD15785] - (AF050114) alginate lyase [Pseudomonas sp. W7]				264604
57	11223386 (113, 114)			Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264557

58	91227506 (115, 116)	Novel Protein sim. GBank gi 5616074 gb AAD45816.1 AF06194 - (AF061943) protease- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	56182575, 264259, 60432049, 35686052, 66712502, 264909, 265008, 265010, 265011, 264681, 29148784, 35685917, 60170615, 264691, 264692, 264693, 18108374, 35686423, 56182323, 60432113 264600, 264689, 264638
59	80077371 (117, 118)	Novel Protein sim. GBank gi 1172920 sp P45830 PFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00953) - Glycosyl transferase	264689 264766
60	12958341 (119, 120)	Novel Protein sim. GBank gi 1710216 (U79260) - unknown		264630
61	80426806 (121, 122)	[Homo sapiens]	glycoprotein	265019
62	13504966 (123, 124)			264602
63	16474553 (125, 126)		UNCLASSIFIED	
64	20724578 (127, 128)	Novel Protein sim. GBank gi 420845 pir A47041 - transposase homolog (insertion element [SAE1] - Alcaligenes eutrophus	UNCLASSIFIED	
65	79326308 (129, 130)	Novel Protein sim. GBank gi 3122312 sp O06134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	264563
66	46854384 (131, 132)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter (Streptomyces coelicolor]	transport	22278996, 264558
67	78952543 (133, 134)	Novel Protein sim. GBank gi 231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)	dehydrogenase	265021
68	79817382 (135, 136)			264909
69	79841764 (137, 138)		UNCLASSIFIED	264908
70	79871329 (139, 140)			264906, 264908
71	65897456 (141, 142)		UNCLASSIFIED	264602, 265021
72	87734977 (143, 144)	Novel Protein sim. GBank gi 415926 gb AAD20157 - (AC006282) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264511, 265008, 264910, 264758, 87168474, 264682, 264766, 264686, 264689, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 264629, 264631, 264639, 22279000
73	80025241 (145, 146)		UNCLASSIFIED	60424179, 264508, 264908, 265007, 264603, 264687, 264689, 264692, 18108387
74	20377410 (147, 148)		UNCLASSIFIED	264605
75	11819032 (149, 150)	Novel Protein sim. GBank gi 265309 emb CAA16914 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]	UNCLASSIFIED	264689
76	95105303 (151, 152)	Novel Protein sim. GBank gi 446881 emb CAB38212 - (AL035601) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	83373044, 264906, 264557
77	10144718 (153, 154)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264563
78	8758258 (155, 156)		UNCLASSIFIED	264604

79	94140190 (157, 158)	Novel Protein sim. GBank gj15689453[dbj BAA83010.1] - (AB028981) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain		35696286, 22278998, 29331822, 29331824, 29331825, 29331827, 264905, 264906, 264907, 66712502, 264908, 264909, 265008, 265009, 264910, 60170831, 55812038, 33109954, 265017, 265018, 264288, 264768, 56181562, 21906765, 21906769, 29148784, 265020, 264690, 264691, 264692, 264693, 60431528, 35696423, 264631, 264632, 264634, 264636, 264639, 83373044, 264564, 264566, 264567
80	82314840 (159, 160)			UNCLASSIFIED	264769, 264801, 265006, 264910, 264604, 264605, 264634, 264635, 264905, 264762, 264637, 264592, 264628, 264907, 264691, 264908, 264567, 264909, 264766
81	20467247 (161, 162)	Novel Protein sim. GBank gj1723442[sp Q10258]YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C56F8.10 IN CHROMOSOME I		reductase	264605
82	16331388 (163, 164)	Novel Protein sim. GBank gj12895866 (AF045770) - methylmalonate semi-aldehyde dehydrogenase (Oryza sativa)		dehydrogenase	264567
83	94741180 (165, 166)	Novel Protein sim. GBank gj13402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 264508, 264509, 264905, 264908, 264909, 264511, 264591, 264593, 264594, 264595, 264596, 264758, 264603, 264760, 264681, 18108351, 264762, 264682, 264764, 264684, 264766, 264686, 264632, 264637, 264557, 264638, 264639, 18108385, 264566
84	80355375 (167, 168)	Novel Protein sim. GBank gj1173364[sp P45380]SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)		transport	264508, 264906, 264907, 264908, 264909, 264910, 264760, 264763, 264764, 264766, 264768, 264769, 35695855, 264636, 264637
85	80499600 (169, 170)	Novel Protein sim. GBank gj1210998[pir J S70682] - glycosyltransferase homolog - Bordetella pertussis		transferase	264605, 264762, 264687, 264769, 18108374, 264636, 264486
86	39559043 (171, 172)	Novel Protein sim. GBank gj13256023[emb CAA17228.1] - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			264910
87	13856808 (173, 174)			UNCLASSIFIED	264093

88	95344718 (175, 176)	Novel Protein sim. GBank gi 559703 dbj BAA07552 - (D38549) ha1025 is new [Homo sapiens]		52644507, 52646365, 18108398, 65274572, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 264105, 264508, 264905, 264906, 264907, 264908, 29331830, 66712502, 52644045, 56182435, 265007, 265009, 264910, 60170831, 264592, 60431735, 60433356, 33657402, 264757, 60433438, 55812038, 264758, 21906754, 52646317, 33109954, 52644296, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264766, 52844229, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 60170615, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35695763, 264628, 263972, 18108374, 55810764, 35696423, 55811576, 65274791, 35695855, 60431850, 264636, 52644332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264564, 264488, 264600
89	80077389 (177, 178)	Novel Protein sim. GBank gi 1710383 sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115998 (178, 180)			
91	78906950 (181, 182)	Novel Protein sim. GBank gi 2499891 sp P76403 YEQQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGK INTERGENIC REGION	UNCLASSIFIED protease	264760 265006
92	79554871 (183, 184)	Novel Protein sim. GBank gi 3367754 emb CAA20079 - (AL031155) hypothetical protein SC3A7.16c [Streptomyces coelicolor]	UNCLASSIFIED	264691
93	80496778 (185, 186)	Novel Protein sim. GBank gi 2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase associated	264907, 264908, 264910, 265009, 264605, 264769
94	78646649 (187, 188)	Novel Protein sim. GBank gi 1171919 sp P46920 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - CBS domain	264906
95	11090238 (189, 190)			264594

96	94322125 (191, 192)	Novel Protein sim. GBank gi 4589560 dbj BAA76802.1 - (AB023175) KIAA0958 protein (Homo sapiens)		UNCLASSIFIED	22278995, 22278999, 264259, 29331822, 29331826, 35696052, 29146499, 264509, 264906, 264907, 264908, 264909, 265007, 265008, 264910, 265009, 264593, 265010, 265017, 264604, 265019, 18108351, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264692, 33657182, 35695763, 264628, 264629, 18108379, 264631, 264636, 18108381, 264559, 18108382, 83373044, 22278902
97	79605200 (193, 194)	Novel Protein sim. GBank gi 4583559 emb CAB40388.1 - (AJ005255) OxyR [Enwinia chrysanthemi]		UNCLASSIFIED	264508
98	79427000 (195, 196)	Novel Protein sim. GBank gi 1001693 dbj BAA10430 - (D64002) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	264909
99	20466524 (197, 198)	Novel Protein sim. GBank gi 169479 sp P43925 EFG_HAEIN - ELONGATION FACTOR G (EF-G)		UNCLASSIFIED	264605
100	79640113 (199, 200)	Novel Protein sim. GBank gi 408087 pir S37485 - gene msg1 protein - mouse		UNCLASSIFIED	264693
101	80203298 (201, 202)	Novel Protein sim. GBank gi 2894166 emb CAA11773.1 - (AJ223998) PCZA361.18 [Amycolatopsis orientalis]		UNCLASSIFIED	265020, 264102, 263972
102	20467259 (203, 204)	Novel Protein sim. GBank gi 1731040 sp P54509 YQH_H_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	synthase	264605
103	20466368 (205, 206)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264605
104	80247572 (207, 208)	Novel Protein sim. GBank gi 1685117 U70770 - furrowed [Drosophila melanogaster]		UNCLASSIFIED	264591, 264595, 264602
105	79605206 (209, 210)	Novel Protein sim. GBank gi 1705505 sp P54729 BS4_MOUSE - BS4 PROTEIN	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complement	264508
106	28382058 (211, 212)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264511, 265009
107	80057781 (213, 214)	Novel Protein sim. GBank gi 299120 similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]		ATPase_associated	29331824, 264591, 21906754, 265019
108	80237836 (215, 216)	Novel Protein sim. GBank gi 2330791 emb CAB11265 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]	Contains protein domain (PF00005) - ABC transporter	transport	18108374, 35695917, 22278996, 264113, 264600, 264602, 264603, 265017, 264910, 264906, 264636, 264766
109	95194148 (217, 218)	Novel Protein sim. GBank gi 2330791 emb CAB11265 - (Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	264758, 264603, 264630, 264636, 264637
110	79582823 (219, 220)				264687
111	39565458 (221, 222)				264564
112	79856038 (223, 224)			UNCLASSIFIED	264908
113	17959439 (225, 226)			UNCLASSIFIED	265007
114	80502101 (227, 228)			UNCLASSIFIED	264769

115	80251003 (229, 230)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52645156, 52645080, 33656970, 264592, 21906754, 27486264, 18108379, 35698423, 264635, 52644332, 18108382
116	81298689 (231, 232)				264905, 264906, 264907, 264908, 264909, 264910, 264758, 285010, 264763, 264682, 264764, 264766, 264685, 264686, 264768, 264769, 33657023, 284693, 33657109, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56526486, 264565, 264566
117	79636695 (233, 234)				264639, 264693
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263974
119	91013071 (237, 238)	Novel Protein sim. GBank gij732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264689, 265020, 264534, 27486261, 264558, 83373044, 18108385, 264564
120	8756491 (239, 240)	Novel Protein sim. GBank gij2131219 [pir]IS0157 - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	264603
121	80026153 (241, 242)				264595
122	20457620 (243, 244)	Novel Protein sim. GBank gij2052147 [emb]CAB08137 - (Z94752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gij2833385 [sp]Q43134 [UGST, SORBI - GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108379, 18108380, 18108384
125	87797986 (249, 250)	Novel Protein sim. GBank gij475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gij5102785 [emb]CAB45200.1 - (AL079308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)				264605
128	80248473 (255, 256)	Novel Protein sim. GBank gij130120 [sp]P23620 [PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED - phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95290543 (257, 258)	Novel Protein sim. GBank gij2506493 [sp]P38036 [YGC8, ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	35698423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264906, 264564, 264628, 264682, 264565, 264683
130	80085583 (259, 260)	Novel Protein sim. GBank gij85405 [emb]CAA58371 - (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gij1076038 [pir]IS54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331826, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264636

132	10867692 (263, 264)	Novel Protein sim. GBank gj11877340[emb]CAB07068] - (Z92771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)		264636
133	94630883 (265, 266)	Novel Protein sim. GBank gj14585839[emb]CAB40932.1] - (AL049630) putative NADH dehydrogenase [Streptomyces coelicolor]	dehydrogenase		264905, 264689
134	79834660 (267, 268)	Novel Protein sim. GBank gj1460074[emb]CAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			264634
135	19885057 (269, 270)	Novel Protein sim. GBank gj125899[emb]CAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]	synthase		264508
136	79846083 (271, 272)	Novel Protein sim. GBank gj125899[emb]CAA73511] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]			264683, 264685, 264686, 264691, 264692, 264693
137	79619770 (273, 274)	Novel Protein sim. GBank gj15420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		18108374, 18108385, 33657109, 33657182, 265010, 22278998, 265006, 265007, 265008, 265009, 264693
138	79635971 (275, 276)	Novel Protein sim. GBank gj15688912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	dehydrogenase		22278996, 265007, 264910, 60433356, 265010, 264602, 264605, 264768, 264688, 264769, 264693, 32833986, 18108374, 18108387
139	86688076 (277, 278)	Novel Protein sim. GBank gj15688912[emb]CAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	UNCLASSIFIED		264908
140	79825759 (279, 280)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	nuclease		264600
141	20700094 (281, 282)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]			264602, 265017
142	80028104 (283, 284)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	UNCLASSIFIED		264600
143	11072274 (285, 286)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]			263978, 264600, 264910, 264632, 264508, 264563, 264564, 264591, 264556, 264908, 264629, 264639
144	95009102 (287, 288)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	UNCLASSIFIED		264600
145	80027058 (289, 290)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	UNCLASSIFIED		22278996, 264602
146	13085662 (291, 292)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	Contains protein domain (PF01675) - Transposase		264687
147	94320366 (293, 294)	Novel Protein sim. GBank gj13581916[emb]CAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]	helicase		264905, 264906, 264909, 264510, 265009, 60433356, 264600, 264601, 264604, 264605, 264687, 264769, 18108365, 65274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank gj12916947[emb]CAA17585] - (AL021999) hypothetical protein Rv0986 [Mycobacterium tuberculosis]	transport		265009, 265010, 264600, 264602, 264603, 264604, 264605, 264693, 33657109, 264636

149	80249373 (287, 298)	Novel Protein sim. GBank gi 1723073 sp Q11040 Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CV50.01	Contains protein domain (PF00005) - ABC transporter	transport	265010, 264600, 264601, 264603, 264604, 27486285, 264636
150	20294748 (289, 300)	Novel Protein sim. GBank gi 3724125 emb CAA11905 - (AJ224340) mallophosphorylase [Lactobacillus sanfrancisco]			264600
151	20726398 (301, 302)	Novel Protein sim. GBank gi 729312 sp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	264602
152	95002877 (303, 304)	Novel Protein sim. GBank gi 2497952 sp P55667 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	264602
153	80256665 (305, 306)	Novel Protein sim. GBank gi 3123021 sp Q90508 VIT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	264593
154	82305968 (307, 308)	Novel Protein sim. GBank gi 419687 pir JUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	264910, 264762, 264691, 264634 264605
155	20429859 (309, 310)	Novel Protein sim. GBank gi 628710 pir J541739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	264565
156	39564742 (311, 312)	Novel Protein sim. GBank gi 3695013 (AF052586) - CitA [Pseudomonas aeruginosa]	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HnfX family	hydrolase	264691
157	10358887 (313, 314)	Novel Protein sim. GBank gi 1073072 pir J55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	264905
158	79761938 (315, 316)	Novel Protein sim. GBank gi 173023 sp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	265008 264605
159	78890376 (317, 318)	Novel Protein sim. GBank gi 5304869 emb CAB46028.1 - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomalprot	22278996, 264600, 264603, 35695917, 32833986, 35696423, 264636
160	11075119 (319, 320)	Novel Protein sim. GBank gi 266169 emb CAA15795 - (AL009204) putative protease [Streptomyces coelicolor]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	264112, 264532, 22279002
161	80055007 (321, 322)	Novel Protein sim. GBank gi 4416478 gb AAD20378 - (AF125999) transposase [Mycobacterium avium]		UNCLASSIFIED	264639
162	80016371 (323, 324)	Novel Protein sim. GBank gi 76177 pir JQCECF - hypothetical 38.8K protein (ftsI 5' region) - Escherichia coli		UNCLASSIFIED	264905, 264907, 264600
163	11692306 (325, 326)			UNCLASSIFIED	264891
164	80077902 (327, 328)			UNCLASSIFIED	264805, 264486
165	10856067 (329, 330)			UNCLASSIFIED	265010
166	88095003 (331, 332)			UNCLASSIFIED	264600
167	16395460 (333, 334)			UNCLASSIFIED	
168	80079362 (335, 336)			UNCLASSIFIED	
169	80239581 (337, 338)				264556, 264557, 264558, 264559

170	78612364 (339, 340)	Novel Protein sim. GBank gi 140888 sp P27847 YICK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLDB INTERGENIC REGION (F138)	Contains protein domain (PF01810) - LysE type translocator	264906	
171	95293073 (341, 342)	Novel Protein sim. GBank gi 4210905 gb AAD12048.1 - (AF045609) AglG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	264595, 264604	
172	37797007 (343, 344)	Novel Protein sim. GBank gi 132854 sp P02387 RL2_ECOLI - 50S RIBOSOMAL PROTEIN L2	transport	264769	
173	57529660 (345, 346)	Novel Protein sim. GBank gi 1881350 dbj BAA19377 - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIBIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]	ribosomalprot	264769	
174	95293078 (347, 348)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR-A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	transport	264510, 264593, 264602, 264603, 264605, 264762, 264693	
175	79756270 (349, 350)	Novel Protein sim. GBank gi 207272 emb CA808326 - (Z95121) manA [Mycobacterium tuberculosis]	isomerase	264565	
176	80066898 (351, 352)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR-A41724 chicken LD (limb deformity) gene product and to formin; also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	264907, 264910, 264681, 264558	
177	86684862 (353, 354)	Novel Protein sim. GBank gi 2326738 emb CAB10952 - (Z98268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	UNCLASSIFIED	264788, 60424179, 264687, 264688, 264769, 29331826, 60432289, 18108376, 264689, 18108387, 32833986, 22278996, 265020, 264600, 264601, 264602, 264603, 264604, 264605, 264635, 264762, 264636, 264906, 264564, 264637, 264638, 264486, 60433356, 264766	
178	79559526 (355, 356)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73 [Drosophila melanogaster]	struct	264693, 33657109, 264635	
179	20263112 (357, 358)	Novel Protein sim. GBank gi 169367 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE	UNCLASSIFIED	264563	
180	80488958 (359, 360)	Novel Protein sim. GBank gi 3170615 (AF059485) - DOC4 [Mus musculus]	helicase	264769	
181	79585369 (361, 362)	Novel Protein sim. GBank gi 1076627 pir S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED	21906767, 264635, 264639, 18108384	
182	80577899 (363, 364)	Novel Protein sim. GBank gi 4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 35696052, 56182435, 264511, 265018, 33657109, 264555, 264566	
183	11614017 (365, 366)	Novel Protein sim. GBank gi 1076627 pir S54172 - inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED	284690	
184	10174167 (367, 368)	Novel Protein sim. GBank gi 4371280 gb AAD18138 - (AC006260) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	264510	

185	21660822 (369, 370)	Novel Protein sim. GBank gij3006178[emb]CAA18398.1] - (AL022304) putative mma transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij2829802[sp]P94408[YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION]		transport	264595
187	80186611 (373, 374)	Novel Protein sim. GBank gij3150260[emb]CAA19179] - (AL023634) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264359
188	20464942 (375, 376)	Novel Protein sim. GBank gij2145853[pil]S72938 - hnx protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[dbj]BAA19271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]		UNCLASSIFIED	35696052, 264602, 264605, 264762, 264689, 35695917, 18108370, 18108372, 264638, 264585
190	80086821 (379, 380)	Novel Protein sim. GBank gij120226[sp]P28725[FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PIPIASE) (ROTAMASE)]		synthase	264583
191	88095012 (381, 382)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		isomerase	264508, 264604, 264605, 264769, 264555
192	16333379 (383, 384)	Novel Protein sim. GBank gij4980892[gb]AAD35474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]			264567
193	79910127 (385, 386)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264908, 264693
194	20464949 (387, 388)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264605
195	13518369 (389, 390)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		transport	264636
196	95005569 (391, 392)	Novel Protein sim. GBank gij1705461[sp]P53656[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]			264600, 264689, 264638
197	80248665 (393, 394)	Novel Protein sim. GBank gij3123305[sp]Q27778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)]		gaba	
198	78163635 (395, 396)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]		kinase	264602, 264682, 264692, 18108374
199	78890715 (397, 398)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83859) gnd [Mycobacterium tuberculosis]			264636
200	79413849 (399, 400)	Novel Protein sim. GBank gij2842222 (AF030885) - telomere-associated recQ-like helicase [Usilago maydis]			265008
201	86945924 (401, 402)	Novel Protein sim. GBank gij2894379[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	264595, 264596
				UNCLASSIFIED	29331826, 265007, 264512, 33657402, 264596, 265017, 18108351, 264682, 264683, 264767, 264629, 55810764, 264634, 264635, 56182323, 60432113, 22278000

202	7958046 (403, 404)	Novel Protein sim. GBank gi 231772 sp P30598 CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)	Contains protein domain (PF01644) - Chitin synthase	264600	
203	79843927 (405, 406)	Novel Protein sim. GBank gi 1504042 dbj BAA13220 - (D6984) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 29331822, 29331825, 29331827, 264906, 21908754, 264683, 21908766, 21906769, 35896423, 264556	
204	79855186 (407, 408)	Novel Protein sim. GBank gi 2633808 emb CAB13310 - (Z59111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED [transport]	264909	
205	10090583 (409, 410)			264909	
206	8758473 (411, 412)		UNCLASSIFIED	264604	
207	20754522 (413, 414)	Novel Protein sim. GBank gi 2134381 pir S60678 - polybromo 1 protein - chicken	UNCLASSIFIED	264556	
208	20289281 (415, 416)			264605	
209	80071069 (417, 418)	Novel Protein sim. GBank gi 2501040 sp O5814 SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE--TRNA LIGASE) (PRORS)		264605, 264689	
210	80168800 (419, 420)			264905, 264907, 264909, 264766, 264687, 264691, 264629, 18108374, 264638	
211	80034539 (421, 422)			263978	
212	82442474 (423, 424)	Novel Protein sim. GBank gi 5031809 ref NP_005536.1 pISLR - immunoglobulin superfamily containing leucine-rich repeat	UNCLASSIFIED	264508, 264905, 264906, 264907, 264908, 264500, 264762, 264534, 264632, 264634, 264635, 264639, 264486	
213	80249562 (425, 426)	Novel Protein sim. GBank gi 3122359 sp O33123 LEU2_MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	22278996, 264508, 264600, 264602, 264603, 264605, 33657023, 264565, 264486	
214	80079381 (427, 428)	Novel Protein sim. GBank gi 116236 sp P19421 CH60_COXBU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	264600, 264693	
215	14973283 (429, 430)		UNCLASSIFIED	264629	
216	80177716 (431, 432)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264448	
217	79603634 (433, 434)	Novel Protein sim. GBank gi 2506924 sp P49754 VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)		264508	
218	80256475 (435, 436)	Novel Protein sim. GBank gi 1173288 sp P38106 RSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	mapolymerase	264594	
219	20438797 (437, 438)	Novel Protein sim. GBank gi 1781097 emb CAB06231 - (Z83864) giB [Mycobacterium tuberculosis]	synthase	264604	
220	13499572 (439, 440)	Novel Protein sim. GBank gi 2984703 (AF052427) - unknown [Trypanosoma cruzi]	nucleaseinhib	264689	
221	11287498 (441, 442)	Novel Protein sim. GBank gi 4587313 dbj BAA76709.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	UNCLASSIFIED	264555	

222	79862802 (443, 444)	Novel Protein sim. GBank gij1877268[emb]CAB07049] - (Z92770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264769, 35696423
223	83053869 (445, 446)			UNCLASSIFIED	264906, 264907, 264603
224	79557920 (447, 448)			UNCLASSIFIED	264684, 264693
225	79559541 (449, 450)	Novel Protein sim. GBank gij2274851[dbj]BAA21515] - (D64159) 3-7 gene product [Homo sapiens]		UNCLASSIFIED	264692
226	79172397 (451, 452)	Novel Protein sim. GBank gij668245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 264112, 33657023, 263981
227	81777196 (453, 454)			UNCLASSIFIED	35695917, 264636, 264907
228	79872285 (455, 456)			UNCLASSIFIED	264768, 264907, 264908, 264692, 264593, 264639
229	79838266 (457, 458)			UNCLASSIFIED	264906, 264910
230	11013209 (459, 460)			UNCLASSIFIED	264631
231	20622207 (461, 462)	Novel Protein sim. GBank gij1835114[emb]CAA71733] - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]		UNCLASSIFIED	264906, 264600, 264603, 264692
232	80055035 (463, 464)			UNCLASSIFIED	264600, 264603, 264605, 264687, 264769
233	80063054 (465, 466)	Novel Protein sim. GBank gij2642340 (AF032970) - imidazolone propionate hydrolase [Pseudomonas putida]	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
234	7523998 (467, 468)	Novel Protein sim. GBank gij3510505 (AF030881) - polypeptide [Fugu rubripes]		UNCLASSIFIED	264369
235	80203671 (469, 470)			UNCLASSIFIED	264106
236	78940001 (471, 472)	Novel Protein sim. GBank gij2104609[emb]CAB08805] - (Z95398) PckA [Mycobacterium leprae]		UNCLASSIFIED	264905
237	11755273 (473, 474)			UNCLASSIFIED	264681
238	79461401 (475, 476)			UNCLASSIFIED	264639
239	82435190 (477, 478)	Novel Protein sim. GBank gij2495617[sp]Q57252[VDIJ]_HAEIN - HYPOTHETICAL PROTEIN H1163	Contains protein domain (PF00037) - 4Fe-4S ferredoxins and related iron-sulfur cluster binding domains.	UNCLASSIFIED	264906, 265010, 264603, 264762, 264682, 264636, 264638, 264486
240	21635575 (479, 480)	Novel Protein sim. GBank gij183458[sp]P75796[YLIA]_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA		transport	264259, 264769
241	80377307 (481, 482)	Novel Protein sim. GBank gij3675920[emb]CAB04111] - (Z81503) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264908, 264909, 264764, 264639
242	82148454 (483, 484)			UNCLASSIFIED	264489, 264907, 264908, 264511, 264760, 264764, 264692, 264635, 264637
243	79633207 (485, 486)			UNCLASSIFIED	264906
244	80248682 (487, 488)	Novel Protein sim. GBank gij2624302[emb]CAA15575] - (AL008987) ald [Mycobacterium tuberculosis]		UNCLASSIFIED	264600, 264602, 264605, 264769, 264689
245	79863543 (489, 490)	Novel Protein sim. GBank gij2920625 (AF044499) - vgrE protein [Escherichia coli]		UNCLASSIFIED	264907, 264758
246	79162928 (491, 492)	Novel Protein sim. GBank gij5420387[emb]CAB46679:] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01106) - NiRu-like domain		264637, 18108381, 18108387, 264565

247	79873185 (493, 494)	Novel Protein sim. GBank gi 1839006 emb CAB06648 - (Z85982) argB [Mycobacterium tuberculosis]		kinase	264909, 264691, 35698423, 18108387
248	80488983 (495, 496)	Novel Protein sim. GBank gi 168574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35956286, 264907, 264511, 264602, 264768, 264688, 265021, 35695855, 18108385
249	79764645 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264762, 264636
250	79619980 (499, 500)				21908768, 264692
251	84359488 (501, 502)			UNCLASSIFIED	52645156, 29331822, 29331824, 52644045, 265018, 21906765, 21906768, 265020, 27486261, 27486265, 35695763, 18108376, 264556, 264559, 264565
252	79737756 (503, 504)	Novel Protein sim. GBank gi 3327166 dbj BAA31651 - (AB014576) KIAA0676 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 506)	Novel Protein sim. GBank gi 3036880 emb CAA18513 - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank gi 3915488 sp O34961 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COTT-RAPA INTERGENIC REGION (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264508, 264906, 264602, 264687, 265021, 264486
255	11398315 (509, 510)	Novel Protein sim. GBank gi 1665720 dbj BAA04134 - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank gi 465787 sp P34422 YL31_CAEEL - HYPOTHETICAL 86.0 KD PROTEIN F44B9.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Proyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank gi 1172039 sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459484 (515, 516)	Novel Protein sim. GBank gi 3127836 emb CAA18902 - (AL023496) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	264681, 264686, 264692
260	20378437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20285883 (521, 522)	Novel Protein sim. GBank gi 123761 sp P24221 HUTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264389
263	88095045 (525, 526)	Novel Protein sim. GBank gi 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (biasip score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB ...		UNCLASSIFIED	264488, 264905, 264906, 264907, 264908, 264909, 264512, 264910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264763, 264764, 264288, 264766, 264768, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank gi 3043734 dbj BAA25531 - (AB011177) KIAA0605 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264908, 21908754, 265018, 265019, 265020

265	95355646 (528, 530)	Novel Protein sim. GBank gi 4589624 dbj BAA76834.1 - (AB023207) KIAA0990 protein [Homo sapiens]		Kinase	264488, 35696286, 29331824, 56182181, 35896052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264596, 55811386, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21906765, 21906767, 21906769, 265020, 264691, 33857023, 33657109, 33657182, 264628, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526486, 87168518, 264564, 264566, 264486, 264600
266	79588075 (531, 532)			UNCLASSIFIED	264828
267	11362222 (533, 534)			UNCLASSIFIED	264687, 264769, 264689
268	79509566 (535, 536)			UNCLASSIFIED	264602
269	80025810 (537, 538)			UNCLASSIFIED	264693
270	84361144 (539, 540)	Novel Protein sim. GBank gi 4507367 ref NP_003182.1 pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	
271	79552301 (541, 542)	Novel Protein sim. GBank gi 4980738 gb AAD35331.1 AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		UNCLASSIFIED	264909, 264693
272	9674778 (543, 544)	Novel Protein sim. GBank gi 1168224 sp P44569 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		synthase	264908
273	12840694 (545, 546)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	264688
274	39524246 (547, 548)	Novel Protein sim. GBank gi 3253159 (AF005355) - Translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	264564
275	82787041 (549, 550)	Novel Protein sim. GBank gi 129021 sp P20964 QBG_BACSU - SPO08-ASSOCIATED GTP-BINDING PROTEIN		UNCLASSIFIED	264907, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	86671073 (551, 552)	Novel Protein sim. GBank gi 129021 sp P20964 QBG_BACSU - SPO08-ASSOCIATED GTP-BINDING PROTEIN		ribosomalprot	265008, 60432229
277	80079735 (553, 554)	Novel Protein sim. GBank gi 79839 pir J03812 - uvrB protein - Micrococcus luteus		UNCLASSIFIED	264600, 18108387
278	12866947 (555, 556)	Novel Protein sim. GBank gi 3123160 sp Q18964 YLN2_CAEEL - HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II		UNCLASSIFIED	264689
279	95292719 (557, 558)			nuclease	264508, 264604, 21906764, 264638, 264557, 264404
280	5603617 (559, 560)				264259
281	80249599 (561, 562)				18108392, 264634, 264555, 264556, 264557, 264558
282	18598682 (563, 564)			UNCLASSIFIED	265019
283	20814211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (567, 568)	Novel Protein sim. GBank gi 2429094 (U58632) - acetyl xylan esterase. AveA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696052, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21906764, 18108376, 264636, 264559, 18108387
285	8757940 (569, 570)			UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gi 2072674 emb CAB08305 - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	ATPase-associated	35696052, 264769, 264638
287	12745521 (573, 574)			UNCLASSIFIED	264689
288	20756502 (575, 576)	Novel Protein sim. GBank gi 765323 bbs 157676 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori-silkworms, Peptide Partial, 633 aa] [Bombyx mori]		collagen	264557
289	80043804 (577, 578)	Novel Protein sim. GBank gi 1870009 emb CAB06860 - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, telR family	-ribosomalprot	264593, 264600
290	80430175 (578, 580)			UNCLASSIFIED	264768
291	20747431 (581, 582)	Novel Protein sim. GBank gi 250664 sp P40120 YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
292	80052555 (583, 584)	Novel Protein sim. GBank gi 625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
293	80062519 (585, 586)	Novel Protein sim. GBank gi 1718065 sp P53528 UVRD_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase		264909, 264605, 264687, 264689, 264692
294	79830303 (587, 588)	Novel Protein sim. GBank gi 117422 sp P10040 CRB_DROME - CRUMBS PROTEIN PRECURSOR (95F)	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696052, 264906, 265011, 264628, 55811576
295	79444180 (589, 590)	Novel Protein sim. GBank gi 1181819 dbj BAA11565 - (D82384) a variant of TSC-22 [Gallus gallus]			52644507, 29331822, 264592, 265020, 264639
296	79607076 (591, 592)	Novel Protein sim. GBank gi 3649789 dbj BAA33403 - (AB012226) SecA [Vibrio alginolyticus]		synthase	264508
297	79631297 (593, 594)	Novel Protein sim. GBank gi 5689967 emb CAB52004.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
298	80418898 (595, 596)			UNCLASSIFIED	264905, 264681, 264639, 264766

299	95283298 (597, 598)	Novel Protein sim. GBank gij220637[dbj]BAA014771 - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	264488, 263994, 56994075, 22278997, 22278998, 22278999, 20281099, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264906, 264907, 264908, 52644045, 264909, 264511, 265008, 264910, 264595, 264596, 264758, 33657084, 87188559, 265018, 265019, 264764, 264288, 264766, 264687, 56181562, 264769, 21906765, 21906768, 21906769, 33657023, 264692, 33657109, 27486281, 18108370, 264628, 264629, 55811576, 35695855, 264631, 264634, 264635, 264638, 264639, 83373044, 18108387, 87168518, 22279000, 22279002, 264565, 264566, 264567
300	20711340 (599, 600)	Novel Protein sim. GBank gij145922 (M20981) - iron dicitrate transport protein precursor [Escherichia coli]	UNCLASSIFIED	264602
301	13511332 (601, 602)	Novel Protein sim. GBank gij1174681[sp]P44594[GTG_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]	transport	264687
302	9875260 (603, 604)	Novel Protein sim. GBank gij1174681[sp]P44594[GTG_HAEIN - QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]		264908
303	79574895 (605, 606)	Novel Protein sim. GBank gij67985[pir]HJUNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus	helicase	264689
304	20711344 (607, 608)	Novel Protein sim. GBank gij1657554[gb]AAB18082.1 - (U73857) hypothetical protein [Escherichia coli]		264602
305	80412520 (609, 610)	Novel Protein sim. GBank gij728867[sp]P40602[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR	UNCLASSIFIED	264763
306	8515876 (611, 612)	Novel Protein sim. GBank gij1657554[gb]AAB18082.1 - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	263978
307	80222901 (613, 614)	Novel Protein sim. GBank gij1710612[sp]Q10793[RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	UNCLASSIFIED	265010, 21906768, 265020, 18108374, 263977
308	80064305 (615, 616)	Novel Protein sim. GBank gij1710612[sp]Q10793[RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	Contains protein domain (PF01351) - Ribonuclease HII	264910, 264600, 264605, 264687, 264689, 264638, 18108387
309	80504136 (617, 618)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		264769
310	80053616 (619, 620)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	264603
311	11090659 (621, 622)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazolesuccinocarboxamide synthase [Mycobacterium tuberculosis]		264602
312	80054347 (623, 624)		UNCLASSIFIED	264566
313	80046168 (625, 626)		UNCLASSIFIED	264603, 264567

314	87645112 (627, 628)	Novel Protein sim. GBank gi 3661583 (AF092175) - iKaros - [Danio rerio]	Contains protein domain (PF00320) - GATA zinc finger	dna_rna_bind	264259, 60432289, 29331828, 264905, 264906, 264908, 264909, 265008, 264910, 60432229, 33657402, 60433438, 33109954, 265011, 265017, 264603, 265018, 264288, 264766, 264692, 35695763, 264628, 264629, 264639, 60170394, 22279002, 264568
315	82356091 (629, 630)	Novel Protein sim. GBank gi 1652620 dbj BAA17540 - (D90907) pyridine nucleotide transhydrogenase beta subunit [Synechocystis sp.]			264508, 264600, 264762, 264687, 264768, 52644229, 264769, 264689, 264635, 264636, 264638, 264486
316	79911071 (631, 632)	Novel Protein sim. GBank gi 18244 sp P24178 DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (SDAP)		UNCLASSIFIED	264693
317	20466944 (633, 634)	Novel Protein sim. GBank gi 18244 sp P24178 DAPE_ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (SDAP)		UNCLASSIFIED	264605
318	941141836 (635, 636)	Novel Protein sim. GBank gi 4680229 gb AAD27583.1 AF11827 - (AF118274) DNB-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostelium (slime mold) repeats	transport	264908, 264909, 264910, 264593, 264594, 264760, 264288, 264768, 264769, 21906769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264566
319	17289360 (637, 638)	Novel Protein sim. GBank gi 1149693 emb CAA60220 - (X86499) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gi 2811033 sp O05314 GLGC_MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLAASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gi 1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danio rerio]		cyto450	264509, 264906, 264907, 264908, 265009, 264596, 264764, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	66489053 (643, 644)	Novel Protein sim. GBank gi 1160355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810764
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265009, 264593, 264628, 264635
324	79174383 (647, 648)				264687
325	79862691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]			264488, 264905, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	264592
329	10173821 (657, 658)			UNCLASSIFIED	264510
330	86597767 (659, 660)	Novel Protein sim. GBank gi 4191358 (AF087825) - claudin-7 [Mus musculus]		UNCLASSIFIED	264259, 264908
331	79754888 (661, 662)	Novel Protein sim. GBank gi 80741 pir S20912 - regulatory protein whiB - Streptomyces coelicolor		transcriptfactor	264910, 264687, 264689, 264636, 264567
332	80071440 (663, 664)	Novel Protein sim. GBank gi 114049 sp P19480 AHPF_SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		reductase	35696423, 264636, 264638, 264565
333	13009555 (665, 666)				264687

334	80230771 (687, 688)	Novel Protein sim. GBank gij222222[pir][S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80057028 (668, 670)	Novel Protein sim. GBank gij2193938[emb][CAB09602] - (Z96800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264693, 18108374, 264636, 18108387
336	80414319 (671, 672)			UNCLASSIFIED	265009, 264766, 264686
337	11090829 (673, 674)				264602
338	85413134 (675, 676)	Novel Protein sim. GBank gij5454074[ref][NP_006303.1]pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nucl_rept	264569, 18108397, 22278998, 29331822, 20281099, 29331824, 56182181, 66714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87168559, 265017, 265018, 265019, 264760, 55811150, 264681, 264762, 18108351, 264682, 264764, 264766, 264685, 264686, 264768, 52644229, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35696423, 35695855, 264635, 264555, 264636, 264556, 264637, 264557, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87168518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank gij4001713[dbj][BAA35087.1] - (AB015879) DnaK [Porphyromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank gij2842699[sp]Q92353[UBPC_SCHPO - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)]		ubiquitin	264905, 265019, 264769, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank gij2688580 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00290) - Tryptophan synthase alpha chain	isomerase	264605
342	80054196 (683, 684)	Novel Protein sim. GBank gij1684738[emb][CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20466782 (685, 686)				
344	80428670 (687, 688)	Novel Protein sim. GBank gij2117275[emb][CAB09104] - (Z95618) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264605, 264768, 18108370, 18108374, 35695855
345	80258853 (689, 690)	Novel Protein sim. GBank gij3023317[sp]Q48935[APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE]		histone	264593
346	78831058 (691, 692)	Novel Protein sim. GBank gij4239787[emb][CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905

347	79158185 (693, 694)	Novel Protein sim. GBank gi 731675 sp P38795 YHN4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	265006, 265008, 265010, 265018, 263967, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gi 1073610 pir IS4762 - ugpB protein - Escherichia coli		transport	264602, 18108351, 18108387
349	17282112 (697, 698)				265007
350	80502370 (699, 700)	Novel Protein sim. GBank gi 3261599 emb CAB009171 - (Z77137) hypothetical protein RV1277 [Mycobacterium tuberculosis]		nuclease	265009, 264769, 264689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gi 2959367 emb CAA17921 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	264769, 264905, 264908
352	11611585 (703, 704)	Novel Protein sim. GBank gi 4416302 gb AAD20307 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	264595
353	80061653 (705, 706)	Novel Protein sim. GBank gi 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	264604
354	56626130 (707, 708)			UNCLASSIFIED	264628
355	80046344 (709, 710)			UNCLASSIFIED	264909, 264595, 264683, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	-transcriptfactor	264909, 264591, 264592
357	80070566 (713, 714)	Novel Protein sim. GBank gi 497637 (J03939) - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	264605
358	37032756 (715, 716)	Novel Protein sim. GBank gi 2290990 (AF006000) - Brg1 [Bordetella pertussis]		UNCLASSIFIED	264768
359	80501488 (717, 718)			UNCLASSIFIED	264604, 264769
360	80026748 (719, 720)			UNCLASSIFIED	264594
361	80584075 (721, 722)	Novel Protein sim. GBank gi 3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		transferase	22278996, 264259, 29331822, 29331824, 264605, 55811957, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gi 113764 sp P25718 AMY1_ECOLI - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	264688
363	78750145 (725, 726)				264566
364	82443593 (727, 728)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	264769, 264602, 264604, 264508, 264762, 264638, 264488

365	88040288 (729, 730)	Novel Protein sim. GBank gi 4929268 gb AAD33924.1 - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	264488, 21906766, 21906767, 55811576, 21906769, 29148629, 22278995, 22278996, 265020, 265022, 264634, 264691, 264593, 33657023, 33657402, 264693, 264639, 264594, 29331824, 264758, 18108385, 29331827, 87168559, 265018, 22279000, 265019, 264482, 264761, 264681, 18108351, 265017, 264757
366	81821838 (731, 732)			
367	95357471 (733, 734)	Novel Protein sim. GBank gi 4503843 ref NP_003908.1 pG2AD - UNKNOWN	Contains protein domain (PF01602) - Adaplin N terminal region	60424178, 65274572, 56182575, 22278994, 56994075, 22278998, 264259, 29331822, 29331824, 56182181, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264905, 264828, 56182435, 265006, 264512, 265008, 264591, 55812038, 55811386, 265010, 87168559, 265017, 265018, 264604, 265019, 55811150, 264448, 264369, 264288, 264686, 264768, 56181562, 21906768, 21906769, 55811957, 35895917, 265022, 60170615, 33657023, 65274620, 18108365, 263967, 33657109, 33657349, 35895763, 264628, 18108376, 55811576, 65274791, 35695855, 56182323, 83373044, 60432113, 264563, 264564, 264567, 264509
368	78607265 (735, 736)	Novel Protein sim. GBank gi 3913029 sp P94967 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	264508, 264604, 264605, 264636
369	95292917 (737, 738)			
370	88090966 (739, 740)	Novel Protein sim. GBank gi 3249559 (AF018261) - EH domain binding protein Epsin [Rattus norvegicus]		264905, 264592, 264605, 264766, 264691
371	95292599 (741, 742)	Novel Protein sim. GBank gi 2995299 emb CAA18328 - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - IPP transferase	264905, 264906, 264510, 264600, 264601, 264602, 264603, 265018, 264604, 264605, 265021, 264692, 264636, 264564
372	80021107 (743, 744)	Novel Protein sim. GBank gi 2506393 sp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN		264564
373	79863768 (745, 746)			
374	79847568 (747, 748)	Novel Protein sim. GBank gi 3341640 emb CAA13164 - (AJ231122) z611 [Vibrio cholerae]	UNCLASSIFIED	264909
375	91230181 (749, 750)	Novel Protein sim. GBank gi 5456834 gb AAD43716.1 - (AF152322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	264905, 264906
376	80505214 (751, 752)	Novel Protein sim. GBank gi 1805408 dbj BAA08970 - (D50453) homologues to nitrate hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 264259, 29331826, 56182435, 60433356, 60433438, 264757, 55812038, 264758, 55811957, 264690, 33657023, 264769
377	10339083 (753, 754)		UNCLASSIFIED	264906

378	80056153 (755, 756)	Novel Protein sim. GBank gj1076013 pir A49930 - carB protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	Novel Protein sim. GBank gj1216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264769
380	80060937 (759, 760)	Novel Protein sim. GBank gj1216556 dbj BAA02174 - (D12651) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - PQQ enzyme repeat	dehydrogenase	264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)	Novel Protein sim. GBank gj13327136 dbj BAA31636 - (AB014561) KIAA0661 protein [Homo sapiens]			264592
383	83259025 (765, 766)				264595, 265017, 265021, 264638, 87168518, 22279002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264288, 264766, 263987, 85274791, 35695855, 263981, 83373044, 264567
385	10237679 (769, 770)	Novel Protein sim. GBank gj1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00455) - Iron-containing alcohol dehydrogenases	dehydrogenase	264692
386	79633434 (771, 772)				264906
387	17960637 (773, 774)	Novel Protein sim. GBank gj1460074 emb CA801049 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741376 (775, 776)	Novel Protein sim. GBank gj1424016 gb BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	homeobox	35896286, 264905, 66712502, 60432229, 264593, 60433356, 264686, 264688, 21906765, 264691, 22279000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278996, 264630, 264556, 22279002
390	80079949 (779, 780)	Novel Protein sim. GBank gj1854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264600
391	7657302 (781, 782)				264482
392	79796056 (783, 784)	Novel Protein sim. GBank gj13378523 emb CAA08867 - (AJ009832) cyclomaltodextrinase glucanotransferase [Thermotoga neapolitana]		UNCLASSIFIED	264908
393	33206031 (785, 786)			synthase	264602, 21906764
394	10104463 (787, 788)				
395	80229010 (789, 790)			UNCLASSIFIED	264508, 264563
396	20436224 (791, 792)	Novel Protein sim. GBank gj12677780 (U70327) - unknown [Paretioplus polyacilis]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	264556
397	80417014 (793, 794)	Novel Protein sim. GBank gj14507909 ref NP_000368.1 pWAS - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)			265007, 265009, 264508, 264556, 264629, 264766
398	91230517 (795, 796)	Novel Protein sim. GBank gj1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	18108398, 22278995, 22278996, 56994075, 22278999, 264259, 29331824, 29331826, 264905, 264908, 265007, 265008, 265009, 21906754, 33657084, 265017, 264448, 264288, 264766, 21906765, 21906766, 21906767, 265020, 265021, 33657023, 33657109, 264628, 35696423, 35695855, 264952, 18108380, 264567, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gi 335809 dbj BAA31995 - (AB015974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - kinases FGGY family of carbohydrate kinases	kinase	264582, 264595
400	94117480 (799, 800)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - !!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!	Contains protein domain (PF00560) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278999, 264259, 29331824, 265006, 265007, 265009, 60432229, 33657402, 21906754, 265010, 265017, 265018, 265019, 18108351, 18108357, 21906765, 265021, 265022, 264691, 264692, 33657023, 18108370, 65274791, 264634, 264636, 60170394, 56182323
401	11397491 (801, 802)	Novel Protein sim. GBank gi 4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	264594
402	95420294 (803, 804)	Novel Protein sim. GBank gi 5689487 dbj BAA83027.1 - (AB028998) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 264093, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 264907, 264909, 265006, 264511, 265007, 265008, 264910, 264591, 33657402, 60433356, 60433438, 264596, 21906754, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264682, 264448, 264288, 264684, 264766, 264767, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264690, 264693, 65274620, 35695763, 264628, 18108370, 264629, 18108379, 35696423, 55811576, 264635, 264636, 264557, 264639, 18108385, 22279002, 264563, 264564, 264565, 264566
403	80439913 (805, 806)			UNCLASSIFIED	264768, 264632, 264639, 264563
404	11809865 (807, 808)				264682
405	79471280 (809, 810)	Novel Protein sim. GBank gi 2661649 emb CAA15755 - (AL009198) dnaE2 [Mycobacterium tuberculosis]		polymerase	265009, 264682
406	79634172 (811, 812)				
407	80478229 (813, 814)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 264693
408	80079956 (815, 816)			UNCLASSIFIED	264769
409	5640527 (817, 818)	Novel Protein sim. GBank gi 3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		UNCLASSIFIED	264600
				helicase	264259

410	95357496 (819, 820)	Novel Protein sim. GBank gij475016[dbj BAA06184] - (D29801) Unknown [Mus musculus]		UNCLASSIFIED	264489, 52646365, 52646842, 56181686, 35696286, 52645080, 29331822, 29331824, 56182181, 29331825, 60424269, 35696052, 33656970, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 265007, 264512, 265008, 264910, 33657402, 264758, 52646317, 55811386, 265010, 265011, 265017, 264604, 265018, 55811150, 264762, 264764, 264766, 264687, 264768, 264769, 52644229, 21906766, 265020, 265021, 264534, 52644150, 264692, 33657023, 65274620, 33657109, 33657182, 27486261, 35695763, 264628, 264629, 60431528, 18108376, 263978, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 56182323, 264559, 60432113, 22279002, 264563, 264565, 264486
411	80501670 (821, 822)			UNCLASSIFIED	264769
412	80241662 (823, 824)				264907, 264910, 263973, 22279002
413	11076446 (825, 826)	Novel Protein sim. GBank gij3261784[emb CAB08997] - (Z95558) htpX [Mycobacterium tuberculosis]		eph	264605
414	82050554 (827, 828)	Novel Protein sim. GBank gij129038[sp P20707 ODO1_AZOVI - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)		dehydrogenase	18108374, 264760, 264769, 264602, 264638, 264603, 264909, 264605
415	84453144 (829, 830)	Novel Protein sim. GBank gij4868350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]		UNCLASSIFIED	264908, 87168518
416	80402775 (831, 832)	Novel Protein sim. GBank gij2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium elii]		kinase	264488, 264600, 264602, 264764, 264636
417	20153787 (833, 834)	Novel Protein sim. GBank gij1709171[sp P52311 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M. XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase		264605
418	84125841 (835, 836)			UNCLASSIFIED	264689, 264693
419	95314273 (837, 838)			collagen	264908, 264910, 264764, 264639
420	37036349 (839, 840)	Novel Protein sim. GBank gij3261659[emb CAB03751] - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	- phosphatase	264769
421	95282942 (841, 842)	Novel Protein sim. GBank gij2916942[emb CAA17580] - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	Contains protein domain (PF00072) - Response regulator receiver domain	- phosphatase	264906, 264600, 264601, 264603, 264604, 264760, 264769
422	79471293 (843, 844)	Novel Protein sim. GBank gij231752[sp Q00767 CH61_STRAL - 60 KD CHAPERONIN 1 (PROTEIN CPN60 1) (HSP58)]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	- eph	22278996, 264682, 18108376, 18108387
423	79604948 (845, 846)			UNCLASSIFIED	264509

424	7896557 (847, 848)	Novel Protein sim. GBank gij4826814[ref]NP_004977.1 pKTN1 - kinesin receptor		struct	265019
425	80431450 (849, 850)	Novel Protein sim. GBank gij1703701 bbsj178462 - KRP5=kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	- struct	264909, 265007, 55811386, 264768, 55810764
426	80064522 (851, 852)				
427	80057232 (853, 854)	Novel Protein sim. GBank gij231829sp P29929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	264605, 264559 264603, 264636
428	79481798 (855, 856)	Novel Protein sim. GBank gij81286 pir S22697 - extensin - Volvox carter (fragment)		UNCLASSIFIED	264683
429	80091252 (857, 858)	Novel Protein sim. GBank gij1806154 embj CA806451 - (284395) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase	UNCLASSIFIED	35696423, 35695763, 35695855, 265017, 264564, 264762
430	80504192 (859, 860)				264508, 264905, 264509, 264908, 264909, 265008, 264600, 264687, 264769, 264689, 264636, 264638, 18108385, 264486
431	20624249 (861, 862)				264566
432	16525372 (863, 864)				265020
433	81494303 (865, 866)	Novel Protein sim. GBank gij3123552 embj CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0289 LIKE) [Homo sapiens]	UNCLASSIFIED	UNCLASSIFIED	264907, 264908, 264909, 264910, 264592, 264595, 264758, 264604, 264760, 264762, 264763, 264636, 264637, 22279002
434	94326323 (867, 868)	Novel Protein sim. GBank gij2495272sp Q99626 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696052, 55810764, 55811576, 65274791, 35695855, 60432113, 55811150, 264636, 264766
435	80502738 (869, 870)	Novel Protein sim. GBank gij114105sp P0832 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH	transport		264595, 264769
436	41085953 (871, 872)			UNCLASSIFIED	265020, 22279002
437	11399291 (873, 874)			UNCLASSIFIED	264593
438	11773835 (875, 876)			UNCLASSIFIED	264686
439	80019495 (877, 878)	Novel Protein sim. GBank gij3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			264905, 264600, 264602, 264604
440	79841062 (879, 880)	Novel Protein sim. GBank gij2291232 gb AAB65351.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)	ATPase-associated	35696052, 264905, 264908, 264909, 265011, 35696423
441	20396935 (881, 882)	Novel Protein sim. GBank gij5639946 gb AAD45904.1 AF16132 - (AF16132) histidine kinase CstS [Corynebacterium diphtheriae]			264605
442	85281058 (883, 884)	Novel Protein sim. GBank gij1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
443	82456427 (885, 886)	Novel Protein sim. GBank gij5689893 embj CA852056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 264508, 264906, 264512, 264604, 264762, 264769, 264689, 264636
444	11395897 (887, 888)	Novel Protein sim. GBank gij1783249 gb BAA11726 - (B83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	264591

445	79552709 (889, 890)	Novel Protein sim. GBank gi 5531272 emb CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	264693
446	79810937 (891, 892)	Novel Protein sim. GBank gi 538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00086) - Zinc finger, C2H2 type		264509
447	80438888 (893, 894)	Novel Protein sim. GBank gi 1542914 emb CAB02185 - (Z80108) fml [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	transcript factor	264768, 55811576
448	80238110 (895, 896)	Novel Protein sim. GBank gi 118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		dehydrogenase	264508, 264600, 264603, 264605, 264682, 264769, 18108362, 264634, 18108387
449	20460634 (897, 898)	Novel Protein sim. GBank gi 118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	264605, 264559
450	84631210 (899, 900)	Novel Protein sim. GBank gi 4589506 db BAA76775.1 - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	65274572, 22278998, 29331824, 29331826, 264906, 264910, 264592, 52646317, 265017, 21906767, 55811957, 56526486, 22279002
451	21433609 (901, 902)			UNCLASSIFIED	264486
452	10267278 (903, 904)	Novel Protein sim. GBank gi 2650614 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	264692
453	52560096 (905, 906)	Novel Protein sim. GBank gi 2493000 sp Q09450 SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		transferase	264603
454	39523922 (907, 908)				
455	13089692 (909, 910)	Novel Protein sim. GBank gi 4468699 emb CAB38153.1 - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		UNCLASSIFIED	264687
456	79563081 (911, 912)			UNCLASSIFIED	264691
457	79831273 (913, 914)				264905
458	79581227 (915, 916)	Novel Protein sim. GBank gi 3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	55812038, 265010, 265018, 264681
459	80567359 (917, 918)	Novel Protein sim. GBank gi 4506075 ref NP_002733.1 pPRKC - protein kinase C, mu	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	kinase	22278997, 264259, 29331826, 265018, 264448, 264369, 21906765, 35696423
460	79245890 (919, 920)	Novel Protein sim. GBank gi 113158 sp P25516 ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)		UNCLASSIFIED	264906
461	95287618 (921, 922)	Novel Protein sim. GBank gi 1168574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	264602, 264605, 264768, 264769, 265021, 33657023, 264559

462	79606589 (923, 924)	Novel Protein sim. GBank gi1346891 sp P45597 PTF1_XANCP - MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00381) - PEP-utilizing enzymes	UNCLASSIFIED	264807
463	79796417 (925, 926)	Novel Protein sim. GBank gi1854065 emb CAA58337 - (X83413) U88 (Human herpesvirus 6)		UNCLASSIFIED	264905, 264906, 264908, 264909, 264910, 264591, 264595, 265011, 264632, 264635, 264636, 264637, 264638, 264639
464	82340151 (927, 928)	Novel Protein sim. GBank gi15689776 emb CAB52137.1 - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00648) - Calpain family cysteine protease	UNCLASSIFIED	264634
465	83005730 (929, 930)	Novel Protein sim. GBank gi11806175 emb CAB06470 - (Z64395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	265017, 21906764, 265020
466	20460645 (931, 932)			UNCLASSIFIED	264605, 264659
467	80409035 (933, 934)	Novel Protein sim. GBank gi1548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	264764
468	52562208 (935, 936)	Novel Protein sim. GBank gi12114024 emb CAB08957 - (Z95558) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	264692
469	19520527 (937, 938)	Novel Protein sim. GBank gi12909459 emb CAA17347 - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
470	80502756 (939, 940)	Novel Protein sim. GBank gi114921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	synthase		264602, 264769
471	17937351 (941, 942)		transport		265019
472	80047458 (943, 944)	Novel Protein sim. GBank gi1862343 (L10908) - Gcap1 gene product [Mus musculus]		UNCLASSIFIED	264596, 264685, 264557
473	20558793 (945, 946)			UNCLASSIFIED	264369
474	80593365 (947, 948)			UNCLASSIFIED	22278997, 264692, 264288
475	82454665 (949, 950)			UNCLASSIFIED	264907, 264908, 264511, 265009, 264762, 264448, 264636, 264638
476	94143857 (951, 952)	Novel Protein sim. GBank gi15453656 ref NP_006329.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 60432049, 264259, 264508, 52644045, 55812038, 264758, 265011, 264288, 264686, 52644229, 65274791, 264638, 264566
477	79175833 (953, 954)			UNCLASSIFIED	264638
478	79633483 (955, 956)			UNCLASSIFIED	264690, 264693
479	80189746 (957, 958)			collagen	264686, 35695855, 265008, 264631, 264910, 264632, 264638, 265018, 264369, 264909
480	79390729 (959, 960)	Novel Protein sim. GBank gi1127551 (U18939) - orf2 [Batrachocottus baikalensis]		mapolymerase	264369
481	79624578 (961, 962)			UNCLASSIFIED	264693
482	83050611 (963, 964)	Novel Protein sim. GBank gi14063042 (AF068065) - GP900; mucin-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	264909, 264686, 264768, 264693, 55811576, 56182323, 18108385

483	20283306 (965, 966)	Novel Protein sim. GBank gij2104303[embjCAB08632] - (295387) hypothetical protein Rv2610c [Mycobacterium tuberculosis]	Contains protein domain (PF00534) - Glycosyl transferases group 1		264600
484	11618046 (967, 968)	Novel Protein sim. GBank gij3450883 (AF083334) - fibroin [Antheraea pernyi]		UNCLASSIFIED	264594
485	80181234 (969, 970)	Novel Protein sim. GBank gij5042272[embjCAB44526.1] - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]		UNCLASSIFIED	264369, 21906765, 22279000, 22279002
486	80059042 (971, 972)	Novel Protein sim. GBank gij5724778[embjAAC53522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]		dehydrogenase	264604
487	11813339 (973, 974)	Novel Protein sim. GBank gij3882223[dbjBAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain		264638
488	91222383 (975, 976)	Novel Protein sim. GBank gij82091[pirjA25494] - hydroxyproline-rich glycoprotein - tomato (fragment)		kinase	264886, 66714117, 264768, 18108385, 55811576, 265006, 265008, 265009, 265019, 22279002, 264259, 18108370, 264907, 264764, 56182323, 264288, 264693
489	10867710 (977, 978)	Novel Protein sim. GBank gij2894206[embjCAA17072] - (AL021840) hypothetical protein Rv3258c [Mycobacterium tuberculosis]		collagen	264639
490	95361124 (979, 980)	Novel Protein sim. GBank gij5262605[embjCAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]			22278996, 29331822, 29331828, 264107, 264909, 264110, 265009, 264592, 264593, 60433356, 264288, 264693, 263974, 263976, 20281071, 60432113
491	80498412 (981, 982)	Novel Protein sim. GBank gij2791517[embjCAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264769
492	87421264 (983, 984)	Novel Protein sim. GBank gij5262605[embjCAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]			264600
493	11692942 (985, 986)	Novel Protein sim. GBank gij230281[dbjR69] - 434 Repressor (Amino-Terminal Domain) (R1-69)		UNCLASSIFIED	264638
494	87726604 (987, 988)	Novel Protein sim. GBank gij128736[spIP28225]PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/IMP OXIDASE)			264489, 35696286, 60432289, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 33657402, 264762, 264764, 264768, 264769, 264688, 21906765, 21906769, 35695917, 265020, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264638
495	80028599 (989, 990)	Novel Protein sim. GBank gij230281[dbjR69] - 434 Repressor (Amino-Terminal Domain) (R1-69)	Contains protein domain (PF00005) - transport ABC transporter	transport	264602, 264682, 264638
496	78985624 (991, 992)	Novel Protein sim. GBank gij128736[spIP28225]PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/IMP OXIDASE)	Contains protein domain (PF01381) - Helix-turn-helix		264601, 265021
497	78949661 (993, 994)	Novel Protein sim. GBank gij128736[spIP28225]PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/IMP OXIDASE)		oxidase	265006

488	88095488 (895, 996)	Novel Protein sim. GBank gij1145789 (U41662) - neuroigin 2 [Rattus norvegicus]	Contains protein domain (PF00135) - Carboxylesterases	esterase	264259, 29331826, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264591, 33657402, 264758, 265010, 265011, 264600, 264601, 264605, 264683, 264764, 264766, 264767, 264768, 264687, 264769, 21906767, 33657023, 264693, 264628, 264629, 35696423, 264630, 264632, 264634, 264635, 264637, 264638, 264558, 264639, 18108385, 264563, 264564, 264565, 264566, 264567
489	20438222 (987, 998)	Novel Protein sim. GBank gij97480[pil]S19739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	264605
500	11076810 (999, 1000)				264605
501	13418034 (1001, 1002)	Novel Protein sim. GBank gij5708250[emb]CAB52363.1] - (AL109747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264688
502	80021176 (1003, 1004)	Novel Protein sim. GBank gij4486678[emb]CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 265011, 264602, 264605, 264635
503	20264483 (1005, 1006)			UNCLASSIFIED	264564
504	10887321 (1007, 1008)			UNCLASSIFIED	264687
505	95003068 (1009, 1010)			UNCLASSIFIED	264369
506	16454292 (1011, 1012)	Novel Protein sim. GBank gij4033509[sp]P02598[CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	265010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gij2501069[sp]Q46127[SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	264604
508	78841424 (1015, 1016)	Novel Protein sim. GBank gij466068[sp]P34618[YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1236.2 IN CHROMOSOME III		UNCLASSIFIED	264908
509	11776386 (1017, 1018)				264638
510	83373465 (1019, 1020)			UNCLASSIFIED	264687, 264639
511	16525578 (1021, 1022)				265007
512	20399484 (1023, 1024)	Novel Protein sim. GBank gij2497419[sp]P55635[Y4R8_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4R8		UNCLASSIFIED	264565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gij1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	264683, 264689, 35696423, 264639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gij1184790 (U46068) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 264909
515	79462591 (1029, 1030)				22278999, 264690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gij2127400[pil]S65770 - maltotigosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)		amylase	264910

517	95292994 (1033, 1034)	Novel Protein sim. GBank gij2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264565
518	8491831 (1035, 1036)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91677888 (1037, 1038)	Novel Protein sim. GBank gij5689365[dbj]BAA83073.1] - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_rna_bind	52644507, 22278997, 22278998, 60432049, 264259, 52645080, 29331824, 66714117, 60424269, 29331826, 35996052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432228, 33657402, 60433438, 21908754, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21908765, 21906766, 21906767, 21906769, 265021, 60170615, 33657023, 264692, 52645129, 33657109, 27486262, 27486264, 35695763, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56526486, 60432113
520	79869188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gij1169126[sp]P46839[CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A	transport		264605
522	80435060 (1043, 1044)	Novel Protein sim. GBank gij1172869[sp]P44331[RBSK_HAEIN - RIBOKINASE	Contains protein domain (PF00294) - pfkB family carbohydrate kinase	kinase	264905, 264768
523	18356013 (1045, 1046)	Novel Protein sim. GBank gij2132243[pir]S61028 - hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261805 (1047, 1048)	Novel Protein sim. GBank gij4033608[dbj]BAA35136] - (AB012308) B2HC [Anthracidaris crassispina]		ATPase_associated	264092, 264596, 265011
525	79810046 (1049, 1050)				264907
526	36827630 (1051, 1052)	Novel Protein sim. GBank gij4106610[emb]CAA21365] - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap, Fasta scores: opt-468, E(): 8.5e-24, in Q64602 R. norvegicus, (425 aa), 28.6% identl...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)			UNCLASSIFIED	264769
528	65484134 (1055, 1056)			UNCLASSIFIED	56182575, 265017, 265018
529	17936810 (1057, 1058)	Novel Protein sim. GBank gij731088[sp]P24215[XUUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)	hydrolase		265019
530	10887336 (1059, 1060)	Novel Protein sim. GBank gij42144[emb]CAA25200] - (X00513) NusA protein (nusa) [Escherichia coli]		UNCLASSIFIED	264687
531	80226576 (1061, 1062)			UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
532	90933444 (1063, 1064)	Novel Protein sim. GBank gij5262640[emb]CAB45758.1] - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264488, 264490, 264259, 264592, 264780, 265021, 264690, 263976, 264558

533	87761531 (1065, 1066)	Novel Protein sim. GBank gi 4683636 gb AA031593.1 AF11229 - (AF112299) Integral inner nuclear membrane protein MAN1 [Homo sapiens]			264907, 264909, 264768, 35695917, 264630, 264555
534	82368264 (1067, 1068)	Novel Protein sim. GBank gi 2995352 emb CAA04606.1 - (AJ001206) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		264905, 265011, 264601, 264602, 264605, 264762, 264768, 265020, 264693, 264636 264906
535	79641850 (1069, 1070)	Novel Protein sim. GBank gi 3878636 emb CAA88953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	ATPase-associated	
536	79907207 (1071, 1072)	Novel Protein sim. GBank gi 2495628 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5'REGION	reductase		18108376, 264905, 264906, 264907, 264909
537	94147448 (1073, 1074)	Novel Protein sim. GBank			265008, 264605, 65274791
538	87821963 (1075, 1076)	gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen		29331822, 29331824, 29331825, 29331826, 29331827, 264908, 52644045, 33657402, 265017, 264762, 264683, 264288, 264685, 21906765, 35695763, 264558, 60170394, 264559, 22279002
539	28396269 (1077, 1078)	Novel Protein sim. GBank gi 2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		264602, 265019
540	79637077 (1078, 1080)	Novel Protein sim. GBank gi 3882241 dbj BAA34480.1 - (AB018303) KIAA0760 protein [Homo sapiens]	transcript factor		264693
541	87762268 (1081, 1082)		Contains protein domain (PF00096) Zinc finger, C2H2 type		18108394, 22278997, 22278998, 264259, 264112, 265009, 33657402, 55812038, 52646317, 265017, 21906765, 264693, 55811576, 264635, 56526486, 264566 264910, 265018, 264689, 264638, 264486
542	95285836 (1083, 1084)	Novel Protein sim. GBank gi 5042272 emb CAB44526.1 - (AL078618) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		
543	79786280 (1085, 1086)				
544	20437191 (1087, 1088)	Novel Protein sim. GBank gi 2791398 emb CAA15994 - (AL021184) hypothetical protein Rv1464 [Mycobacterium tuberculosis]	UNCLASSIFIED		264602, 264908
545	80434504 (1089, 1090)		UNCLASSIFIED		264605
546	80249016 (1091, 1092)	Novel Protein sim. GBank gi 4887211 gb AA032237.1 AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]			264768, 264634, 264907, 264592, 264909 264600, 264602, 21906765
547	11077563 (1093, 1094)	Novel Protein sim. GBank gi 1350855 sp P19176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase		264604
548	82114936 (1095, 1096)	Novel Protein sim. GBank gi 2330021 AF019250 - Kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		264488, 264905, 264910, 264760, 264693, 264638, 264563, 264564

549	95421904 (1097, 1098)	Novel Protein sim. GBank gi 4337460 gb AAD18133 - (AF056195) neuroblastoma-amplified protein [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33657402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264886, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 33657023, 264692, 264693, 65274620, 52645129, 33657109, 27486261, 27486262, 27486264, 33657349, 55811576, 18108387, 60432113, 22279002
550	10886616 (1089, 1100)			264688
551	80439990 (1101, 1102)	Novel Protein sim. GBank gi 3122893 sp P94985 SYFB MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)	UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)			
553	80105002 (1105, 1106)	Novel Protein sim. GBank gi 552087 (M33753) - crumbs protein [Drosophila melanogaster]	UNCLASSIFIED	264689, 264639, 264563
554	79618379 (1107, 1108)	Novel Protein sim. GBank gi 501977 gb AAD37857.1 AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]	glycoprotein	55811957, 264628
555	78996347 (1109, 1110)	Novel Protein sim. GBank gi 131515 sp P02908 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)	kinase	264906
556	20457127 (1111, 1112)	Novel Protein sim. GBank gi 3914014 sp P96380 IMFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)	transport	264762
557	19523405 (1113, 1114)	Novel Protein sim. GBank gi 5042273 emb CAB44527.1 - (AL078618) nuoE, NADH dehydrogenase subunit [Streptomyces coelicolor]	transcriptfactor	264508, 264605, 264559
558	20724429 (1115, 1116)	Novel Protein sim. GBank gi 1170933 sp P45331 METE_HAEIN - 5-METHYL-TETRAHYDROPTEROYL-TRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)	dehydrogenase	264488
559	80084353 (1117, 1118)	Novel Protein sim. GBank gi 4980567 gb AAD35173.1 AE00169 - (AE001694) iron(III) ABC transporter, permease protein [Thermotoga maritima]	UNCLASSIFIED	264602
			UNCLASSIFIED	264634

560	80066533 (1119, 1120)	Novel Protein sim. GBank gi 2492595 sp Q53193 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - transport ABC transporter	18108396, 264906, 264602, 264604, 18108374
561	20293187 (1121, 1122)		UNCLASSIFIED	264600
562	11698161 (1123, 1124)		UNCLASSIFIED	264689
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi 4104925 (AF042276) - poly(hydroxycarboxylate) granule associated protein GA2 [Pseudomonas putida]	UNCLASSIFIED	264910, 264691
564	56716390 (1127, 1128)	Novel Protein sim. GBank gi 2792310 (AF040570) - unknown [Amycolatopsis mediterranei]	dehydrogenase	264592
565	56465618 (1129, 1130)	Novel Protein sim. GBank gi 3449294 dbj BAA32462 - (AB011532) MEGF6 [Rattus norvegicus]	Contains protein domain (PF00008) - synthase EGF-like domain	265010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi 4539568 emb CAB38487.1 - (AL035636) putative helicase [Streptomyces coelicolor]	helicase	264909, 264510, 265008, 264910, 264758, 264600, 264602, 264604, 264605, 264788, 264687, 264689, 35695917, 264693, 65274620, 264486
567	79560955 (1133, 1134)		UNCLASSIFIED	264681, 264691, 264593
568	94681793 (1135, 1136)	Novel Protein sim. GBank gi 100506 pir S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria Innervia (fragment)	Contains protein domain (PF00390) - Malic enzyme	264689
569	39506897 (1137, 1138)	Novel Protein sim. GBank gi 3915843 sp O31212 IRS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00318) - Ribosomal protein S2	264565
570	78375927 (1139, 1140)			
571	79793961 (1141, 1142)	Novel Protein sim. GBank gi 115122 sp P21627 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	UNCLASSIFIED	18108376, 18108387, 264565
572	36998838 (1143, 1144)		transport	264907, 264909
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi 4539223 emb CAB39881.1 - (AL049497) putative Integral membrane protein [Streptomyces coelicolor]	UNCLASSIFIED	264762
574	13521592 (1147, 1148)		UNCLASSIFIED	265007, 264601
575	13076416 (1149, 1150)	Novel Protein sim. GBank gi 118784 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN	polymerase	264636 264687
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi 5457625 emb CAB49116.1 - (AJ248283) PAB2227 [Pyrococcus abyssi]		264605
577	66727102 (1153, 1154)	Novel Protein sim. GBank gi 5042274 emb CAB44528.1 - (AL078618) nuoD, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	35696052, 264636
578	11804477 (1155, 1156)			264638
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi 1723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09	transport	264682, 264556

580	80059417 (1159, 1160)					22278999, 35696052, 264555, 264556, 264558
581	79230833 (1161, 1162)	Novel Protein sim. GBank gij3243131 (AF045777) - titin [Drosophila melanogaster]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	struct	265008, 264564
582	80049617 (1163, 1164)	Novel Protein sim. GBank gij2501162 (sp77726) [YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION]		transport		265021, 264555, 264557
583	79321392 (1165, 1166)	Novel Protein sim. GBank gij2501162 (sp77726) [YAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION]				264594
584	79845024 (1167, 1168)	Novel Protein sim. GBank gij3882221 (dbj) [BAA34470.1] - (AB018293) KIAA0750 protein [Homo sapiens]		UNCLASSIFIED		264488, 264906, 264766, 264687, 35696423
585	79581454 (1169, 1170)	Novel Protein sim. GBank gij3882221 (dbj) [BAA34470.1] - (AB018293) KIAA0750 protein [Homo sapiens]		UNCLASSIFIED		265018, 264684, 21908769
586	38277486 (1171, 1172)	Novel Protein sim. GBank gij4467250 (emb) [CAB37575] - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		UNCLASSIFIED		264908, 265007
587	80497359 (1173, 1174)	Novel Protein sim. GBank gij5689519 (dbj) [BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]		hydrolase		264600, 264602, 264605, 264769, 264690, 264557
588	79557239 (1175, 1176)	Novel Protein sim. GBank gij5689519 (dbj) [BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]		UNCLASSIFIED		265020, 264692
589	79805828 (1177, 1178)			UNCLASSIFIED		22278996, 264907, 264909, 264510, 265009, 265010, 264687, 264769, 35695917, 18108376, 264634, 264636, 264638
590	79815629 (1179, 1180)	Novel Protein sim. GBank gij2143293 (emb) [CAB09390] - (Z95972) rpoB [Mycobacterium tuberculosis]		UNCLASSIFIED		264906, 264909
591	10313540 (1181, 1182)	Novel Protein sim. GBank gij2143293 (emb) [CAB09390] - (Z95972) rpoB [Mycobacterium tuberculosis]		mapolymerase		264691
592	13889767 (1183, 1184)	Novel Protein sim. GBank gij4511983 (gb) [AAD21543.1] - (AF088896) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]		MHC		263972
593	82348699 (1185, 1186)	Novel Protein sim. GBank gij4511983 (gb) [AAD21543.1] - (AF088896) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]		dehydrogenase		264511, 264762, 264769, 264486
594	20212392 (1187, 1188)	Novel Protein sim. GBank gij1272368 (U51896) - Lige [Vibrio parahaemolyticus]		UNCLASSIFIED		264605
595	10064064 (1189, 1190)	Novel Protein sim. GBank gij131490 (sp20966) [PTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EIIF-FRU)]				264769
596	13085170 (1191, 1192)			UNCLASSIFIED		264636
597	80259003 (1193, 1194)			UNCLASSIFIED		264592
598	84140216 (1195, 1196)			UNCLASSIFIED		264758, 55810764, 264555, 264556, 264637, 83373044
599	20385137 (1197, 1198)	Novel Protein sim. GBank gij125329 (sp) [P04951] [KDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYLTRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)]		UNCLASSIFIED		264603
600	10357663 (1199, 1200)					264906
601	79610404 (1201, 1202)	Novel Protein sim. GBank gij2127414 (pir) [S60064 - hypothetical protein 2 - Corynebacterium glutamicum]		UNCLASSIFIED		264510

602	78250602 (1203, 1204)	Novel Protein sim. GBank gi 3522961 gb AAC34243.1 - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	265007	
603	11466067 (1205, 1206)			UNCLASSIFIED	264595	
604	81675420 (1207, 1208)				284758	
605	20436657 (1209, 1210)	Novel Protein sim. GBank gi 1175322 sp P44917 Y883_HAEIN - HYPOTHETICAL PROTEIN HI0883		UNCLASSIFIED	264605	
606	80334582 (1211, 1212)	Novel Protein sim. GBank gi 5020264 gb AAD38043.1 AF15136 - (AF151363) Cdc42 GTPase-activating protein [Mus musculus]		UNCLASSIFIED	264764	
607	95361506 (1213, 1214)	Novel Protein sim. GBank gi 188864 (M74027) - mucin [Homo sapiens]		UNCLASSIFIED	264508, 264906, 85658542, 264682, 264687, 264689, 264534, 18108376, 35696423, 264636, 264555, 264638	
608	11810888 (1215, 1216)			UNCLASSIFIED	264682	
609	80064775 (1217, 1218)	Novel Protein sim. GBank gi 2496701 sp P55552 Y4LL_RHISN - HYPOTHETICAL 91.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	UNCLASSIFIED	264605	
610	79629413 (1219, 1220)				264692	
611	87586205 (1221, 1222)				264508, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264604, 264684, 264766, 264689, 264692, 264628, 264635, 264636, 264637, 264558	
612	95287851 (1223, 1224)	Novel Protein sim. GBank gi 1877366 emb CAB07118 - (Z92772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	nuclease	264565	
613	7523475 (1225, 1226)	Novel Protein sim. GBank gi 5114231 gb AAD40238.1 AF13670 - (AF136709) histidine kinase YycG [Staphylococcus aureus]		UNCLASSIFIED	264369	
614	79969348 (1227, 1228)	Novel Protein sim. GBank gi 1339500 dbj BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]		kinase	18108372, 264563	
615	39586998 (1229, 1230)	Novel Protein sim. GBank gi 544367 sp P35673 GALE_ERWAM - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		synthase	264600, 264602, 264629	
616	20465331 (1231, 1232)	Novel Protein sim. GBank gi 2498097 sp Q60769 TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)		isomerase	264605	
617	91227222 (1233, 1234)	Novel Protein sim. GBank gi 2498097 sp Q60769 TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00641) - Inf Zn-finger in Ran binding protein and others.		52845156, 21906765, 35696423, 21906768, 21906769, 22278994, 35696286, 22278996, 265020, 265021, 265007, 265008, 264636, 52844150, 33657023, 264692, 264693, 29331822, 29331824, 55812038, 83373044, 58182181, 60424269, 66714117, 29331825, 33657109, 29331826, 33657182, 29331827, 35696052, 29331828, 27486262, 33657349, 56528486, 265018, 265019, 22279002, 264482, 264448, 29331830, 66712502, 264909	

618	20632843 (1235, 1236)	Novel Protein sim. GBank gij5459388[emb]CAB50746.1] - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603	
619	91227224 (1237, 1238)					56994075, 29331826, 33656970, 265008, 33657402, 33109954, 87168559, 264448, 18108374, 83373044
620	81183143 (1239, 1240)	Novel Protein sim. GBank gij464335[sp]Q05922[DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 (DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1)]		phosphatase		29146498, 264758, 264369, 29148627
621	80239251 (1241, 1242)					
622	20456427 (1243, 1244)	Novel Protein sim. GBank gij2633557[emb]CAB13060] - (Z99110) yjF [Bacillus subtilis]		UNCLASSIFIED	264556, 264558, 264639	
623	10131798 (1245, 1246)	Novel Protein sim. GBank gij1857710[gb]AAB48482] - (U87224) contacin associated protein [Rattus norvegicus]		UNCLASSIFIED	264605	
624	19534127 (1247, 1248)	Novel Protein sim. GBank gij1705703[sp]P52225[CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		Contains protein domain (PF00054) - laminin Laminin G domain	264906	
625	13084619 (1249, 1250)	Novel Protein sim. GBank gij2894252[emb]CAA17114.1] - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		cytochrome	264596	
626	8062603 (1251, 1252)	Novel Protein sim. GBank gij416592[sp]P32323[AGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	264688	
627	80255457 (1253, 1254)	Novel Protein sim. GBank gij3098418 (AF040944) - P140 [Mus musculus]		UNCLASSIFIED	29331822, 264905, 264908, 33657023, 33657109, 264558	
628	80077096 (1255, 1256)	Novel Protein sim. GBank gij1711543[sp]P50526[SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1		Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	18108394, 264112, 264593, 265022, 264635	
629	79851602 (1257, 1258)	Novel Protein sim. GBank gij1143204 (U34305) - ORF2: Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264600	
630	39565156 (1259, 1260)	Novel Protein sim. GBank gij3236368 (AF064748) - S3-12 [Mus musculus]		isomerase	264906, 264907	
631	20598718 (1261, 1262)	Novel Protein sim. GBank gij140687[sp]P11666[YGGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)]		UNCLASSIFIED	264490	
632	27843890 (1263, 1264)				263978	
633	80477772 (1265, 1266)			UNCLASSIFIED	264906, 264600, 264605, 264769, 264689, 264486	
634	17938806 (1267, 1268)			UNCLASSIFIED	264769	
635	79574506 (1269, 1270)			UNCLASSIFIED	265019	
636	79910981 (1271, 1272)			UNCLASSIFIED	264689	
				UNCLASSIFIED	264596, 264762, 264693	

637	82455796 (1273, 1274)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z98268) recN [Mycobacterium tuberculosis]		nuclease	264906, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264766, 264687, 264769, 264689, 3595917, 264693, 264634, 264638, 264639, 264559, 18108385, 264636
638	14997457 (1275, 1276)	Novel Protein sim. GBank gi 4678662 emb CAB41074.1 - (AL049645) putative large ATP-binding protein [Streptomyces coelicolor]			
639	80204210 (1277, 1278)	Novel Protein sim. GBank gi 4589628 dbj BAA76836.1 - (AB023209) KIAA0992 protein [Homo sapiens]		struct	264112, 263974
640	17929579 (1278, 1280)	Novel Protein sim. GBank gi 1432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]	Contains protein domain (PF01466) - Skp1 family	-mapolymerase	265009, 265010
641	79636398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264906, 264908, 264758, 264288, 264632, 264635, 264639, 264584
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	95010907 (1289, 1290)			UNCLASSIFIED	264906, 264762, 264693, 264639, 264559
646	80069083 (1291, 1292)				264595, 264566
647	80257085 (1293, 1294)	Novel Protein sim. GBank gi 4507613 ref NP_003736.1 pTNKS - TANKYRASE	Contains protein domain (PF00023) - Ank repeat	transcriptfactor	264908, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank gi 1044963 bbs 169646 - protamine [Monodonta turbinata, gonads, Peptide, 106 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798316 (1299, 1300)			UNCLASSIFIED	264686
651	11776932 (1301, 1302)	Novel Protein sim. GBank gi 1346916 sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			264602, 264638
652	85516704 (1303, 1304)			UNCLASSIFIED	264905, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)	Novel Protein sim. GBank gi 1722977 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	22278996, 264510, 264511, 264512, 264593, 21906754, 264603, 264760, 18108376, 264556
654	95010589 (1307, 1308)			UNCLASSIFIED	264906, 264595, 264632
655	79320692 (1309, 1310)	Novel Protein sim. GBank gi 130327 sp P26647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)	Contains protein domain (PF01553) - Acyltransferase	transferase	264592
656	80416739 (1311, 1312)				
657	20611010 (1313, 1314)			UNCLASSIFIED	264602, 264605, 264766, 264691
				UNCLASSIFIED	264557, 264558

658	87761815 (1315, 1316)	Novel Protein sim. GBank gjl5689493[db][BAA83030.1] - (AB029001) KIAA1078 protein (Homo sapiens)		UNCLASSIFIED	2278996, 60432049, 29331822, 29331824, 29331828, 265007, 265008, 33657402, 33657084, 265017, 264448, 21906765, 21906766, 263967, 20281149, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gjl2137872[pr][l48724 - zinc finger protein PZF - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	22278999, 60432049, 66714117, 29331827, 265007, 264766, 58181562, 18108359, 18108365, 18108370, 18108381
660	81897922 (1319, 1320)			UNCLASSIFIED	264757
661	80026023 (1321, 1322)	Novel Protein sim. GBank gjl134180[sp]P15401[SACY, BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTITERMINATOR	Contains protein domain (PF00874) - Transcriptional antiterminator bglG family	UNCLASSIFIED	264510, 265009, 264600, 264602, 264603, 264604, 264605, 32833986, 18108376, 264636, 18108387, 22279000
662	20463731 (1323, 1324)	Novel Protein sim. GBank gjl4545229[gb][AAD22450.1][AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]		UNCLASSIFIED	264605
663	20626080 (1325, 1326)	Novel Protein sim. GBank gjl5689250[db][BAA82881.1] - (AB024335) similar to orf5 [Comamonas testosteroni]		dehydrogenase	264605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gjl1652848[db][BAA17766] - (D90909) DNA photolyase [Synecocystis sp.]		UNCLASSIFIED	264769
665	80079053 (1329, 1330)	Novel Protein sim. GBank gjl116841[sp]P21640[COBJ, PSEDE - PRECORRIN-3B C17 METHYLTRANSFERASE (PRECORRIN-3 METHYLTRANSFERASE) (PRECORRIN-3 METHYLTRANSFERASE)		isomerase	264600
666	78603142 (1331, 1332)	Novel Protein sim. GBank gjl3261829[emb][CAB10927] - (Z98260) hypothetical protein Rv1230c [Mycobacterium tuberculosis]		glycoprotein	264907, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gjl5688851[db][BAA82702.1] - (AB017438) Orf5 [Streptomyces coelicolor]		UNCLASSIFIED	264689, 264602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gjl3581853[emb][CAA20809] - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	Contains protein domain (PF00453) - Ribosomal protein L20	ribosomal prot	264905, 264906, 264908, 264600, 264601, 264603, 264605, 264760, 264689, 264636, 264638, 264639
669	12967154 (1337, 1338)			UNCLASSIFIED	264637
670	80238549 (1339, 1340)	Novel Protein sim. GBank gjl2582531 (AF028444) - 2-isopropylmalate synthase [Streptomyces coelicolor]		synthase	264905, 264906, 264908, 264601, 264762, 264766, 264689, 264638, 18108385, 264486
671	79601368 (1341, 1342)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264690, 264692, 264693, 264636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gjl2114430 (U92703) - Olf-1/EBF-like-3 transcription factor [Mus musculus]		transcript factor	264910, 265017
673	82285798 (1345, 1346)	Novel Protein sim. GBank gjl4589285[gb][AAD26430.1][AF13515 - (AF135154) ferric alcaligin siderophore receptor [Bordetella pertussis]			264759
674	79199259 (1347, 1348)			UNCLASSIFIED	264629

675	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AAD35347.1 AE001708 D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-alanine D-alanine ligase	UNCLASSIFIED	264488, 22278999, 66714117, 264508, 264511, 265008, 60433438, 264600, 264601, 264602, 264603, 264604, 264605, 264762, 264687, 264769, 60431602, 18108374, 264636, 264638 265010
676	78899607 (1351, 1352)	Novel Protein sim. GBank gi 1723566 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C9.07		ATPase-associated	264591, 264632
677	21644312 (1353, 1354)	Novel Protein sim. GBank gi 87208 (U03976) - dynein heavy chain isotype 5C [Tripeustes graillia]			
678	84225200 (1355, 1356)	Novel Protein sim. GBank gi 1566274 pf 2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264758, 264682, 264557
679	78868855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278996, 264693
680	20726424 (1359, 1360)				264600, 264602
681	94322017 (1361, 1362)	Novel Protein sim. GBank gi 5174493 ref NP_006050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	264102, 264907, 264908, 265006, 264693, 263972, 83373044, 264566
682	11392476 (1363, 1364)			UNCLASSIFIED	264595
683	80083680 (1365, 1366)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264634
684	20465367 (1367, 1368)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (A1243459) proteophosphoglycan [Leishmania major]			264605
685	80246735 (1369, 1370)				264909, 263967, 263981
686	79208608 (1371, 1372)				264631
687	80085629 (1373, 1374)				264693, 264635
688	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688962 (AF027768) - LspA [Serratia marcescens]		peptidase	264907, 264638
689	88064256 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264908, 264907, 265007, 265009, 60433438, 21908754, 264760, 18108358, 21908786, 21906769, 265021, 18108361, 263974, 18108379, 264557, 18108385, 22279002 264510, 264511, 264764, 264769
690	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A66)		UNCLASSIFIED	
691	81854392 (1381, 1382)			UNCLASSIFIED	264757
692	83608936 (1383, 1384)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (A1243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55812038, 55811957, 265018, 55811150, 18108351, 264908, 60431528, 264594
693	79586116 (1385, 1386)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264635
694	82455983 (1387, 1388)	Novel Protein sim. GBank gi 267327 sp Q01033 VG48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278996, 264510, 264602, 264603, 264762, 264687, 264769, 264693

695	94147849 (1389, 1390)	Novel Protein sim. GBank gjl446339[embjCAB38059.1] - (AJ010501) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 264509, 264905, 264907, 29331830, 264908, 264909, 264511, 265007, 264910, 264758, 264764, 264288, 65274791
696	79830982 (1391, 1392)	Novel Protein sim. GBank gjl2649950 (AE001058) - glutamine ABC transporter, ATP-binding protein (glnQ) [Archaeoglobus fulgidus]	Contains protein domain (PF000005) - ABC transporter	transport	264905, 264595
697	11767889 (1393, 1394)	Novel Protein sim. GBank gjl1731343[spjQ10694]YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY49.25	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	264682
698	66695862 (1395, 1396)			UNCLASSIFIED	264688, 35659817
699	79582558 (1397, 1398)			UNCLASSIFIED	264682
700	79839098 (1399, 1400)				264693
701	80230242 (1401, 1402)	Novel Protein sim. GBank gjl1001235[dbjBAA10471] - (D64003) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	264488, 264510, 264511, 264602, 264605, 264689
702	79814789 (1403, 1404)	Novel Protein sim. GBank gjl2498935[spjQ46338]SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT		UNCLASSIFIED	264909
703	20446820 (1405, 1406)	Novel Protein sim. GBank gjl3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	oxidase		264604
704	94312224 (1407, 1408)	Novel Protein sim. GBank gjl3150513 (AF067219) - contains similarity to the kelch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	264288, 56181562, 33657109, 264629, 55811576
705	17932141 (1409, 1410)	Novel Protein sim. GBank gjl421091[pirjIS30730] - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	265006
706	20288062 (1411, 1412)	Novel Protein sim. GBank gjl3024872[spjQ55790]Y074_SYNY3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074			264600
707	20638065 (1413, 1414)	Novel Protein sim. GBank gjl3420608[gbjAAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		264603
708	20708282 (1415, 1416)	Novel Protein sim. GBank gjl3649741[embjCAA03985] - (AJ000281) mucin [Homo sapiens]			264601, 264692
709	88001439 (1417, 1418)	Novel Protein sim. GBank gjl3080425[embjCAA18744.1] - (AL022604) putative protein [Arabidopsis thaliana]	struct		18108398, 264637, 264908, 264909
710	11356683 (1419, 1420)	Novel Protein sim. GBank gjl4758686[refjNP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)			264369
711	17931418 (1421, 1422)	Novel Protein sim. GBank gjl1703266[spjQ11056]AM12_MYCTU - PUTATIVE AMIDASE CY50.19C	Contains protein domain (PF00058) - Low-density lipoprotein receptor repeat class B	apolipoprotein	265019
712	80258164 (1423, 1424)				264591
713	79263126 (1425, 1426)	Novel Protein sim. GBank gjl4502351[refjNP_001692.1]pBAAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase	hydrolase		264906, 264907
714	27847651 (1427, 1428)				264508, 264555

715	79639423 (1429, 1430)	Novel Protein sim. GBank gj1789035 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	264907	
716	79559072 (1431, 1432)				264692	
717	79491842 (1433, 1434)	Novel Protein sim. GBank gj12494074[sp]P55653[CABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+)] (SSDH)		dehydrogenase	264636	
718	94319658 (1435, 1436)	Novel Protein sim. GBank gj13873679[emb]CAA94886] - (Z71178) similar to pro-collagen domains; cDNA EST EMBL.D27978 comes from this gene; cDNA EST EMBL.D27977 comes from this gene; cDNA EST EMBL.D34199 comes from this gene; cDNA EST EMBL.D64392 comes from this gene; cDNA EST EMBL...	Contains protein domain (PF00093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21906769, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388	
719	17679564 (1437, 1438)	Novel Protein sim. GBank gj12104302[emb]CAB08631] - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	265011	
720	79841684 (1439, 1440)				264908	
721	15020180 (1441, 1442)	Novel Protein sim. GBank gj123530[sp]P04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	264629	
722	9862603 (1443, 1444)	Novel Protein sim. GBank gj1498253 (U02372) - integrase [Vibrio cholerae]			264910	
723	19755599 (1445, 1446)	Novel Protein sim. GBank gj12253054[emb]CAB10705] - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	264691	
724	10126494 (1447, 1448)	Novel Protein sim. GBank gj14063015 (AF083061) - protease PrtA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	264909	
725	79878679 (1449, 1450)			UNCLASSIFIED	264905, 264907	
726	13086282 (1451, 1452)			UNCLASSIFIED	264636	
727	13522872 (1453, 1454)				264634	
728	20268471 (1455, 1456)	Novel Protein sim. GBank gj12633910[emb]CAB1341] - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			264567	
729	11293753 (1457, 1458)					
730	19900373 (1459, 1460)	Novel Protein sim. GBank gj12494660[sp]Q45291[GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		UNCLASSIFIED	264490	
731	80058750 (1461, 1462)	Novel Protein sim. GBank gj1146192 (L47838) - putative [Bacillus subtilis]		isomerase	264564	
732	80258175 (1463, 1464)	Novel Protein sim. GBank gj1168396[sp]P46681[AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		UNCLASSIFIED	264605	
733	20446839 (1465, 1466)			struct	264591, 264594, 264595	
734	20435987 (1467, 1468)	Novel Protein sim. GBank gj13184080[emb]CAA19336] - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264604	
				ubiquitin	264604	

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELIC INTERGENIC REGION				264594
736	10879734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport		264636
737	78945340 (1473, 1474)		Contains protein domain (PF00615) - Regulator of G protein signaling domain	UNCLASSIFIED		265020
738	17895353 (1475, 1476)					265008
739	79833670 (1477, 1478)	Novel Protein sim. GBank gi 2508667 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)		oxidase		264910
740	19881557 (1479, 1480)					264907, 264764, 264634, 264637
741	79827273 (1481, 1482)	Novel Protein sim. GBank gi 3261828 emb CAA10925 - (Z98260) mtp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - Domain of unknown function	UNCLASSIFIED		264689, 35696286, 264510, 264908, 18108362
742	82393795 (1483, 1484)	Novel Protein sim. GBank gi 3877494 emb CAA88472.1 - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D68340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D6845...		UNCLASSIFIED		29331822, 264910, 264762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi 127420 sp P19888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	UNCLASSIFIED		264488, 264259, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264596, 264759, 265010, 265011, 18108351, 264763, 264288, 264766, 264768, 264693, 18108370, 264629, 18108372, 264630, 264631, 264634, 264558, 18108385, 264482, 264564, 264567
744	80230421 (1487, 1488)					18108397, 264511, 264690, 264628, 264638, 264692, 264639, 264768
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi 78921 pr I S04846 - UDP-N- acetylmutamoylalanine-D-glutamyl-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli		glycoprotein		264906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]		synthase		264600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 288741 db BAA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	oxidase		66714117, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264681, 264288, 264766, 264687, 264768, 264769, 21906768, 35695917, 264691, 264693, 264628, 264634, 264635, 264639, 56182323, 83373044
748	11617923 (1495, 1496)					264690

749	20469118 (1497, 1498)	Novel Protein sim. GBank gi 1169727 sp P44948 FPG_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	264604 264600
750	20296427 (1499, 1500)	Novel Protein sim. GBank gi 5360088 gb AAD42851.1 AF159689 - (AF159689) serine/threonine kinase PKN3 [Myxococcus xanthus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		264605, 264559
751	21635169 (1501, 1502)	Novel Protein sim. GBank gi 1168662 sp P44426 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7-8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	264508, 264907, 264510, 265011, 264762, 264689, 35595855, 264638, 18108387
752	82450366 (1503, 1504)	Novel Protein sim. GBank gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORF8)		UNCLASSIFIED	264908, 264600, 264602, 264604, 264760, 264769, 264634
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi 2851530 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORF8)		UNCLASSIFIED	264508, 264906, 264907, 264908, 264909, 264759, 264602, 264764, 264769, 264628, 264629, 264630, 264632, 264634, 264635, 264637, 264638, 83373044, 18108385
754	95083741 (1507, 1508)	Novel Protein sim. GBank gi 3449276 emb CAA20420 - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	264448, 264690 264769, 264689, 264638, 264639
755	80185449 (1509, 1510)	Novel Protein sim. GBank gi 4580331 emb CAB40107.1 - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		UNCLASSIFIED	264682, 264685
756	78963176 (1515, 1516)	Novel Protein sim. GBank gi 2911858 (AF047659) - No definition line found [Caenorhabditis elegans]	amylase	UNCLASSIFIED	265007, 18108387, 265007, 18108387
757	79475667 (1517, 1518)	Novel Protein sim. GBank gi 3451312 emb CAA20449 - (AL031324) membrane alipase [Schizosaccharomyces pombe]		UNCLASSIFIED	264684, 264686
758	87628888 (1519, 1520)	Novel Protein sim. GBank gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermoplasma maritima]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	29331822, 264908, 52644045, 56182435, 60170831, 21906754, 265017, 265019, 264681, 264687, 264688, 21906766, 21908768, 265020, 265021, 265022, 264635, 22279000
759	79877968 (1521, 1522)	Novel Protein sim. GBank gi 3327158 dbj BAA31647 - (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED	264766
760	80023563 (1523, 1524)	Novel Protein sim. GBank gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermoplasma maritima]		UNCLASSIFIED	264907, 264593, 265020
761	79877968 (1521, 1522)	Novel Protein sim. GBank gi 3327158 dbj BAA31647 - (AB014572) KIAA0672 protein [Homo sapiens]		UNCLASSIFIED	264600
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermoplasma maritima]		UNCLASSIFIED	264600
763	20294813 (1525, 1526)	Novel Protein sim. GBank gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermoplasma maritima]		UNCLASSIFIED	264600
764	39515024 (1527, 1528)	Novel Protein sim. GBank gi 4981266 gb AAD35822.1 AE00174 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermoplasma maritima]		UNCLASSIFIED	264603

765	80025347 (1529, 1530)	Novel Protein sim. GBank glj3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	264905, 264906, 264594, 264686, 33657023
766	82417404 (1531, 1532)				264605, 264762, 18108374
767	10298742 (1533, 1534)	Novel Protein sim. GBank glj541121 [pir]S40827 - hypothetical protein o300 - Escherichia coli		UNCLASSIFIED	264907
768	79416080 (1535, 1536)			UNCLASSIFIED	264592, 264595
769	80085554 (1537, 1538)	Novel Protein sim. GBank glj2982501 [emb]CAA06164 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 264559
770	80417847 (1539, 1540)	Novel Protein sim. GBank glj283437 [pir]S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	264905, 264907, 264828, 264909, 265010, 264766, 264628, 264629, 264634, 264636, 264555
771	93329509 (1541, 1542)	Novel Protein sim. GBank glj4769004 [gb]AAD29715.1 [AF14059] - (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	56182575, 35696286, 264259, 66714117, 264107, 66712502, 56182435, 264112, 55812038, 87168559, 264288, 21906766, 33657023, 65274620, 65274791, 18108381
772	78971362 (1543, 1544)			UNCLASSIFIED	264910
773	78945363 (1545, 1546)			UNCLASSIFIED	265020
774	79856129 (1547, 1548)	Novel Protein sim. GBank glj5531324 [emb]CAB51045.1 - (AJ009579) putative alkane 1-monooxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	264909
775	20620141 (1549, 1550)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	UNCLASSIFIED	264555
776	78942693 (1551, 1552)		Contains protein domain (PF01344) - Ketch motif		265019
777	79960378 (1553, 1554)	Novel Protein sim. GBank glj4505461 [ref]NP_003624.1 [pNRPB - nuclear restricted protein, BTB domain-like (brain)]		protease	21906754, 265020, 60170615, 264691
778	20691310 (1555, 1556)			UNCLASSIFIED	264511
779	80054024 (1557, 1558)				264603
780	95288987 (1559, 1560)	Novel Protein sim. GBank glj1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	264907, 264600, 264601, 264602, 264603, 264604, 264605, 264486
781	80250049 (1561, 1562)				264905, 264907, 265010, 264600, 264601, 18108362, 18108374, 264556
782	8758529 (1563, 1564)	Novel Protein sim. GBank glj4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	264605
783	16410791 (1565, 1566)				265020
784	80051197 (1567, 1568)			UNCLASSIFIED	264635, 33657023, 29331828, 265017, 264565, 264566
785	56073541 (1569, 1570)	Novel Protein sim. GBank glj3451335 (AC005525) - F22162_1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 264604
786	20438842 (1571, 1572)	Novel Protein sim. GBank glj136748 [sp]P10905 [UGPA, ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA]		transport	264603
787	80258364 (1573, 1574)			UNCLASSIFIED	264593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	264909, 264602, 264603, 264769, 264638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium cutriburum]		UNCLASSIFIED	265007
790	86284408 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA83099.1 - (AB026118) MALT1 [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	22278999, 29331824, 264828, 87168559, 265018, 21906765, 21906767, 21906768, 21906769, 265020, 264692, 22279000, 264563
791	94651627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb]CAB51985.1 - (AL109663) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			264601, 264605, 264636
792	80058786 (1583, 1584)	Novel Protein sim. GBank gij393194 (L02375) - S-antigen [Plasmodium falciparum]		struct	265021, 264631, 264635, 264556
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046 - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gij105894 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	264603, 264604, 264910, 264762, 264906, 264639, 264909, 264757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CAB07082 - (Z92771) birA [Mycobacterium tuberculosis]		carboxylase	264488, 35696052, 264905, 264907, 265010, 35696423, 264636
796	86669451 (1591, 1592)				60432229, 55811150, 264630, 264637, 264565
797	87771781 (1593, 1594)	Novel Protein sim. GBank gij2995447 [emb]CAA71519 - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 264093, 264094, 66714117, 21906767, 21906769, 265020, 265022
798	79865209 (1595, 1596)			transcript factor	264687, 264768, 264693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gij4467250 [emb]CAB37575 - (AL035569) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	264909, 264910, 264636, 264638
800	79970189 (1599, 1600)				
801	80499399 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA16054 - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		UNCLASSIFIED	264488
802	79834598 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744 - (AF147449) penicillin binding protein 1B [Pseudomonas aeruginosa]		transport	264508, 264511, 265006, 265009, 264769, 264567, 264486
803	20467520 (1605, 1606)				264905, 264693
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H1009]		struct	264605
				kinase	264510
805	79599993 (1609, 1610)				
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683 - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	transferase	264508
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNFD_CAEEL - HYPOTHETICAL 18.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			264769
					264764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi 3913092 sp Q46170 ARCD_CLOPE - ARGININE/ORNITHINE ANTIporter			transport	264909, 264602, 21906764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi 3913016 sp P74309 ALF1_SYN3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)		Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	264508, 264906, 264909, 265007, 264910, 264758, 264600, 264602, 264603, 264605, 264687, 264769, 264689, 264636, 264486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi 401472 sp P30863 YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION		Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264369
811	80079280 (1621, 1622)			UNCLASSIFIED	UNCLASSIFIED	264558
812	10297654 (1623, 1624)			UNCLASSIFIED	UNCLASSIFIED	264692
813	79612280 (1625, 1626)			UNCLASSIFIED	UNCLASSIFIED	264906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi 146168 (J01617) - glutaminyl- [rRNA synthetase [Escherichia coli]			synthase	264905, 264602, 264605, 264682, 264687, 264769, 264636
815	95419513 (1629, 1630)	Novel Protein sim. GBank gi 4589652 db BAA76848.1 - (AB023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	UNCLASSIFIED	264488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29146499, 264905, 264908, 265007, 33657402, 60433356, 60433438, 264758, 265011, 265017, 265018, 265019, 264369, 264288, 264685, 21906765, 21906767, 265020, 265021, 264692, 65274620, 33657109, 264629, 18108376, 264635, 264638, 60170394, 58182323, 264564
816	19881910 (1631, 1632)					264600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi 1781144 emb CAB06254 - (Z83866) hypothetical protein Rv3069 [Mycobacterium tuberculosis]		UNCLASSIFIED	UNCLASSIFIED	264595
818	90938190 (1635, 1636)	Novel Protein sim. GBank gi 1477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]				65274572, 22278999, 60424269, 35696052, 55812038, 21906768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810764, 35696423, 55811576, 264636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi 1001352 db BAA10839 - (D64006) ABC transporter [Synechocystis sp.]			transport	264565
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi 586814 sp P37484 YYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION			UNCLASSIFIED	264600, 264602, 264604
821	79762590 (1641, 1642)			UNCLASSIFIED	UNCLASSIFIED	264910
822	80215310 (1643, 1644)			UNCLASSIFIED	UNCLASSIFIED	264510, 264594, 264637
823	94992299 (1645, 1646)	Novel Protein sim. GBank gi 3878400 emb CAA95828 - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL:D32742 comes from this gene; cDNA EST EMBL:D33617 comes from this gene; cDNA EST....		struct		264509, 264687, 264691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi 1370076 emb CAA66887 - (X98235) type I [Drosophila melanogaster]		Contains protein domain (PF01429) - Methyl-CpG binding domain		264910, 264763, 264769, 264693

825	20638600 (1649, 1650)	Novel Protein sim. GBank gi 3025132 sp P77391 YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank gi 3242281 emb CAA16669 - (AL021646) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank gi 3417424 emb CAA20312 - (AL031261) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank gi 4336892 gb AAD17897 - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264508, 264505, 264509, 264906, 264907, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264766, 264768, 21908768, 35895917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264563, 264566, 264486
829	81742215 (1657, 1658)	Novel Protein sim. GBank gi 3820539 (AF080002) - UDP-N- acetyluramyl tripeptide synthetase MurC [Helicobacillus mobilis]		UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)			UNCLASSIFIED	264603
831	87112435 (1661, 1662)			UNCLASSIFIED	66714117, 264910, 264639
832	19536322 (1663, 1664)	Novel Protein sim. GBank gi 1870004 emb CAB06855 - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	264906
833	20726654 (1665, 1666)	Novel Protein sim. GBank gi 2500056 sp Q46267 PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank gi 2497531 sp Q46078 KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - kinase Pyruvate kinase		264600, 264602, 264769, 264689, 264636
835	84140482 (1669, 1670)				264768, 263994, 21906767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35896052, 22279002, 264508, 264905, 264906, 264448, 263972, 264908, 264909
836	66126552 (1671, 1672)	Novel Protein sim. GBank gi 699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		transport	35895917, 264557
837	79450450 (1673, 1674)			UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank gi 728867 sp P40602 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR		UNCLASSIFIED	264687
839	79641125 (1677, 1678)	Novel Protein sim. GBank gi 2496533 sp Q50598 Y0D8_MYCTU - HYPOTHETICAL 69.9 KD PROTEIN CY1A11.08		UNCLASSIFIED	264906
840	80059851 (1679, 1680)	Novel Protein sim. GBank gi 4557753 ref NP_000372.1 pMID1 - midline 1 protein finger)	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264762, 264556

841	80376318 (1681, 1682)	Novel Protein sim. GBank gi 139805 sp P08045 XFIN_XENLA - XFIN PROTEIN	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264764
842	80078724 (1683, 1684)	Novel Protein sim. GBank gi 2114321 db BAA20037 - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	264905, 264908, 265008, 265009, 18108374, 56182323, 284558
843	87002847 (1685, 1686)	Novel Protein sim. GBank gi 3882325 db BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	264091, 29331825, 264906, 264768, 264563
844	17941439 (1687, 1688)	Novel Protein sim. GBank gi 2224721 db BAA20844 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	265011
845	18346844 (1689, 1690)				264629
846	79863441 (1691, 1692)	Novel Protein sim. GBank gi 625679 pir JA36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	284907
847	78695348 (1693, 1694)				264909
848	78489365 (1695, 1696)			UNCLASSIFIED	265020
849	79756367 (1697, 1698)			UNCLASSIFIED	264566
850	79817849 (1699, 1700)	Novel Protein sim. GBank gi 3183245 sp P78061 YC_KJ_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	264909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gi 5454130 ref NP_006280.1 pTLN - talin	Contains protein domain (PF01608) - ILWEQ domain		264488, 52644507, 264489, 18108398, 65274572, 56182575, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 20281171, 264490, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264107, 264905, 264906, 264907, 264908, 52644045, 56182435, 265006, 265007, 265008, 265009, 264910, 60432229, 60431735, 60433356, 33657402, 60433438, 264595, 264758, 264759, 21906754, 33109954, 52644288, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 264762, 264681, 18108351, 264763, 264448, 264682, 264764, 264683, 18108354, 264288, 264369, 264685, 264766, 264687, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 29148629, 55811957, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264691, 264692, 33657023, 264693, 263966, 33657109, 27486261, 27486262, 27486264, 27486265, 35695763, 60431602, 18108370, 20281089, 264629, 18108374, 18108376, 55811576, 35696423, 35695855, 264634, 264635, 264636, 264555, 60431850, 264556, 264691
852	10147366 (1703, 1704)				

853	13032587 (1705, 1706)	Novel Protein sim. GBank gij3402836[embjCAA76082] - [Y16136] 2-enoate reductase [Moorella thermoacetica]		reductase	264636 264566
854	80052438 (1707, 1708)				
855	79641130 (1709, 1710)				264592
856	11594236 (1711, 1712)			UNCLASSIFIED	264591
857	79210165 (1713, 1714)			UNCLASSIFIED	264630, 264634
858	80248910 (1715, 1716)				265008, 265009, 264601, 264602, 264603, 18108351
859	20296634 (1717, 1718)				264559
860	80041749 (1719, 1720)			UNCLASSIFIED	264489
861	65857045 (1721, 1722)			UNCLASSIFIED	33657023, 264630
862	80079467 (1723, 1724)				264600
863	80579931 (1725, 1726)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	264488, 18108398, 35696286, 264259, 18108351, 264288, 265021
864	94939904 (1727, 1728)				
865	80045310 (1729, 1730)	Novel Protein sim. GBank gij5689884[embjCAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain	UNCLASSIFIED	264259, 264112, 263974 264635, 264600, 264636, 264591, 264602, 264693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gij4557876[ref]NP_000341.1 pABCR - ATP binding cassette transporter	transport		264288, 264557, 264558
867	80062402 (1733, 1734)				
868	10075384 (1735, 1736)			UNCLASSIFIED	264605
869	80062406 (1737, 1738)				264909
870	80249651 (1739, 1740)	Novel Protein sim. GBank gij628660[prj]S37755 - Adenyltransferase - Escherichia coli	transferase		264605, 264687, 18108374 264601, 264636
871	20378295 (1741, 1742)	Novel Protein sim. GBank gij1708180[sp]Q10602 HEMK_MYCTU - HEMK PROTEIN HOMOLOG	UNCLASSIFIED		264603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gij1545959[embjCAA67763] - (X99384) paladin [Mus musculus]	UNCLASSIFIED		35696286, 22278998, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 264910, 264591, 60433356, 264596, 52646317, 87168474, 265010, 264602, 264603, 265017, 265018, 264605, 18108351, 264764, 264766, 264768, 52644229, 264769, 21906765, 265021, 264534, 264691, 52645129, 264628, 264629, 35696423, 65274791, 264631, 264632, 264635, 264636, 264556, 264637, 264638, 264639, 60432113, 22279000, 22279002, 264584
873	20189728 (1745, 1746)	Novel Protein sim. GBank gij4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264595

874	80077692 (1747, 1748)	Novel Protein sim. GBank gij134319[sp]P07819[SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)]			UNCLASSIFIED	264600	
875	86608446 (1749, 1750)	Novel Protein sim. GBank gij481000[p]irj[S37594 - mucin - human (fragment)]				264259, 264448, 264288, 264557, 87168518	
876	86465157 (1751, 1752)	Novel Protein sim. GBank gij3128283 (AF010496) - iron(iii) dicitrate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF00005) - ABC transporter		transport	264907, 264601, 264602, 264605, 265020, 60431602	
877	87802548 (1753, 1754)	Novel Protein sim. GBank gij731074[sp]P40349[URB1 - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1]	Contains protein domain (PF00320) - GATA zinc finger		transcriptfactor	22278998, 264909, 264369	
878	80187288 (1755, 1756)	Novel Protein sim. GBank gij1351614[sp]Q09853[YAED_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I]			ATPase_associated	264369, 264555	
879	94328862 (1757, 1758)	Novel Protein sim. GBank gij3875304[emb]CAA8434] - (Z74030) predicted using Genefinder; cDNA EST EMBL: C07609 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...				56182575, 29331824, 264508, 264906, 265018, 18108351, 264448, 264683, 21906768, 21908768, 60170615, 33657023, 65274620, 33657109, 18108374, 35695855, 264563	
880	8491135 (1759, 1760)	Novel Protein sim. GBank gij137120[sp]P11214[UR0T_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)]	Contains protein domain (PF00051) - Kringle domain		cathepsin	264508	
881	11280122 (1761, 1762)				UNCLASSIFIED	264508	
882	11077011 (1763, 1764)	Novel Protein sim. GBank gij2632098[emb]CAA75667] - (Y15513) Prodos protein [Drosophila melanogaster]			UNCLASSIFIED	264558	
883	79582969 (1765, 1766)				UNCLASSIFIED	264688	
884	13517921 (1767, 1768)	Novel Protein sim. GBank gij1155068[emb]CAA84425] - (X94976) cell wall-plasma membrane linker protein [Brassica napus]			UNCLASSIFIED	264636	
885	80052457 (1769, 1770)	Novel Protein sim. GBank gij2078027[emb]CAB08467] - (Z95208) hypothetical protein Rv2372c [Mycobacterium tuberculosis]			UNCLASSIFIED	264605, 18108362	
886	11685138 (1771, 1772)					264690	
887	94315307 (1773, 1774)	Novel Protein sim. GBank gij2695834[emb]CAA15904] - (AL021006) sucA [Mycobacterium tuberculosis]			dehydrogenase	35696052, 264906, 264600, 264603, 35695917, 35695855, 264636	
888	10083398 (1775, 1776)	Novel Protein sim. GBank gij5689395[dbj]BAA82981.1] - (AB028952) KIAA1029 protein [Homo sapiens]			UNCLASSIFIED	264908	
889	20385917 (1777, 1778)	Novel Protein sim. GBank gij11861338[dbj]BAA19365] - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE. [Bacillus subtilis]				264603	
890	19904337 (1779, 1780)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]				264629	

891	13516879 (1781, 1782)	Novel Protein sim. GBank gi 4959396 gb AAD3431.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	264636
892	87634157 (1783, 1784)	Novel Protein sim. GBank gi 545526 bbs 143833 - LBP- 1b=transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Namalwa cells, Peptide, 541 aa]		transcriptfactor	22278996, 22278999, 29331828, 35696052, 264908, 264909, 265009, 265011, 264602, 265019, 264766, 21906765, 21906766, 21906769, 265020, 265021, 56526486
893	79168037 (1785, 1786)	Novel Protein sim. GBank gi 2829688 sp P80608 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIOL)-LYASE) (CSASE)		synthase	264689, 263967
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	264508, 264600, 264555, 264559
896	79747803 (1791, 1792)				264632
897	94991923 (1793, 1794)			UNCLASSIFIED	264686, 28331828, 264511
898	87695109 (1795, 1796)		Contains protein domain (PF00047) - Immunoglobulin domain		56182575, 60432289, 56182435, 60432229, 55811957, 22279000, 264486
899	11100463 (1797, 1798)				264601
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi 1750127 (U66480) - YncC [Bacillus subtilis]		transport	264769, 264691, 264563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi 3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	264907, 264602, 264605, 264769, 35695917, 18108376, 264563
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi 335570 emb CAA20001 - (AL031124) 3-isopropylmalate dehydratase large subunit [Streptomyces coelicolor]	Contains protein domain (PF00330) - aconitase family (aconitate hydratase)	isomerase	264909, 265008, 264602, 264604, 264769, 264689, 264693
903	82060206 (1805, 1806)	Novel Protein sim. GBank gi 2960120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	35696052, 264905, 264510, 264511, 264512, 264605, 264760, 18108351, 264762, 264687, 264768, 264769, 264688, 21906764, 35695917, 27486282, 35695955, 264634, 264636, 264486
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi 728887 sp P40906 ARGI_COCIM - ARGINASE	Contains protein domain (PF00491) - Arginase family	hydrolase	264604*
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi 4567200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264909
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi 3738200 emb CAA21292 - (AB01855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			264595, 264605
907	87913201 (1813, 1814)				
908	11754482 (1815, 1816)			UNCLASSIFIED	60432289, 264601, 264690
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi 3668940 bbs BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	264638
910	16776206 (1819, 1820)	Novel Protein sim. GBank gi 4589726 bbs BAA76883.1 - (AB003137) DnaJ homolog protein [Salix gligiana]	Contains protein domain (PF00684) - DnaJ central domain (4 repeats)	eph	264602 265009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P35685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomalprot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07921.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26695]		hydrolase	264559
913	20459357 (1825, 1826)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED	264604
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 417657 sp Q03604 RIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)		reductase	264636
915	87606703 (1829, 1830)	Novel Protein sim. GBank gi 568957 dbj BA83069.1 - (AB029040) KIAA1117 protein [Homo sapiens]			18108398, 22278996, 66714117, 264906, 264591, 21906768, 265020, 55811576, 264638
916	79444081 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264595
917	20195985 (1833, 1834)	Novel Protein sim. GBank gi 1655699 emb CAA69032 - (Y07752) pherophorin-S [Volvox carter]		UNCLASSIFIED	264605
918	91226795 (1835, 1836)	Novel Protein sim. GBank gi 568957 dbj BA83069.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]		synthase	264259, 26331826, 264808, 265019, 264448, 265020, 264635, 83373044
919	80436785 (1837, 1838)	Novel Protein sim. GBank gi 568957 dbj BA83069.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264602, 264604, 264768, 18108370, 264563
920	79606095 (1839, 1840)	Novel Protein sim. GBank gi 168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858634 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1 - (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	7982605 (1843, 1844)	Novel Protein sim. GBank gi 267079 sp P28514 TBB6_ARATH - TUBULIN BETA-6 CHAIN			265019, 22279002
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267079 sp P28514 TBB6_ARATH - TUBULIN BETA-6 CHAIN		tubulin	264807, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385
924	21431341 (1847, 1848)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264510
925	20630332 (1849, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...			264603
926	79397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811957, 263972, 264639
927	37036201 (1853, 1854)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]		UNCLASSIFIED	264769

928	80070610 (1855, 1856)	Novel Protein sim. GBank gij156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20630336 (1857, 1858)			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gij115936gip[AAD03446.1] - (AF118223) No definition line found [Arabidopsis thaliana]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gij4490609[emb]CAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - Ribonucleotide reductase	reductase	264486
932	80420613 (1863, 1864)	Novel Protein sim. GBank gij545939[emb]CAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264508, 264905, 264906, 264907, 264908, 264909, 264600, 264602, 264603, 264605, 264766, 264558, 18108387, 264486
933	94326010 (1865, 1866)	Novel Protein sim. GBank gij5689523[dbj]BAA83045.1] - (AB029016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22279002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gij119111[sp]P12978[EBN2_EBV - EBNA-2 NUCLEAR PROTEIN]			264369, 22279002
935	80063162 (1869, 1870)				
936	80026632 (1871, 1872)	Novel Protein sim. GBank gij845686 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
937	80250273 (1873, 1874)	Novel Protein sim. GBank gij1360669[pil]CGHU1V - collagen alpha 1(V) chain precursor - human		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
938	80026633 (1875, 1876)	Novel Protein sim. GBank gij2226243[emb]CAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		synthase	263978
939	11071694 (1877, 1878)			UNCLASSIFIED	264602
940	94144252 (1879, 1880)	Novel Protein sim. GBank gij3560166[emb]CAA20678] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264600
941	11388414 (1881, 1882)				264905, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264759, 264760, 264683, 264766, 264768, 264769, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
942	19484122 (1883, 1884)				264593
943	80080258 (1885, 1886)	Novel Protein sim. GBank gij4033729 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264760
944	80216096 (1887, 1888)	Novel Protein sim. GBank gij2494764[sp]Q50729[GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)]		UNCLASSIFIED	264600, 264687, 264689, 264563
945	80052477 (1889, 1890)	Novel Protein sim. GBank gij732353[sp]P39606[YWCH_BACSU - HYPOTHETICAL 36.6 KD PROTEIN IN QOXD_VPR INTERGENIC REGION]	Contains protein domain (PF00818) - Ice nucleation protein repeat	synthase	264511, 264603
946	79248402 (1891, 1892)			UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
					265017

947	81802698 (1893, 1894)	Novel Protein sim. GBank gjl2896770[embjCAA17247] - (AL021899) hypothetical protein Rv2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278996, 264907, 264909, 265008, 265009, 264910, 264758, 264600, 264602, 265018, 264605, 264769, 264689, 264693
948	88165538 (1895, 1896)	Novel Protein sim. GBank gjl2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		lgf	18108398, 56182575, 22278997, 22278999, 60432049, 29331822, 29331826, 264907, 56182435, 55811386, 265011, 264600, 265017, 265018, 265019, 18108351, 265020, 265021, 265022, 27486265, 263972, 55811576, 264638, 60170394, 264566
949	88081786 (1897, 1898)	Novel Protein sim. GBank gjl4507985[refjNP_003427.1]pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	29331825, 21906764, 27486261, 21906766, 52844298, 33657349, 87168518, 58994075, 265020, 265021, 87168559, 52644150, 264637
950	79485872 (1899, 1900)	Novel Protein sim. GBank gjl1079461[pirjS43865 - cytochrome b, type II - polonoo (fragment)]	Contains protein domain (PF00039) - Intermediate filament proteins	struct	264683, 18108361
951	20451411 (1901, 1902)	Novel Protein sim. GBank gjl5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264604
952	79566954 (1903, 1904)	Novel Protein sim. GBank gjl5305702[gbIAAD41779.1]AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	264910, 264691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gjl2495642[spQ47142]YFHS, ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION		transport	264510
954	8893326 (1907, 1908)	Novel Protein sim. GBank gjl2360965 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	264508
955	96313410 (1909, 1910)	Novel Protein sim. GBank gjl5454064[refjNP_006319.1]pSIP1 - SYT interacting protein	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	58994075, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264910, 264758, 264759, 265010, 264601, 264760, 18108351, 264762, 264763, 264764, 264766, 264686, 264767, 264687, 264768, 264769, 264689, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 56182323, 264639, 18108388, 264563, 264564
956	80064224 (1911, 1912)	Novel Protein sim. GBank gjl2052129[embjCAB08155] - (Z94752) rimJ [Mycobacterium tuberculosis]			264605
957	80056208 (1913, 1914)	Novel Protein sim. GBank		UNCLASSIFIED	264603, 18108362
958	80036446 (1915, 1916)	Novel Protein sim. GBank gjl1709787[spQ00451]PRF1_LYCES - 36.4 KD PROLINE-RICH PROTEIN		UNCLASSIFIED	264908, 264910, 264762, 263978, 264637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gjl2131050[embjCAB09260] - (Z95844) opa [Mycobacterium tuberculosis]		UNCLASSIFIED	264602, 264692
960	37815406 (1919, 1920)	Novel Protein sim. GBank gjl2129478[pirjS51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264259
961	20567383 (1921, 1922)				263978
962	11399318 (1923, 1924)				264593

963	80580374 (1925, 1926)				UNCLASSIFIED	264510, 264288, 264555, 264556, 264559, 264486
964	79832019 (1927, 1928)	Novel Protein sim. GBank gij4589622[dbj BAA76833.1] - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	264112, 264910, 264689
965	91229485 (1929, 1930)	Novel Protein sim. GBank gij5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	264488, 265017, 264448, 264634, 264558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	264906, 264592, 264596, 264604, 264768, 21906764, 264692, 264693, 264629, 264636, 264638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gij1731207[sp Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REGX3		Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264760
968	79560269 (1935, 1936)	Novel Protein sim. GBank gij2661836[emb CAA75187] - (Y14964) putative transport protein [Methylophilus methylotrophus]			transport	264693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gij5419878[emb CAB46422.1] - (AL096747) hypothetical protein [Homo sapiens]		Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	35696286, 264685, 264686, 35695917, 264692, 18108374, 264635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147620, 264828, 265006, 265007, 265008, 265009, 18108348, 33109954, 265010, 265011, 18108351, 264288, 21906767, 21906768, 18108370, 18108374, 18108377, 264630, 264635, 18108380, 83373044, 18108387, 18108388
971	79919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)					264557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gij1723119[sp P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				264604
974	80057103 (1947, 1948)				UNCLASSIFIED	264565
975	10196018 (1949, 1950)				UNCLASSIFIED	264510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gij3881459[emb CAA92988.1] - (Z68753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27680 comes from this gene; cDNA EST EMBL:D27679 comes from this gene; cDNA EST EMBL:D64477 comes from this ge...			UNCLASSIFIED	264508, 264906, 264758, 264632, 264639, 264563
977	10355349 (1953, 1954)	Novel Protein sim. GBank gij549456[sp Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	264906
978	80025927 (1955, 1956)					
979	80447820 (1957, 1958)	Novel Protein sim. GBank gij3171904[emb CAA75669] - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	264600, 264602, 264603, 264604
980	80025928 (1959, 1960)				UNCLASSIFIED	264767, 264768, 265006, 265007, 264906
981	80098550 (1961, 1962)	Novel Protein sim. GBank gij3599940 (AF017368) - facicongenital dysplasia protein 2 [Mus musculus]			UNCLASSIFIED	264600, 264602, 264605
					UNCLASSIFIED	264692, 264555, 264556, 264557, 264559

982	80195670 (1963, 1964)	Novel Protein sim. GBank gij2950220[emb]CAA71575] - (Y10545) fused-ccdB [Escherichia coli]	UNCLASSIFIED	264404
983	90895041 (1965, 1966)	Novel Protein sim. GBank gij476389[pri]JB43402 - myosin heavy chain-B, neuronal - chicken	struct	65274572, 56182575, 264908, 264909, 265007, 265008, 264758, 265010, 55811150, 33657023, 264634, 264557, 264558
984	20466878 (1967, 1968)		UNCLASSIFIED	264605
985	55461368 (1969, 1970)	Novel Protein sim. GBank gij3451504[emb]CAA07660.1] - (AJ007747) hypothetical protein BbLPS1.21 [Bordetella bronchiseptica]	transferase	56182435, 264600
986	87102868 (1971, 1972)		UNCLASSIFIED	264106, 264110, 265020, 60170615
987	79867231 (1973, 1974)		UNCLASSIFIED	264909
988	19858661 (1975, 1976)		UNCLASSIFIED	264600
989	88095329 (1977, 1978)		UNCLASSIFIED	264508, 265017, 264534, 264564
990	88057746 (1979, 1980)	Novel Protein sim. GBank gij572506[gb]AAD48080.1[AF06015] - (AF060152) METH1 protein [Homo sapiens]	oxidase	264259, 264908, 265009, 264910, 264596, 264369, 264288, 264766, 264628, 264635, 264568
991	10106140 (1981, 1982)		UNCLASSIFIED	264909
992	79845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[emb]CAB08835] - (Z85436) hypothetical protein Rv3645 [Mycobacterium tuberculosis]	UNCLASSIFIED	264508, 264593
993	10814053 (1985, 1986)			
994	11090590 (1987, 1988)	Novel Protein sim. GBank gij329297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]	reductase	264907
995	94321911 (1988, 1990)	Novel Protein sim. GBank gij5106572[gb]AAD39760.1[AF14394] - (AF143946) transcriptional activator SRCAP [Homo sapiens]	helicase	18108398, 65274572, 22278996, 264490, 60432049, 29331827, 29146498, 264508, 264905, 264907, 264908, 56182435, 265008, 264591, 264592, 60432228, 60431735, 33657402, 264595, 264758, 21906754, 265010, 265017, 265018, 264605, 264760, 264448, 264763, 264768, 21906765, 21906768, 21906769, 55811957, 264692, 264693, 264629, 35896423, 55811576, 35695855, 264636, 264555, 264556, 264558, 83373044, 22278002, 264563
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2911719 (AC004227) - KIA0071LB [Homo sapiens]	phosphatase	83373044, 29331824, 263978, 55811957, 56526486, 87168518, 264910, 264908, 264565, 264566, 264693, 264768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2649101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	transport	35696286, 22278997, 22278999, 264508, 264905, 264908, 265010, 264600, 264602, 264605, 264688, 264769, 265021, 264565, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[sp]P04929[HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR	helicase	264595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2506697 sp P46490 YFCA_HAEIN - HYPOTHETICAL PROTEIN H10198		UNCLASSIFIED	264682	
1000	20727944 (1998, 2000)			UNCLASSIFIED	264602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 dbj BAA20833 - (AB002377) KIAA0379 [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED kinase	60432049, 264907, 264908, 264511, 264603, 264683, 264684, 264687, 264689, 29148827, 21906769, 264692, 18108385, 22279000 265009, 264369, 265020	
1002	80189603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		struct		
1003	17933491 (2005, 2006)				265019	
1004	16314987 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			264635	
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gi 114073 sp P07672 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	264508	
1006	37815429 (2011, 2012)			UNCLASSIFIED	264259	
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi 4062979 dbj BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		synthase	264905	
1008	88094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1 - (AJ001206) putative trehalose synthase [Streptomyces coelicolor]		synthase	265007, 264602, 264605, 264760, 264636	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	kinase	264102, 264288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Sinorhizobium meliloti]		dehydrogenase	264592	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342647 gb AAB86591.1 - (U90653) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35896052, 264905, 264764, 264768, 35895917, 264629	
1012	85294456 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35896052, 264905, 264600, 264601, 264602, 264605, 264762, 264766, 264768, 264689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	264591, 21906768	
1014	86608828 (2027, 2028)				29331824, 265019, 265020	

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gjl4159995 (AF063095) - SELIL [Mus musculus]	Contains protein domain (PF00040) - Fibronectin type II domain	struct	22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331825, 29331828, 264907, 56182435, 264510, 264591, 264593, 60433358, 264594, 55812038, 264758, 21906754, 33657084, 265010, 264600, 265017, 265018, 265019, 18108351, 21906765, 21906766, 21906767, 21906768, 55811957, 265022, 33657023, 65274620, 33657182, 32833986, 18108370, 18108377, 55811576, 35696423, 264630, 22279000, 264565
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gjl2506989 [sp]P41407 [ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)]	esterase		264686, 264693
1017	11069213 (2033, 2034)	Novel Protein sim. GBank gjl5103943 [dbj]BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	transport		264600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gjl4493973 [emb]CAB39032.1 - (AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa [Plasmodium falciparum]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5		22278996, 29148627, 264563
1019	11703607 (2037, 2038)		UNCLASSIFIED		264686
1020	80234432 (2039, 2040)				264508, 264509, 264512, 264600, 264762, 264769, 264689, 18108370, 264636, 264638, 264486
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gjl4633807 [gb]AAD26859.1 [AF12779] trehalose biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]	synthase		264769
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gjl1781230 [emb]CAB06277 - (Z83867) hypothetical protein Rv3137 [Mycobacterium tuberculosis]	phosphatase		35696052, 264508, 265008, 265009, 264769, 18108387, 264563
1023	11399341 (2045, 2046)	Novel Protein sim. GBank gjl3777495 (U92083) - calcium transporting ATPase [Pichia angusta]	ATPase-associated E1-E2 ATPase		264593
1024	80057129 (2047, 2048)		UNCLASSIFIED		52646842, 33657402, 33657023, 18108379, 55811576, 264631, 264556, 264557, 264559, 18108388, 264566
1025	79644200 (2049, 2050)	Novel Protein sim. GBank gjl3483045 [emb]CAA20556j - (AL031371) putative transport system permease protein [Streptomyces coelicolor]	transport		264693
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gjl1174922 [sp]Q02322 [UVRD_HAEIN - DNA HELICASE II]	helicase		264602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gjl4757728 [ref]NP_004886.1 [pAGTA - angiotensin/vasopressin receptor AII/AVP-like]	UNCLASSIFIED		265017

1028	20297828 (2055, 2056)	Novel Protein sim. GBank gij2791409[emb]CAA16003] - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	264600
1029	94665090 (2057, 2058)			UNCLASSIFIED	264595
1030	80095343 (2059, 2060)			UNCLASSIFIED	264907, 264908, 264510, 264512, 265009, 265010, 265011, 264600, 264602, 264603, 264605, 264769, 18108372, 18108374
1031	95289117 (2061, 2062)			UNCLASSIFIED	264905, 264906, 264909, 264595, 264692, 264630, 264634, 264638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gij4503895[ref]NP_000145.1pGALK - galactokinase 1		UNCLASSIFIED	264689
1033	86464818 (2065, 2066)	Novel Protein sim. GBank gij2982990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35696052, 264906, 264510, 18108354, 264687, 264769, 264689, 60433438, 265019, 18108385, 264486
1034	79245937 (2067, 2068)	Novel Protein sim. GBank gij405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	264906
1035	79956355 (2069, 2070)			UNCLASSIFIED	264692
1036	85804998 (2071, 2072)			UNCLASSIFIED	264905, 66712502, 264908, 264766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 264909, 60433438, 265019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gij790819 (L39891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLATLH2 domain		264604, 264634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gij2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	264092, 264093, 264094, 264683, 264689, 263967
1040	80026840 (2079, 2080)	Novel Protein sim. GBank gij2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase	isomerase	264595
1041	10156682 (2081, 2082)	Novel Protein sim. GBank gij3256535[dbj]BAA29218.1] - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		kinase	264907
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gij2058299[emb]CAA66953] - (X98309) ARI protein [Drosophila melanogaster]			264605
1043	80057136 (2085, 2086)	Novel Protein sim. GBank gij1870167[emb]CAA70125] - (Y08921) msik [Streptomyces reticuli]	Contains protein domain (PF00005) - ABC transporter	transport	264565, 264567
1044	80025952 (2087, 2088)	Novel Protein sim. GBank gij5689890[emb]CAB52053.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	265006, 264602, 265017, 29331825, 264637
1045	52415482 (2089, 2090)				
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gij854065[emb]CAA58337] - (X83413) U98 [Human herpesvirus 6]		helicase	264686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gij4210471[dbj]BAA74535.1] - (AB019033) orISA [Pseudomonas sp.]		UNCLASSIFIED	264769
1048	79186400 (2095, 2096)	Novel Protein sim. GBank gij3413419[emb]CAA20279] - (AL031232) hypothetical protein SC-10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	264687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gij5051636[gb]AAD38326.1[AF07372] EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	264905, 264634
1050	79471521 (2099, 2100)			UNCLASSIFIED	264686

1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	824242862 (2103, 2104)	Novel Protein sim. GBank gi 3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank gi 5441319 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			264686, 18108374, 29331824, 83373044, 21906754, 52645156, 56182435, 264689, 29331827, 27486261, 35698052, 21908765, 35696423, 21906768, 56182575, 21906769, 55811957, 87168518, 35696286, 22278997, 265020, 265011, 265021, 265022, 265007, 265018, 22279000, 22279002, 264482, 264906, 52644150, 264909, 264288, 29331822, 52645080, 264766
1054	79580225 (2107, 2108)			UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank gi 5052508 gb AAD38584.1 AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	264907, 264602, 264681, 264288, 21906768, 33657109, 55810764, 35695855, 264631
1056	17682319 (2111, 2112)	Novel Protein sim. GBank gi 3021676 dbj BAA25359 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		mapolymerase	264906
1057	85667216 (2113, 2114)	Novel Protein sim. GBank gi 1226281 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264682
1058	80376576 (2115, 2116)				264764
1059	84662754 (2117, 2118)	Novel Protein sim. GBank gi 170016 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA)		transcriptfactor	35696052, 35695855, 265009, 264636
1060	79481169 (2119, 2120)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146499, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank gi 90254 pir J28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	264634
1062	39567937 (2123, 2124)	Novel Protein sim. GBank gi 3334200 sp O49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank gi 2499966 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)			264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank gi 82654 pir JUA0086 - 10K zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2128, 2130)	Novel Protein sim. GBank gij2120998 pir S70682 - glycosyltransferase homolog - <i>Bordetella pertussis</i>		transferase	264600, 264602, 264689
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gij2506362 sp P15042 DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))		synthase	265009
1067	10132178 (2133, 2134)				264909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4007669 emb CAA22355 - (AL034443) putative oxidoreductase [<i>Streptomyces coelicolor</i>]	Contains protein domain (PF00248) - Aldo/keto reductase family	reductase	264688, 18108362, 264558, 264600, 264760
1069	83002954 (2137, 2138)	Novel Protein sim. GBank gij4589484 dbj BAA76770.1 - (AB023143) KIAA0926 protein [<i>Homo sapiens</i>]		UNCLASSIFIED	264604
1070	82101992 (2139, 2140)	Novel Protein sim. GBank gij120304 sp P15932 FLGK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)		UNCLASSIFIED	264604, 264760
1071	20710589 (2141, 2142)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [<i>Pseudomonas aeruginosa</i>]		synthase	264602
1072	82356540 (2143, 2144)			UNCLASSIFIED	264687, 264688, 21908764, 35696052, 35695917, 35695855, 264600, 264601, 264602, 265009, 264605, 264508, 264905, 264690, 264908, 264762, 264628, 264766
1073	79814400 (2145, 2146)				264909
1074	80105992 (2147, 2148)	Novel Protein sim. GBank gij477532 pir J49175 - Match B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	264906
1075	81850293 (2149, 2150)	Novel Protein sim. GBank gij3893109 emb CAA76940 - (Y17920) CALO protein [<i>Drosophila melanogaster</i>]		UNCLASSIFIED	56994075, 22278998, 264594, 264757, 264596, 265018, 265019, 264681, 264369, 264688, 265020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij1176203 sp P46442 YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)		ATPase_associated	264769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487 sp Q44472 TUD4_AGRVI - PUTATIVE HYDROXYPYRUVATE REDUCTASE		kinase	264905
1078	20288874 (2155, 2156)				
1079	80494516 (2157, 2158)	Novel Protein sim. GBank gij3413828 emb CAA20296 - (AL031260) hypothetical protein SC9A10.09 [<i>Streptomyces coelicolor</i>]		UNCLASSIFIED	264600
1080	11767188 (2159, 2160)			UNCLASSIFIED	18108394, 264769, 264634, 264636
1081	94747080 (2161, 2162)			UNCLASSIFIED	264684
1082	81490656 (2163, 2164)			UNCLASSIFIED	83373044, 265019, 22279002, 264482, 18108351, 264682, 264908, 264693, 264487, 264758, 264768, 264769, 21906767, 264511, 264910, 264634, 264635, 264905, 264636, 264906, 264637, 264907, 264908, 264764, 264638, 20281099, 264766, 264595

1083	87446717 (2165, 2166)	Novel Protein sim. GBank gi 1722945 sp Q10523 Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427 23		UNCLASSIFIED	60424179, 264905, 264906, 264510, 60432229, 264759, 87188474, 264605, 264769, 264689, 18108364, 18108376, 35695855, 264636 264769
1084	37799308 (2167, 2168)	Novel Protein sim. GBank gi 18384 sp P32057 WCAI_ECOLI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475368 (2169, 2170)	Novel Protein sim. GBank gi 1899190 (U02004) - heat shock protein 60 [Tsukamurella tyrosinosolvens]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	60432229, 264687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gi 1172956 sp P46176 RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	264486
1087	79603979 (2173, 2174)	Novel Protein sim. GBank gi 4160198 emb CAA15431 - (AL008583) dJ327 J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHRromatin Organization MOfifier) domain	helicase	29331827, 264693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gi 2983155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aerophilus]		UNCLASSIFIED	264905, 264601, 18108387
1089	80216800 (2177, 2178)	Novel Protein sim. GBank gi 4981768 gb AAD36290.1 AE00177 - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	264488, 264511, 265011, 264682, 264768, 264689, 21906764, 35695917, 265020, 32833986, 18108370, 35695855
1090	11083825 (2179, 2180)	Novel Protein sim. GBank gi 4007680 emb CAA22366 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			264604
1091	12817471 (2181, 2182)	Novel Protein sim. GBank gi 2495582 sp P77239 YLCD_ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gi 2960098 emb CAA17996.1 - (AL022121) nt1 [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	264566 264769, 35695917, 35695855, 264600, 264602, 264603, 264605, 18108351
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gi 1001642 dbj BAA10373 - (DG4002) dGTP triphosphohydrolase [Synecocystis sp.]		UNCLASSIFIED	264686
1094	10880972 (2187, 2188)	Novel Protein sim. GBank gi 4585587 emb CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	264906, 265007, 264595, 264600, 264602, 264803, 264604, 264605, 264762, 264766, 264769, 264636, 264558, 18108387, 60432113, 264482, 264486
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gi 4585587 emb CAB40855.1 - (AL049628) putative adenine glycosylase [Streptomyces coelicolor]		synthase	264600, 264602, 264603, 264604, 264605, 35695917, 264692, 264631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gi 15001 sp P19208 BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		UNCLASSIFIED	265019
1097	79239550 (2193, 2194)	Novel Protein sim. GBank gi 114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	264687
1098	79186424 (2195, 2196)	Novel Protein sim. GBank gi 114135 sp P08205 ARGA_ECOLI - AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)			

1099	39523838 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (M1G- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	264603	
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp O64420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	264259, 264636	
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	264769	
1102	79777814 (2203, 2204)	Novel Protein sim. GBank gi 1906596 (U81788) - kinesin-73		UNCLASSIFIED	264910, 264909	
1103	81897259 (2205, 2206)	[Drosophila melanogaster]		struct	264757	
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2935448 (AF048976) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21908754, 264555, 264556, 264558, 22279002	
1105	80255121 (2209, 2210)				264566	
1106	79314110 (2211, 2212)			UNCLASSIFIED	264555, 264369	
1107	80470019 (2213, 2214)				264908, 264769	
1108	80440616 (2215, 2216)	Novel Protein sim. GBank gi 1173421 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		transport	264907, 264510, 264511, 264600, 264602, 264605, 264768, 264769	
1109	80064615 (2217, 2218)	Novel Protein sim. GBank gi 2995310 emb CAA18338 - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	264602, 264605, 264636	
1110	80503554 (2219, 2220)					
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2622039 (AE000868) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			264908, 264593, 265010, 264601, 264603, 264604, 264605, 264682, 264769, 264693, 264636	
1112	95010088 (2223, 2224)				18108370, 264557	
1113	82456352 (2225, 2226)	Novel Protein sim. GBank gi 3218376 emb CAA19628 - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	264908 264600, 264602, 264604, 264605, 264762, 264769, 264565	
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir J554876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	264636	
1115	11765583 (2229, 2230)					
1116	79841152 (2231, 2232)			UNCLASSIFIED	264686	
					264908	

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gi 3255965 emb CAA94089 - (Z70200) U5 snRNP-specific 200kD protein [Homo sapiens]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108392, 264488, 263994, 264489, 18108398, 56182575, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264909, 52644045, 56182435, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264596, 264758, 264759, 21906754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264604, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 264448, 264682, 264764, 264683, 264288, 264389, 264684, 264685, 264766, 264767, 264686, 264687, 264768, 264769, 264688, 18108359, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 264691
1118	79563326 (2235, 2236)			UNCLASSIFIED	264907
1119	79642463 (2237, 2238)			UNCLASSIFIED	
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		collagen	29331827, 265018, 265019, 264681, 265021, 60170615, 18108387
1121	79471716 (2241, 2242)	Novel Protein sim. GBank gi 1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264683, 264632, 18108388
1122	79456246 (2243, 2244)			UNCLASSIFIED	264639, 264563
1123	79637119 (2245, 2246)	Novel Protein sim. GBank gi 98800 pir S17768 - 3-dehydroquinase synthase (EC 4.6.1.3) - Mycobacterium tuberculosis		synthase	264693, 27486265
1124	79811596 (2247, 2248)			UNCLASSIFIED	264909
1125	79757861 (2249, 2250)			UNCLASSIFIED	264910
1126	79758914 (2251, 2252)	Novel Protein sim. GBank gi 138154 sp P03643 VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)		eph	264905, 264909, 264910
1127	11800930 (2253, 2254)			UNCLASSIFIED	264682
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gi 5002704 emb CAB44358.1 - (AJ242630) DNA polymerase I [Methylobacterium sp. DMA]	Contains protein domain (PF00476) - DNA polymerase family A	UNCLASSIFIED - polymerase	264511

1129	80422480 (2257, 2259)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264766
1130	79420151 (2259, 2260)	Novel Protein sim. GBank gi 4981328 gb AAD35881.1 AE001174 - (AE001174) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264595
1131	80055391 (2261, 2262)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	35696286, 22278998, 29331828, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank gi 1841552 (U89336) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 264906, 265009, 264600, 264602, 264604, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80029393 (2269, 2270)	Novel Protein sim. GBank gi 4539171 emb CAB39700.1 - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264600, 264602, 264603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank gi 4982454 gb AAD36931.1 AE001823 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank gi 4972746 gb AAD34768.1 - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22278998, 22278999, 35696052, 264907, 265009, 60433356, 264596, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811576, 35695855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank gi 731607 sp P3879YHC8_YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR	struc		264908
1139	78633561 (2277, 2278)	Novel Protein sim. GBank gi 3650031 (AC005396) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	79638019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635848 (2283, 2284)			UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank gi 3928000 emb CAA05880 - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain		56182575, 264908, 264600, 264632, 87168518
1144	80086988 (2287, 2288)			UNCLASSIFIED	264635, 264636, 264907, 264593, 264908, 264566, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35696286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank gi 2499003 sp P76422 THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP- PHOSPHATE KINASE) (HMP-P KINASE)	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank gi 2896734 emb CAA17213.1 - (AL021897) hypothetical protein Rv1097c [Mycobacterium tuberculosis]			264591

1150	81325074 (2298, 2300)	Novel Protein sim. GBank gij2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase associated	264488, 35696286, 264907, 264908, 264909, 264910, 264593, 264596, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264564, 264566, 264567, 264595
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gij4324655[gib AAD16978] - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gij3874275[jemb CAB07311.1] - (Z92825) predicted using GeneFinder. Similarity to Yeast low affinity glucose transporter HXT4 (PS:32467); cDNA EST EMBL: C12555 comes from this gene; cDNA EST yk4D4c10.3 comes from this gene; cDNA EST yk4D4c10.5 comes from thi...		glycoprotein	264488, 22278988, 264905, 264629, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gij4240315[dbj BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557, 265008
1154	83002995 (2307, 2308)			UNCLASSIFIED	264690, 264636, 264603
1155	79411098 (2308, 2310)	Novel Protein sim. GBank gij586655[jsp P37617 ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZINC)-TRANSLATING P. TYPE ATPASE]	Contains protein domain (PF00122) - E1-E2 ATPase		
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gij418480[jsp P32139 YJHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION]		UNCLASSIFIED	264906, 264907, 264758, 264766, 264769, 264689, 264638, 264566
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gij2496481[jsp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C]		UNCLASSIFIED	264906, 264762, 264687, 264769, 264689, 18108374, 35695855
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gij2496481[jsp Q50724 Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C]			264687
1159	76186451 (2317, 2318)	Novel Protein sim. GBank gij1138406[dbj BAA11490] - (D79995) similar to pig tubulin-tyrosine ligase. [Homo sapiens]			29331822, 29331824, 66714117, 29331828, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563, 264369
1160	91229893 (2319, 2320)			UNCLASSIFIED	264693
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gij2443342[dbj BAA22380] - (D88764) alpha 2 type I collagen [Rana catesbeiana]		UNCLASSIFIED	29331827, 264906
1162	79635357 (2323, 2324)	Novel Protein sim. GBank gij4503375[jef NP_001376.1 pDPYS - dihydropyrimidinase]		UNCLASSIFIED	18108398, 29331827, 29331828, 29146498, 29146499, 18108354, 21906768, 29148827, 21906769, 264693, 18108382, 18108385
1163	79563186 (2325, 2326)	Novel Protein sim. GBank gij5052554[jgb AAD38607.1 AF145632] - (AF145632) BcDNA GH06032 [Drosophila melanogaster]		transport	264602, 264605, 264769, 18108370, 18108374, 264565
1164	79650829 (2327, 2328)	Novel Protein sim. GBank gij5052554[jgb AAD38607.1 AF145632] - (AF145632) BcDNA GH06032 [Drosophila melanogaster]		UNCLASSIFIED	264488, 35696286, 22278989, 264259, 66714117, 60432289, 35696052, 264905, 56182435, 265006, 60433438, 264759, 21906754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113
1165	80491888 (2329, 2330)				
1166	88096456 (2331, 2332)	Novel Protein sim. GBank gij4589476[dbj BAA76766.1] - (AB023139) KIAA0922 protein [Homo sapiens]			

1167	79963862 (2333, 2334)	Novel Protein sim. GBank gi 2580433 dbj BAA23138 - (D76414) ppGpp hydrolase [Staphylococcus aureus]		kinase	264488
1168	88094678 (2335, 2336)			UNCLASSIFIED	264259, 29331827, 56182435, 60433438, 265019, 33657023, 35695855, 264566
1169	11805403 (2337, 2338)			UNCLASSIFIED	264681
1170	21632244 (2339, 2340)			UNCLASSIFIED	264602
1171	20434582 (2341, 2342)	Novel Protein sim. GBank gi 2772914 (AF029249) - procollagen D [Mytilus edulis]		UNCLASSIFIED	264556
1172	79610113 (2343, 2344)	Novel Protein sim. GBank gi 4757846 ref NP_004317.1 pBCL9 - B-cell CLL lymphoma 9		UNCLASSIFIED	55810764, 35696052, 264634, 264486
1173	80235713 (2345, 2346)	Novel Protein sim. GBank gi 2564053 dbj BAA22946 - (AB007832) Bm trachealless [Bombyx mori]			264508, 264906, 264907, 264909, 264591, 264632, 264638, 264639
1174	20293077 (2347, 2348)	Novel Protein sim. GBank gi 2911027 emb CAA17520 - (AL021958) mmsA [Mycobacterium tuberculosis]		dehydrogenase	264600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank gi 118333 sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	264601
1176	80252845 (2351, 2352)	Novel Protein sim. GBank gi 1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00586) - AIR synthase related protein	synthase	264509, 264905, 264593, 264602, 264605
1177	80064647 (2353, 2354)	Novel Protein sim. GBank gi 119791 sp P28643 FABG_CUPLA - 3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00106) - short chain dehydrogenase	reductase	264605
1178	94128641 (2355, 2356)	Novel Protein sim. GBank gi 5031697 ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase associated	65274572, 18108398, 22278998, 22278999, 29331826, 264508, 264908, 264828, 33657402, 33109954, 264769, 21906765, 21906766, 21906768, 55811957, 33657023, 264629, 55811576, 35696423, 264636, 264556, 56182323, 60432113, 22279000, 22279002
1179	80055575 (2357, 2358)	Novel Protein sim. GBank gi 2960030 emb CAA17988.1 - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00496) - Bacterial extracellular solute-binding proteins, family 5	transport	264603
1180	11794446 (2359, 2360)	Novel Protein sim. GBank gi 2558614 emb CAA04787 - (AJ001493) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	264638
1181	17946362 (2361, 2362)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	265017
1182	81494284 (2363, 2364)				265007, 265008, 264564, 264909, 264693
1183	79574044 (2365, 2366)	Novel Protein sim. GBank gi 4091877 (AF061331) - alpha galactosidase precursor [Saccharopolyspora erythraea]		UNCLASSIFIED	264689, 35696423, 264638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank gi 2129478 pir J51939 - chitinase (EC 3.2.1.14) precursor - beet		glycoprotein	264602
1185	79491185 (2369, 2370)				263967

1186	20224012 (2371, 2372)				UNCLASSIFIED	264559	
1187	79248834 (2373, 2374)				UNCLASSIFIED	29331825, 265017, 18108351	
1188	79831387 (2375, 2376)	Novel Protein sim. GBank gi 2996039 (AF054525) - hypothetical protein [Synecococcus PCC7002]			UNCLASSIFIED	264905, 264906	
1189	79609367 (2377, 2378)					264892	
1190	79930589 (2379, 2380)				UNCLASSIFIED	265018	
1191	80310105 (2381, 2382)				UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486	
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRFamide related peptide family			264636	
1193	11103584 (2385, 2386)				UNCLASSIFIED	263978	
1194	78893947 (2387, 2388)	Novel Protein sim. GBank gi 854065 emb CAA58337 (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	265007, 265008	
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1790277 (AE000459) - putative oxidoreductase [Escherichia coli]			UNCLASSIFIED	264605	
1196	13000688 (2391, 2392)					264689	
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2497360 sp Q50715 IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain		dehydrogenase	264594	
1198	95290101 (2395, 2396)					264603	
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1709525 sp P54673 P3K1_DICD1 - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)				264259, 264757, 33109954, 21906768	
1200	9848880 (2399, 2400)						
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 2499877 sp P70645 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)			UNCLASSIFIED	264910	
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 606342 (U18997) - ORF_0622; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]			cathepsin	264766, 264769	
1203	82125373 (2405, 2406)				ribosomalprot	264600, 264558	
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT			UNCLASSIFIED	264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909, 264766	
1205	8053961 (2409, 2410)					264905, 264769, 264636	
1206	80241985 (2411, 2412)				UNCLASSIFIED	264566	
1207	79841192 (2413, 2414)				UNCLASSIFIED	264556, 264557, 264558	
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2-related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family			29331824, 264909, 265021, 18108370, 29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689	

1209	79185742 (2417, 2418)	Novel Protein sim. GBank gi 1175033 sp P44398 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	264687, 264688
1210	56426884 (2419, 2420)			UNCLASSIFIED	264907, 264693
1211	94656555 (2421, 2422)	Novel Protein sim. GBank gi 421095 pr JIS0688 - hypothetical protein o246 - Escherichia coli		transferase	264591, 264592, 264595
1212	79167929 (2423, 2424)	Novel Protein sim. GBank gi 3880625 emb CAB07858 - (Z93785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		264689, 263967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gi 226292 pr JIS05375A - vir gene [Bordetella pertussis]		kinase	264909
1214	10144306 (2427, 2428)	Novel Protein sim. GBank gi 5726285 gb AAD48396.1 AF12616 - (AF126162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	264908
1215	80050108 (2429, 2430)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z98269) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 264601, 264602, 264603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi 417329 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOLPYRUVYLTRANSFERASE) (EPT)		transferase	264604
1217	95011344 (2433, 2434)			UNCLASSIFIED	264905, 264907, 264908, 264591, 264766, 264691, 264693, 264629, 264630, 264636, 264564 264601
1218	11093680 (2435, 2436)	Novel Protein sim. GBank gi 1805460 dbj BAA09022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		dehydrogenase	
1219	91216252 (2437, 2438)				56181686, 29331822, 60432289, 264601, 264692, 264629
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi 4240315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	52844507, 264905, 264909, 265008, 265019, 265020, 52644150, 33657023, 264693, 33657182, 35695763, 264634, 22279000, 22279002, 264482
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi 2143886 pr JIS2523 - nucleoporin p82 homolog - rat (fragment)		UNCLASSIFIED	264768, 265020, 264906
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi 730805 sp P39663 SPHR_SYN7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00486) - Transcriptional regulatory protein, C terminal	phosphatase	264601
1223	11615647 (2445, 2446)				264593
1224	80432645 (2447, 2448)	Novel Protein sim. GBank gi 1172627 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	264593, 264600, 264601, 264603, 264605, 264768, 18108376, 264635, 18108387

1225	80434427 (2449, 2450)	Novel Protein sim. GBank gij2105050[emb]CAB08836] - (Z95436) hypothetical protein Rv3644c [Mycobacterium tuberculosis]			264768
1226	80237518 (2451, 2452)	Novel Protein sim. GBank gij1706768[sp]P98133[FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)]	polymerase		264905, 264512, 264689
1227	79422138 (2453, 2454)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	UNCLASSIFIED		264908, 264637, 264639
1228	79209027 (2455, 2456)	Novel Protein sim. GBank gij1653901[dbj]BAA18811] - (D90917) acriflavine resistance protein [Syrnechocystis sp.]			264605, 264634
1229	94329135 (2457, 2458)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	UNCLASSIFIED		87168474, 265011, 87168559, 264681, 264689, 264693, 65274820, 18108374
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230[sp]P28598[CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)]	UNCLASSIFIED	- eph	264909, 264605, 18108388
1231	79843141 (2461, 2462)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED	transport	264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij116298[sp]P20730[CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)]	UNCLASSIFIED		264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED		265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED	histone	265008, 265010, 18108381
1235	79914423 (2469, 2470)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			264634, 264762
1236	81927147 (2471, 2472)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED		265018, 55811150, 264565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	glycoprotein		264259, 28331822, 28331824, 35696052, 264508, 264906, 52644045, 52646317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	oncogene		264509, 264511, 264759, 264760, 264764, 264557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			264769
1242	79775890 (2483, 2484)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]	UNCLASSIFIED		264601, 264604, 264638
					264906, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank gij335567[emb]CAA19971] - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank gij2970646 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank gij4586338[jdb]BAA76357.1] - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF00115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank gij3581849[emb]CAA20805] - (AL031541) putative phenylalanine-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank gij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank gij1352403[sp]P09467[F16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 29331826, 264106, 264508, 264907, 264828, 285009, 60433356, 264757, 264758, 21906754, 265010, 265011, 265018, 265019, 264760, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank gij2791407[emb]CAA16001] - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]		transport	264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2499, 2500)	Novel Protein sim. GBank gij112785[sp]P05100[3MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)]		UNCLASSIFIED	264689
1251	78850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264683, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank gij567017[gb]AAD46616.1[AF16131 - (AF161317) NRAMP manganese transport protein MntA [Salmonella typhimurium]		glycoprotein	264600, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank gij103160[pir]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906767, 55811957, 264892, 264556, 264639
1255	78169728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank gij2995353[emb]CAA04608.1] - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	60432289, 264600, 264605, 264764, 264687, 264769, 264689, 27486265, 18108374, 18108376
1257	80201435 (2513, 2514)	Novel Protein sim. GBank gij3193306 (AF069300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)			UNCLASSIFIED	264602, 263978
1259	80186012 (2517, 2518)			UNCLASSIFIED	264906, 264448, 264908
1260	80084606 (2519, 2520)			UNCLASSIFIED	264634, 264639

1261	87412802 (2521, 2522)	Novel Protein sim. GBank gjl5689511[dbj]BAA83039.1] - (AB029010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	- cadherin	29331824, 264906, 264909, 264768, 264769, 264689, 264693, 264639, 18108384, 264563, 264634
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gjl95100[pir]S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	
1263	20710997 (2525, 2526)			struct	264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gjl3550958 (AF004840) - CDO [Rattus norvegicus]			264634
1265	80253578 (2529, 2530)			UNCLASSIFIED	264563
1266	79914604 (2531, 2532)			UNCLASSIFIED	264768, 264636, 264638, 264567
1267	80556918 (2533, 2534)	Novel Protein sim. GBank gjl1085002[pir]S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	264259, 21906754, 264369
1268	88178473 (2535, 2538)	Novel Protein sim. GBank gjl4886445[emb]CAB43370.1] - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278995, 56994075, 60424269, 29331827, 264109, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87168559, 264600, 265018, 265019, 264369, 264688, 21906787, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264488
1269	79821846 (2537, 2538)	Novel Protein sim. GBank gjl3334791[emb]CAA19939] - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264906, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gjl2851634[sp]Q50591[Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	- dehydrogenase	265010, 264601
1271	79840498 (2541, 2542)			ATPase-associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gjl1655665[emb]CAB03731] - (Z81368) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)	Novel Protein sim. GBank gjl123726[sp]P10413[HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C62.5)	Contains protein domain (PF00183) - Hsp90 protein	UNCLASSIFIED	264905, 264908, 264909, 264769
1275	20730763 (2549, 2550)			- eph	264602
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gjl2129478[pir]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264369
1277	20438195 (2553, 2554)				
1278	11088365 (2555, 2556)	Novel Protein sim. GBank gjl175473[sp]P44555[YAAJ_HAEIN - HYPOTHETICAL PROTEIN H0183		UNCLASSIFIED	264556
1279	21656756 (2557, 2558)	Novel Protein sim. GBank gjl1929513 (U64318) - ATP synthase subunit beta [Moorilla thermocellae]		UNCLASSIFIED	264603
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gjl4938504[emb]CAB43862.1] - (AL078465) putative protein [Arabidopsis thaliana]		synthase	264605
				struct	263976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gj1136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	29331825, 29331828, 264766, 83373044
1282	87537695 (2563, 2564)	Novel Protein sim. GBank gj13328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	265008
1283	20466305 (2565, 2566)	Novel Protein sim. GBank gj13261721 (emb) CAB070571 - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	264605
1284	20636325 (2567, 2568)	Novel Protein sim. GBank gj13929022 (AF057696) - LspB [Haemophilus ducreyi]			264604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gj14171541 (sp) p33126HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - Hsp90 protein	eph	264766, 264689, 263967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gj12078004 (emb) CAB08451 - (Z95207) gorA [Mycobacterium tuberculosis]		reductase	264605, 264639
1287	80417530 (2573, 2574)			UNCLASSIFIED	265011, 264602, 264766, 264687, 264769, 264689, 18108370, 264636, 18108385, 264563
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gj15353510 (gb) AAD42161.1 (AF08891) - (AF088916) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - C1q domain	collagen	35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 33657402, 264595, 264758, 265011, 265019, 264760, 18108351, 264681, 264764, 264288, 264685, 264766, 264687, 264768, 264769, 265020, 285021, 264534, 264692, 18108370, 264628, 18108374, 35696423, 264555, 264556, 264557, 264558, 18108385, 264564, 264566, 264567, 264486, 18108391
1289	11813647 (2577, 2578)	Novel Protein sim. GBank	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	264637
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gj11699951 (sp) P46023GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR		im7	264563
1291	80470268 (2581, 2582)	Novel Protein sim. GBank gj12072674 (emb) CAB08305 - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	265007, 265008, 264769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gj11835755 (U86338) - zinc finger protein Png-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	264092, 264259, 29331822, 29331824, 264508, 264908, 264909, 264512, 265008, 265009, 264591, 265019, 264369, 264288, 264686, 264768, 264693, 18108374, 264632, 56182323, 264639, 83373044, 22279002, 264482, 264563
1293	80067536 (2585, 2586)	Novel Protein sim. GBank gj12129173 (pir) IF64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	265006, 55812038, 264369, 264556
1294	82125908 (2587, 2588)			biotindep	264602, 264605, 264760, 18108351, 264689, 33657023, 264559
1295	11686851 (2589, 2590)	Novel Protein sim. GBank gj15441779 (emb) CAB6803.1 - (AL096811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]		dehydrogenase	264689

1296	11687904 (2591, 2592)	Novel Protein sim. GBank			UNCLASSIFIED	264591, 264639
1297	79639300 (2593, 2594)	Novel Protein sim. GBank gi 4982191 gb AAD36686.1 AE001805 DNA- directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'-3' exonuclease		polymerase	264693
1298	84239506 (2595, 2596)	Novel Protein sim. GBank gi 1943770 (U97191) - F53F10.1 gene product [Caenorhabditis elegans]			struct	18108348, 265017
1299	80255378 (2597, 2598)	Novel Protein sim. GBank gi 3445181 (AC005498) - R31665_2 [Homo sapiens]				
1300	80064867 (2599, 2600)	Novel Protein sim. GBank gi 4062973 dbj BAA36204.1 - (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box		transcriptfactor	264488, 264906, 264909, 22278002, 264566 264605
1301	17839814 (2601, 2602)	Novel Protein sim. GBank gi 3242273 emb CAB07017 - (Z92669) hypothetical protein Rv0236c [Mycobacterium tuberculosis]			UNCLASSIFIED	264906
1302	95416188 (2603, 2604)					85658542, 265020
1303	9684121 (2605, 2606)					264908
1304	79377196 (2607, 2608)				UNCLASSIFIED	264508
1305	19905899 (2609, 2610)					264566
1306	13069230 (2611, 2612)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			UNCLASSIFIED	264636
1307	82201029 (2613, 2614)	Novel Protein sim. GBank gi 1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120		UNCLASSIFIED	264907, 264592, 264764
1308	21426814 (2615, 2616)	Novel Protein sim. GBank gi 95819 pir S16298 - ferric enterobactin transport protein fepC - Escherichia coli			transport	264555
1309	78263011 (2617, 2618)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			UNCLASSIFIED	264906, 18108354
1310	20466319 (2619, 2620)	Novel Protein sim. GBank gi 5459220 emb CAB48893.1 - (AL096837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]			UNCLASSIFIED	264605
1311	87613142 (2621, 2622)					35696286, 29331827, 264908, 265008, 264764, 264766, 264686, 21908787, 21906769, 35695917, 264691, 264693
1312	88061720 (2623, 2624)	Novel Protein sim. GBank gi 4455118 gb AAD21084 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		dna_rna_bind	22278995, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21906768, 265020, 265021, 33657023, 22279002, 264564
1313	91225458 (2625, 2626)	Novel Protein sim. GBank gi 4929733 gb AAD34127.1 AF15189 - (AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16		ribosomalprot	22278998, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906765, 21906767, 29148627, 21908768, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390
1314	56926053 (2627, 2628)					264693
1315	84357192 (2629, 2630)	Novel Protein sim. GBank gi 2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		interleukinrecept	264691

1316	85381609 (2631, 2632)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181686, 20281171, 29331822, 29331824, 60424269, 29331825, 3586052, 52644045, 264591, 60432229, 265018, 265019, 55811150, 56181562, 21906765, 21906767, 21906768, 35695917, 60170615, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87168518, 60432113, 22279002, 264564
1317	88055167 (2633, 2634)	Novel Protein sim. GBank gi 4836757 gb AAD3054.1 AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 264906, 264909, 264369, 264684
1318	95322893 (2635, 2636)	Novel Protein sim. GBank gi 4680204 gb AAD27567.1 AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	94238546 (2637, 2638)				264908, 264909, 265006, 265008, 264592, 265019, 264766, 56181562, 18108368, 264628, 264629, 18108377, 264636
1320	86603587 (2639, 2640)	Novel Protein sim. GBank gi 4240183 dbj BAA74870.1 - (AB020654) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696288, 55812038, 265018, 21906768, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank gi 4686505 emb CAB43377.1 - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcription factor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank gi 5262591 emb CAB45736.1 - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264693, 264404
1323	94845931 (2645, 2646)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87168474, 18108351, 264288, 21906766, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278996, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 265018, 264288, 264768, 264769, 21906768, 265022, 18108376, 264631, 264632, 264634, 264636, 264638, 264563, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank gi 3294501 UG4857 - similar to the DPT/Kunitz family of inhibitors, most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF000090) - Thrombospondin type 1 domain	protease	35696288, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85658542, 264760, 264768, 264769, 264691, 35696423
1326	87316289 (2651, 2652)	Novel Protein sim. GBank gi 397275 U61947 - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 264682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 284091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21908754, 265010, 265011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264685, 264768, 264688, 21908767, 21908769, 29148629, 285020, 284690, 264691, 264692, 264693, 263957, 33657109, 33657182, 27486282, 33657349, 18108370, 18108374, 55810764, 35695855, 264634, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	264488, 22278997, 29331828, 264595, 18108351, 264766, 22279002, 264482, 264567
1329	87755276 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26969.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2659, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265019, 265021, 264555, 264558, 56528488
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 dbj BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 35696052, 29331828, 60170831, 264448, 264686, 21906765, 55811957, 265020, 33657023, 33657109, 263973, 55811576, 35696423, 35695855, 56182323
1332	84845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 dbj BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]	synthase		65274572, 22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 21908754, 87168559, 265018, 265019, 264448, 264288, 264369, 264686, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	86098476 (2665, 2666)	Novel Protein sim. GBank gi 5689527 dbj BAA83047.1 - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526486
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662536 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]	phosphatase		264905
1335	87644798 (2669, 2670)	Novel Protein sim. GBank gi 4240285 dbj BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21906754, 87168559, 265017, 264288, 21906765, 21908767, 21908768, 21908769, 265020, 33657109, 27486284, 18108374, 264556, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi 465445 sp P33485 VNUA_PrvKA - PROBABLE NUCLEAR ANTIGEN			264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi 5689471 dbj BAA83019.1 - (AB028990) KIAA1067 protein [Homo sapiens]		UNCLASSIFIED	56182575, 56994075, 22278998, 22278999, 264092, 264259, 60432289, 29331826, 264906, 264908, 264909, 264112, 265008, 265009, 60433356, 55812038, 33657084, 265011, 265017, 265018, 265019, 264682, 264448, 264683, 264369, 264688, 264689, 21906768, 21906769, 265020, 264691, 27486261, 20281069, 18108379, 55811576, 35695855, 56182323, 60432113, 22279002, 264567
1338	80366114 (2675, 2676)			UNCLASSIFIED	29331822, 265010, 264288, 264689, 18108370, 35695855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	35696052, 264909, 264688, 264556, 264558
1340	88316311 (2679, 2680)				264905, 264907, 87168559, 264764
1341	86101485 (2681, 2682)				264681, 264685, 264686, 264692
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi 5019564 emb CAB44507.1 - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Contains protein domain (PF00001) - Im7 7 transmembrane receptor (rhodopsin family)		264629
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi 4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2	Contains protein domain (PF00560) - struct Leucine Rich Repeat		264910, 264686, 264534
1344	20562559 (2687, 2688)				263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi 2144101 pir I55210 - tricarboxylate carrier - rat (fragment)		glycoprotein	264909, 60170394
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi 3881052 emb CAA19523 - (AL023843) predicted using GeneFinder; similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 264568
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi 4504379 ref NP_003658.1 pHG38 - orphan G protein- coupled receptor HG38	Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		264908, 264908, 264909, 265006, 264910, 265011, 265017, 264764, 264766, 264767, 264769, 264631, 264634, 264638, 264567, 264486
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi 3399720 dbj BAA32100 - (AB010999) peptidylarginine deiminase type IV [Rattus norvegicus]		UNCLASSIFIED	264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 264592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264486

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101 pir 55210 - tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52646842, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264591, 60433438, 264757, 21906754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22279000, 22279002, 264583, 264584
1350	87093136 (2699, 2700)			UNCLASSIFIED	52646842, 264259, 29331825, 264908, 264511, 264604, 264288, 21906769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22279002, 264486
1351	87361327 (2701, 2702)	Novel Protein sim. GBank gij4887239 gb AAD32246.1 - (AF064584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101 pir 55210 - tricarboxylate carrier - rat (fragment)			35696286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264596, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264583, 264584, 264566
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4889108 gb AAD27763.1 AF07703 - (AF077030) hypothetical 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 29331826, 264906, 265008, 33657402, 21906754, 265011, 87168559, 264684, 264398, 264769, 264689, 21906765, 21906768, 52644150, 33657023, 264692, 264693, 18108374, 83373044, 87168518, 22279000
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij1469199 gb BAA09487 - (D50828) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21906754, 265010, 264769, 264689, 21906765, 21906768, 264532, 27486262, 264629, 264636, 264556, 264638, 264639, 264482, 264484

1356	95313981 (2711, 2712)	Novel Protein sim. GBank gj1113865 (U40342) - ninein [Mus musculus]			sludr	18108397, 22278995, 22278996, 22278998, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264764, 18108354, 264689, 21906765, 265022, 18108384, 35696423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gj897693[emb]CAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]		Contains protein domain (PF01852) - START domain		264259, 29331822, 29331825, 264510, 87168559, 265018, 264448, 264288, 21906765, 21908766, 21908768, 265021, 264893, 18108376
1358	38719455 (2715, 2716)	Novel Protein sim. GBank gj556219 (L36831) - transcription regulator [Mus musculus]				264757
1359	87771643 (2717, 2718)				UNCLASSIFIED	264907, 264809, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gj2588282[emb]CAA75612] - (Y15417) acetate--CoA ligase [Coprinus cinereus]			synthase	18108374, 264634, 264635, 264638, 264639, 18108385, 264486, 264567
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gj5689443[db]BAA83005.1] - (AB028976) KIAA1053 protein [Homo sapiens]		Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	60432289, 264605
1362	95287961 (2723, 2724)	Novel Protein sim. GBank gj5689411[db]BAA82989.1] - (AB028960) KIAA1037 protein [Homo sapiens]		Contains protein domain (PF00400) - WD domain, G-beta repeat	eph	35696286, 22278997, 22278999, 264259, 29331826, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264683, 264288, 264766, 264769, 264689, 21908768, 265020, 265021, 33657023, 55811576, 35696423, 264634, 60432113, 22279002, 264482, 264486
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gj1130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]		Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	56182575, 56181686, 60432049, 264259, 29331822, 56182181, 29331827, 35696052, 29331828, 264905, 264906, 264908, 264595, 55812038, 85658542, 55811150, 264681, 264288, 264369, 56181562, 60431528, 55810764, 35696423, 60431850, 264558
1364	88179488 (2727, 2728)					264488, 29331826, 264907, 264687, 264689, 264693
1365	83003108 (2729, 2730)	Novel Protein sim. GBank gj4589562[db]BAA76803.1] - (AB023176) KIAA0959 protein [Homo sapiens]				60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21908766, 35696423, 60432113
1366	87003282 (2731, 2732)	Novel Protein sim. GBank gj1084944[pir]S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)			oncogene	264766
				Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265007

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gi 4884088 emb CAB43240.1 - (AL050019) hypothetical protein [Homo sapiens]	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52646842, 52646365, 22278995, 56994075, 35696286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265009, 60170831, 33657402, 55812038, 21908754, 265011, 87168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264369, 264686, 264767, 264689, 21908765, 21906766, 21906768, 21906769, 55811957, 265020, 265021, 265022, 264534, 60170615, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gi 464561 sp P35289 RB15_RAT RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87168559, 264600, 264601, 264760, 264764, 264765, 264768, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264486, 264567, 265008, 60432229, 60433356, 33657084, 21906764, 21906769, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gi 2062702 (U90550) - butyrophilin [Homo sapiens]		UNCLASSIFIED	
1370	95316910 (2739, 2740)	Novel Protein sim. GBank gi 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 28331822, 29331824, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264768, 21906767, 35695917, 18108362, 35696423, 264632, 264635, 264636, 264555, 264638, 264558, 264639, 18108385, 65274727, 264404, 264563, 264566, 264486
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gi 5032203 ref NP_005714.1 TSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 284758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657182, 33657349, 35695855, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gjl840708dbj[BAA09334] - (D50685) trans-sialidase [Trypanosoma cruzi]		collagen	263978	264769, 21906765, 21906767, 22278999, 264691, 264910, 55812038, 265010, 264681, 264684
1373	80499421 (2745, 2746)			UNCLASSIFIED		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 65274791, 264555, 264556, 264557, 83373044, 60432113
1374	95087036 (2747, 2748)	Novel Protein sim. GBank gjl11876[pir][JC1241 - beta-interferon-induced protein - rat		interferon		52644507, 52645156, 52646842, 52646365, 56182575, 56181686, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 60432229, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264906, 264907, 264908, 29331830, 264909, 265006, 264511, 265007, 265008, 265009, 33657402, 60433356, 52646317, 33109954, 33657084, 52644296, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 27486261, 33657349, 27486265, 35695763, 18108376, 55810784, 35698423, 35698555, 264630, 264631, 264634, 264636, 264555, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264553, 264564, 264566, 264567
1375	84236942 (2749, 2750)	Novel Protein sim. GBank gjl5649176[gbl][AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase		264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35696052, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264909, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526488, 265010, 265011, 264800, 264563, 264762, 264564, 264565, 264764, 264486, 264766
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gjl138350[sp][P28968][VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22279002
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gjl1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		

1378	87595071 (2755, 2756)	Novel Protein sim. GBank gi 4107015 dbj BAA36293 - (AB001772) PEM-5 [Ciona savignyi]				22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264369, 264288, 29148627, 55811957, 264691, 18108368, 33657109, 18108368, 264635, 263981, 18108385, 265020
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gi 3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]				264510, 264512, 265009, 264288, 264564
1380	87627862 (2759, 2760)	Novel Protein sim. GBank gi 4637737 gb AAD30662.1 - (AF098834) germ cell specific Y-box binding protein [Homo sapiens]			nucl_rept	
1381	88179656 (2761, 2762)	Novel Protein sim. GBank gi 4731580 gb AAD28508.1 AF12538 - (AF125384) L82A [Drosophila melanogaster]			UNCLASSIFIED	87168559, 265017, 264628, 22279002
1382	84847576 (2763, 2764)		Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED		22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433356, 85858542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486261, 27486262, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)			UNCLASSIFIED		18108396, 264692
1384	86915895 (2767, 2768)			UNCLASSIFIED		264488, 264508, 264509, 264905, 264906, 264908, 264909, 264511, 264512, 264910, 264760, 18108351, 264766, 264769, 35695855, 264630, 264636, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gi 2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]			UNCLASSIFIED	35696052, 55811386, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gi 2384910 (AF022982) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]		Inf		60432289, 29331828, 264906, 264907, 55812435, 265011, 264681, 60170615, 33657023, 83373044, 264566
1387	87787958 (2773, 2774)	Novel Protein sim. GBank gi 4160304 emb CAA10600 - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gi 4895164 gb AAD32753.1 AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]			glycoprotein	65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265006, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1389	91256016 (2777, 2778)	Novel Protein sim. GBank gi 5689387 dbj BAA82977.1 - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29146499, 264906, 68712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 264692, 33657023, 33657349, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564, 52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264906, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644229, 21906765, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486261, 27486264, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1390	94111916 (2779, 2780)	Novel Protein sim. GBank gi 3702295 (AC005783) - R33083_1 [Homo sapiens]	peptidase		52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391, 264763, 264631
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gi 1346910 sp P28650 PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP--ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gi 726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656970, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906764, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486261, 27486262, 27486265, 33657349, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108391, 264763, 264631
1393	80409472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264629, 265009, 18108381
1394	15028819 (2787, 2788)			UNCLASSIFIED	
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gi 2274845 dbj BAA21534 - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	

1396	95563253 (2791, 2792)	Novel Protein sim. GBank gij2135904[pir]j54810 - pHL EIF1 - human			22278997, 22278999, 264259, 29331825, 60432289, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 265006, 265007, 265008, 265009, 60433356, 265010, 264802, 265017, 265018, 265019, 18108354, 52644229, 18108358, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 18108368, 18108374, 56182323, 18108385, 264563, 264567, 35696286, 264907, 66712502, 264510, 35695917, 264892, 264693, 35696423
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gij5420389[emb]CAB46880.1 - (AJ243460) proleophosphoglycan [Leishmania major]			264259, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 87168474, 265018, 265019, 264682, 264768, 21906767, 265020, 33657023, 27486261, 55811576, 264632, 264639, 83373044, 87168518, 22279002
1399	87631076 (2797, 2798)	Novel Protein sim. GBank gij2496887[sp]Q09232[YQ22, CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264768, 18108370, 264555, 264557
1400	95419064 (2799, 2800)	Novel Protein sim. GBank gij283920[pir]S27939 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	56182575, 22278994, 22278997, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264908, 56182435, 264112, 265009, 265011, 265017, 265018, 265019, 264760, 264762, 264765, 264288, 264685, 264687, 56181562, 264769, 21906766, 21906767, 55811957, 264691, 264692, 264628, 264629, 55811576, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226379 (2801, 2802)	Novel Protein sim. GBank gij3256185[emb]CAA15485 - (AL008635) dJ510H16.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 264909, 264758, 264768, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gij1515427 (U57523) - nel homolog [Homo sapiens]	Contains protein domain (PF00008) - EGF-like domain	lgl	264905, 264907, 264908, 264909, 264112, 264693, 33657109, 264634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21906765, 21906769, 264693, 55811576, 65274791, 60432113
1404	90935393 (2807, 2808)			UNCLASSIFIED	65274572, 22278998, 29331822, 29331828, 66712502, 265008, 60433438, 265017, 264693, 18108385

1405	95095088 (2809, 2810)	Novel Protein sim. GBank gij854065[embjCAA58337] - (X83413) U88 [Human herpesvirus 6]			264488, 56994075, 35696286, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264906, 264907, 264908, 264510, 264511, 264910, 33657402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33657023, 33657109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264486, 264567
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij624076[jb]AAC96425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramedum bursaria Chlorella virus 1]	collagen		264907, 264605
1407	94129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696286, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 29146498, 264107, 264908, 265006, 265008, 264910, 60433438, 285011, 265017, 18108351, 264448, 264288, 264686, 21906765, 21906769, 264692, 33657109, 18108370, 264628, 263972, 18108374, 35696423, 55811576, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95361477 (2815, 2816)	Novel Protein sim. GBank gij2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264766, 264687, 264689, 21906767, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567
1409	86644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[dbj]BAA23714] - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			264693
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2493790[sp]Q60994]ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)	Contains protein domain (PF00386) - complement C1q domain		29331826, 264112, 264512, 265009, 265010, 264601, 264686, 264769, 21906767, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gij3123155jip91343YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME I	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	22278995, 22278997, 22278999, 29331822, 60432289, 29331828, 264907, 265017, 265019, 264682, 21908767, 21908768, 21906769, 265020, 264690, 264691, 33657023, 33657109, 27486264, 264628, 263972, 264634, 264558, 18108385 264757
1412	84390919 (2823, 2824)			UNCLASSIFIED	
1413	95416559 (2825, 2826)	Novel Protein sim. GBank gij3879121[emb]CAA94370] - (Z70310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 29331822, 35696052, 29331828, 29331830, 264909, 52644045, 264510, 52644296, 85658542, 87168474, 265017, 265018, 264681, 264687, 21906768, 35695917, 265020, 52644150, 264692, 263987, 27486264, 35695763, 264639, 18108387, 264566
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gij3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264682, 264683, 265022, 264636
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gij1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 66712502, 29331830, 52644045, 264113, 264511, 33657402, 264757, 21906754, 55811386, 265017, 265018, 265019, 264761, 264683, 264369, 264288, 264686, 264689, 21906766, 21906767, 29148627, 21906769, 55811957, 265020, 265021, 264690, 33657023, 65274620, 52645129, 27486262, 27486264, 60431528, 264629, 35695855, 56182323, 264559, 60432113, 264404, 22279002, 264482

1416	94325977 (2831, 2832)	Novel Protein sim. GBank gi 5106557 gb AAD39749.1 AF12305 - (AF123052) MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 264905, 264907, 264908, 264828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264682, 264683, 264766, 52644229, 264688, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 55811957, 29148629, 265020, 52644150, 18108381, 33657023, 18108362, 18108368, 264628, 18108370, 264629, 18108374, 18108378, 55811576, 65274791, 264634, 264636, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22279000
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi 4958935 dbj BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	264107, 264448
1418	87594276 (2835, 2836)		UNCLASSIFIED	264259, 264908, 265010, 52644229, 21906764, 21906768, 264690, 264639, 18108388
1419	87757168 (2837, 2838)	Novel Protein sim. GBank gi 2072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264288
1420	87298628 (2839, 2840)	Novel Protein sim. GBank gi 5174421 ref NP_008023.1 pCPNE - copine VI (neuronal) (Z89635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)	Novel Protein sim. GBank gi 3876090 emb CAA93459.1 - (Z89635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	kinase	18108358, 18108396, 18108397, 21906766, 18108398, 21906767, 56182575, 21906768, 21906769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27486261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 60431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21906754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22279002, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	88178777 (2843, 2844)	Novel Protein sim. GBank gi 4505939 ref NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		mapolymerase	56994075, 35696286, 87168559, 55811957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00620) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264908, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264766, 264687, 21906765, 21906768, 21906767, 21906768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22279002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi 100798 pir S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi 2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21906754, 265018, 264288, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi 5616074 gb AAD45616.1 AF06194 - (AF061943) prolute- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	kinase	22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264683, 264288, 18108354, 21906765, 21906768, 29148629, 33657023, 18108374, 35695855, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi 138350 sp P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	56181686, 264259, 264907, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 65274791, 22279002, 264566
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi 1181619 dbj BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264681, 21906765, 21906767, 65274620, 55811576, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	87463004 (2863, 2864)	Novel Protein sim. GBank gi 414797 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264682, 264691

1435	94708213 (2869, 2870)	Novel Protein sim. GBank gi 3970850 dbj BAA34789.1 - (AB015330) HRIHFB2007 [Homo sapiens]		transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33656970, 264508, 264905, 66712502, 29331830, 284909, 285007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22279000, 22279002, 264563, 264482, 264565
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515 - (X56044) protein HIFC [Mus musculus]		UNCLASSIFIED	263978, 264557, 264559
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264692, 264693
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1905906 (AD000092) - hypothetical human serine-threonine protein kinase R31240_1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264906, 264909, 264757, 264600, 264601, 264605, 264768, 264769, 264890, 35698423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi 3876299 emb CAA94892 - (Z71180) similar to BPTI/KUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249e6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	264489, 18108394, 65274572, 56182575, 22278994, 22278996, 35698286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264638, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423643 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714 - (AB007902) HH-0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264887, 264259, 264906, 264907, 264908, 264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gl 493956 emb CAB11123.2 - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa. Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....	Contains protein domain (PF00646) - F-box domain.	helicase	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85658542, 87168474, 265010, 87168559, 264600, 264602, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264881, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52644150, 264691, 264692, 33657023, 65274620, 33657109, 35695763, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264486
1442	83367491 (2883, 2884)	Novel Protein sim. GBank gl 5103027 dbj BAA78765.1 - (AB023419) mSox7 [Mus musculus]		transcript factor	264906, 265007, 264693, 264558
1443	87109935 (2885, 2886)	Novel Protein sim. GBank gl 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - Spectrin repeat	struc1	52645080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gl 3874447 emb CAB02772 - (Z81039) predicted using Genefinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk278a11.5 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94990470 (2889, 2890)	Novel Protein sim. GBank gl 2959886 emb CAA11022 - (AJ222968) L-peritaxin [Mus musculus]		UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank			264369
1447	86945392 (2893, 2894)	gl 5081610 gb AAD39464.1 AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01846) - FF domain		18108396, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gl 3980411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain		29331827, 264509, 264909, 265008, 264595, 18108357, 18108385, 264566, 264486

1449	87860859 (2897, 2898)				UNCLASSIFIED	66714117, 264906, 264908, 264591, 264601, 264764, 264632
1450	87456696 (2899, 2900)	Novel Protein sim. GBank gij1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35696286, 35696052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35696423, 35695855, 56526486
1451	87797970 (2901, 2902)	Novel Protein sim. GBank gij4160304[emb]CAA10600] - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85692899 (2903, 2904)	Novel Protein sim. GBank gij2832906[dbj]BAA24608.1] - (DB9340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]			kinase	264510, 264768
1454	11204696 (2907, 2908)					
1455	87797896 (2909, 2910)				UNCLASSIFIED	264556 29331822, 66714117, 29331825, 264905, 29331830, 265006, 265008, 265009, 265011, 265019, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gij729230[sp]P41004[CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3]			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906765, 21906766, 21906767, 21906769, 29148628, 18108370, 22279000, 264107, 264556
1457	80076800 (2913, 2914)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 264102, 264107, 264110, 265009, 60432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264556
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gij5524667[gb]AAD44333.1[AF15935] Munc13-4 protein [Rattus norvegicus]			kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264556
1459	95360920 (2917, 2918)	Novel Protein sim. GBank gij5524667[gb]AAD44333.1[AF15935] Munc13-4 protein [Rattus norvegicus]			UNCLASSIFIED	29331822, 264591, 55811957, 264691, 264693, 65274620
1460	95354602 (2919, 2920)				UNCLASSIFIED	264693, 65274620
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gij1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]			- gaba Aminotransferases class-III pyridoxal phosphate	264758, 265017, 265018, 265019, 264760, 264369, 264687, 21906765, 21906768, 265022, 33657109, 27486261, 264555, 83373044
1462	87732018 (2923, 2924)	Novel Protein sim. GBank gij1770466[emb]CAA66912] - (X98259) M-phase phosphoprotein 8 [Homo sapiens]			UNCLASSIFIED	264555, 264556
1463	88090605 (2925, 2926)				- struct 'chromo' (CHRromalin Organization Modifier) domain	60432049, 264259, 29146499, 264906, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264638, 18108385, 18108388

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1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AA027743.1 AF13296 (AF132968) CGI-34 Protein [Homo sapiens]			UNCLASSIFIED	264905, 18108351, 21906765, 264486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC		18108394, 22278995, 56994075, 22278999, 29331822, 29331824, 66714117, 29331825, 29331826, 35696052, 264906, 264907, 56182435, 265007, 264758, 265018, 265019, 264760, 264784, 264288, 264685, 264686, 264768, 21906769, 55811957, 265021, 264693, 264693, 264629, 55811576, 264634, 264638, 56182323, 22279002, 264566, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - WD domain, G-beta repeat	struct		264488, 35695917, 35696286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264906, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264639, 264758, 60432113, 264604, 264605, 264565, 264566, 264764, 264486, 264685, 264766 264681, 264682, 264288, 264566
1475	86871835 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED		
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004664.1 pANGP - angiopoietin 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein		60424179, 56181686, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002
1477	87774279 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 pP1_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)		UNCLASSIFIED		264259, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1478	11754412 (2955, 2956)					264686

1479	91640140 (2957, 2959)	Novel Protein sim. GBank gi 5499741 gb AAD43978.1 AF15296 - (AF152961) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 66714117, 264906, 264907, 56182435, 265006, 60170831, 33657402, 264758, 33109954, 21906754, 265017, 265019, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 18108370, 60431528, 263976, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2959, 2960)	Novel Protein sim. GBank gi 3550456 emb CAA06329.1 - (AJ005073) Alix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 29148499, 264103, 264105, 264108, 264907, 52644045, 264112, 265007, 265008, 265009, 60433358, 60433438, 264598, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2961, 2962)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF146793) PFT27 [Mus musculus]		MHC	265006, 265007, 265010, 18108374
1482	85320442 (2963, 2964)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2965, 2966)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33109954, 265017, 264288, 21906768, 21906769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2967, 2968)	Novel Protein sim. GBank gi 1911774 bbs 180090 - (S83364) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148627, 33657023, 27486262, 18108374, 35696423, 83373044, 60432113
1485	80194441 (2969, 2970)	Novel Protein sim. GBank gi 5360129 gb AAD42883.1 AF15511 - (AF155117) NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - Kinesin motor domain	struct	264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi 4589516 dbj BAA76780.1 - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	56182575, 22278999, 264906, 264907, 21906754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566
1487	86452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB44431.1 - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	21906754, 264486
1488	87732026 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	lgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265006, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264762, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 sp Q62786 FPRP_RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21906767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35696423, 35695855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87390127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21906767, 21906768, 55811957, 60170615, 33657109, 35695855, 264635, 60170394, 56526486, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805363 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - rit [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2986)	Novel Protein sim. GBank gi 5689515 dbj BAA83041.1 - (AB029012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 52646365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52644045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264682, 264685, 264686, 52644229, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108364, 18108365, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264629, 18108374, 52644332, 56182323, 87168518, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!	Contains protein domain (PF01352) - kinase KRAB box	264907, 265009, 264769, 18108370, 55811576, 264639, 264565, 264486
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gi 4589588 dbj BAA76816.1 - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - transcript factor KRAB box	22278997, 264259, 264906, 264907, 265009, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264568, 264486, 264567
1496	87784322 (2991, 2992)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gi 3874925 emb CAA92591 - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33256 comes from this gene;....	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264910, 264758, 265011, 264764, 264288, 264690, 264634, 264635, 56526486
1498	80934938 (2995, 2996)	Novel Protein sim. GBank gi 728836 sp P39193 ALU6_HUMAN - !!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!	oncogene	264488, 65274572, 29331822, 265017, 265018, 21906765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gi 2570198 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]	glucoamylase	263978, 264566
1500	80499386 (2999, 3000)		UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gi 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus salda]	UNCLASSIFIED	264559
1502	80206141 (3003, 3004)			264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486
1503	87012701 (3005, 3006)	Novel Protein sim. GBank gi 3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:gi1171989) [Homo sapiens]	transferase Glycosyl transferases	29331822, 265007, 264369

1504	79640051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693	
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gi 473775 emb CAB41970.1 - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35696052, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 55812038, 264759, 264763, 264764, 264689, 35695917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264566	
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gi 1304201 dbj BAA06170 - (D29766) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 60432049, 264259, 52845080, 29331822, 29331827, 264108, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21908754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264369, 264687, 264689, 21906765, 29148627, 21906768, 21906769, 29148629, 52644150, 33657023, 18108376, 65274791, 56182323, 284558, 264559, 18108385, 87168518, 60432113, 22279000, 264565	
1507	83738250 (3013, 3014)	Novel Protein sim. GBank gi 5689513 dbj BAA83040.1 - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639	
1508	11618758 (3015, 3016)	Novel Protein sim. GBank gi 5031975 ref NP_005875.1 pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264593	
1509	87318451 (3017, 3018)	Novel Protein sim. GBank gi 113161 sp P28614 ACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556	
1510	95362643 (3019, 3020)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563	
1511	88318073 (3021, 3022)	Novel Protein sim. GBank gi 4559353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108396, 56994075, 60432289, 265006, 60433356, 60433438, 21906754, 87168474, 87168559, 265018, 264762, 264763, 264687, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482	
1512	95345390 (3023, 3024)	Novel Protein sim. GBank gi 1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636	
1513	87436228 (3025, 3026)					

1514	95345392 (3027, 3028)	Novel Protein sim. GBank gi 459353 gb AAD23014.1 AC00658 - (AC006585) putative extragenic suppressor protein [Arabidopsis thaliana]	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family	UNCLASSIFIED	52644507, 52645156, 52646365, 52646842, 65274572, 22278994, 35698286, 56994075, 284259, 52645080, 29331822, 29331825, 35986052, 29331830, 52644045, 56182435, 265006, 60433358, 60433438, 55812038, 21906754, 52646317, 52644296, 87168474, 87168559, 264448, 52644228, 21906765, 21906768, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108376, 35696423, 35695855, 52644332, 18108385, 18108387, 87168518, 60432113 265020, 264639
1515	79163536 (3029, 3030)	Novel Protein sim. GBank gi 387950 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33368 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...	ubiquitin		
1516	88073539 (3031, 3032)	Novel Protein sim. GBank gi 498015 (L27479) - X123 [Homo sapiens]	UNCLASSIFIED		265008, 56182323, 22278902
1517	87793325 (3033, 3034)	Novel Protein sim. GBank gi 3415134 (AF082024) - Phyb1 [Pimpinella brachycarpa]			264091, 18108370, 264404
1518	87350697 (3035, 3036)	Novel Protein sim. GBank gi 728838 sp P39195 ALU8_HUMAN - IIII ALU SUBFAMILY SX WARNING ENTRY IIII	Im7		66714117, 264508, 264509, 264905, 264510, 264910, 264591, 264595, 264288, 264766, 264769, 18108374, 264638, 264638, 264486 264569, 264489, 60432049, 265009, 33657402, 264596, 21906754, 265019, 264369, 21906765, 21906768, 21906769, 264691, 65274620, 33657182, 27486261, 18108374, 264557, 264639, 87168518, 22278902
1519	94328689 (3037, 3038)	Novel Protein sim. GBank gi 526268 emb CAB45771.1 - (AL080198) hypothetical protein [Homo sapiens]	UNCLASSIFIED		
1520	87592855 (3039, 3040)	Novel Protein sim. GBank gi 266216 dbj BA23712 - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438- bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]	UNCLASSIFIED		18108392, 60432049, 264259, 29331824, 265007, 60433356, 265010, 21906768, 264636
1521	86970696 (3041, 3042)	Novel Protein sim. GBank gi 5052351 gb AAD38516.1 AF13542 - (AF135421) GDP- mannose pyrophosphorylase B [Homo sapiens]	Contains protein domain (PF00483) - Nucleotidyl transferase	synthase	18108394, 264259, 66714117, 265011, 264603, 265019, 18108364, 35698423, 264557, 264558, 18108388
1522	78960687 (3043, 3044)	Novel Protein sim. GBank gi 3776587 (AC005388) - Strong similarity to F21B7.33 gi 2809264 from A. thaliana BAC gb AC002560. EST gb N65119 comes from this gene. [Arabidopsis thaliana]	UNCLASSIFIED		29331824, 265018, 285020, 265021
1523	91005151 (3045, 3046)		UNCLASSIFIED		63274572, 21906768, 264693
1524	80203723 (3047, 3048)		UNCLASSIFIED		
1525	87799867 (3049, 3050)	Novel Protein sim. GBank gi 4759040 ref NP_004283.1 pRIN1 - ras inhibitor	UNCLASSIFIED		264112, 21906754, 263974 264683, 264687, 264689, 264690, 264692, 264693

1526	95105344 (3051, 3052)	Novel Protein sim. GBank gij728850j P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906765, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	86262512 (3053, 3054)	Novel Protein sim. GBank gij2792496 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264288, 21906766, 21906769, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265022, 264693, 83373044, 18108385
1529	94120793 (3057, 3058)	Novel Protein sim. GBank gij4406663 gb AAD20053] - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	264488, 263994, 56182575, 22278995, 35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35696052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 285009, 264910, 60433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264766, 18108357, 264768, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 60432113, 22279002, 264563, 264564, 264486, 264567
1530	95012765 (3059, 3060)	Novel Protein sim. GBank gij2828710 (AF043642) - malrin cyclophilin [Rattus norvegicus]			264488, 264489, 35696286, 29331825, 35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gij1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - Kinase PDZ domain (Also known as DHR or GLGF).		56182575, 35696286, 264037, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811386, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264566

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gij3874716[emb CAA91265] - (Z66494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...			UNCLASSIFIED	264689
1533	94239830 (3065, 3066)	Novel Protein sim. GBank gij1490324[emb CAB01543] - (Z78141) unknown [Mus musculus]			struct	29331824, 29146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263967, 20281149, 18108374, 263981, 264566
1534	95343941 (3067, 3068)	Novel Protein sim. GBank gij81286[pir S22697] - extensin - Volvox carter (fragment)			UNCLASSIFIED	264905, 264907, 264766, 264637
1535	80936732 (3069, 3070)					65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146499, 265006, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21906768, 29148629, 265021, 265022, 18108377, 56182323, 60432113, 22279000, 22279002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gij106024[pir B32891] - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor		264686, 18108357, 18108394, 21906767, 21906768, 29148629, 3569286, 265020, 265021, 52844150, 264693, 6671417, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35695855, 265009, 264634, 264636, 264638, 18108385, 56526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	95354556 (3073, 3074)	Novel Protein sim. GBank gij3876332[emb CAB02096] - (Z79754) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk426f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...				65274572, 56182575, 60432049, 264259, 29331826, 265006, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gij403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gij3218411 emb CAA19575.1 - (AL023859) SPBC19C7.07c, putative tRNA splicing endonuclease ga mma subunit, len.284aa, similar eg. to YAR008W, YAH8_YEAST, P39707, YAR008W, tRNA splicing endonuclease gamma subunit, (275aa), fasta scores, opt:269, E(j):6.4e-2...		nuclease	22278994, 22278996, 35696286, 56594075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 265017, 265018, 265019, 18108351, 264288, 52844229, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22279000, 22279002, 264566
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gij5052634 gb AAD38647.1 AF14567 - (AF145672) BcDNA GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gij5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 55811957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264563, 264564, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gij5305702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 65274572, 29331822, 264508, 265007, 265008, 265009, 265011, 264682, 18108354, 18108355, 52644150, 18108368, 264636, 18108381, 18108382
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gij728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	264106, 33109954, 265019, 264683, 35695917, 264690, 264692, 33657109
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gij3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nucl_recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264683, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gij1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP:P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86999584 (3093, 3094)	Novel Protein sim. GBank gij2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	264259, 29331822, 66714117, 265007, 55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3095, 3096)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank gi 5689519 dbj BAA83043.1 - (AB029014) KIAA1091 protein [Homo sapiens]		eph	60424179, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264906, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 55181562, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 264691, 33857109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank gi 544463 sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	im7	65274572, 60432289, 265008, 264910, 265011, 265017, 265019, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank gi 4758566 ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 28331828, 66712502, 264764, 264288, 264686, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank gi 4589570 dbj BAA76807.1 - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	dehydrogenase	56182575, 35696286, 29146499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233069 (3107, 3108)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	transferase	35696286, 22278997, 264259, 29331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812038, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gij2257495[dijBAA21392] - (AB004534) p1015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 5264045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87168559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21906765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56526488
1556	91228268 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011, 60432229, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264564, 264486
1557	87640609 (3113, 3114)	Novel Protein sim. GBank gij3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; zlf-C3HC4.hmm, score: 34.08); most similar to drosophila goliath protein (SW: Q06003) [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278994, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22278997, 22279002, 264259, 29331822, 60432229, 35696052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1558	84840376 (3115, 3116)	Novel Protein sim. GBank gij5360105[gjAAD42871.1]AF155105 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278994, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21906754, 265017, 265018, 264448, 21906767, 265021, 265022, 33657023, 33657109, 18108370, 55811576, 83373044, 87168518, 22278997, 22279002, 264259, 29331822, 60432229, 35696052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gij112908[spP02750]A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432229, 35696052, 264107, 264110, 21906754, 33109954, 87168559, 264760, 264763, 21906764, 21906765, 21906769, 265021, 264690, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gij3880146[emb]CAA92704] - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from this gene...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263987
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87766371 (3127, 3128)	Novel Protein sim. GBank gij1168287[spP45953]ACDV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	18108394, 35696286, 264259, 29331822, 60432229, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21906754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21906765, 21906768, 265021, 60170615, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22279002, 264482

1565	87763381 (3128, 3130)	Novel Protein sim. GBank gij129726 sp P05307 PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264688, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264638, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264565, 264567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445 emb CAA20329 - (AL031266) VM106R.1 [Caenorhabditis elegans]		Inf	22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21906765, 21906767, 21906768, 21906769, 33657109, 264555, 264639, 264482, 56182575, 21906769, 264692
1567	84999006 (3133, 3134)	Novel Protein sim. GBank gij4929689 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gij4827063 ref NP_005072.1 pZNF1 - zinc finger protein 142 (clone pHZ-49)	Contains protein domain (PF00006) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21906767, 21906768, 264691, 264693, 22279000, 22279002
1569	90936668 (3137, 3138)	Novel Protein sim. GBank gij5889451 dbj BAA83009.1 - (AB028980) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265019, 264764, 21906765, 21906769, 55811957, 60170615, 52644150, 264692, 33657023, 33657109, 18108377, 264583, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731 ref NP_001081.1 pTUBG - tubulin, gamma polypeptide	Contains protein domain (PF00091) - Tubulin/FtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384
1572	81201684 (3143, 3144)			UNCLASSIFIED	35696052, 264905, 264906, 264908, 264910, 264758, 264766, 35695917, 264637
1573	80207066 (3145, 3146)			UNCLASSIFIED	263972

1574	94216142 (3147, 3148)	Novel Protein sim. GBank gi 4758334 ref NP_004256.1 pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278999, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264369, 264288, 264685, 264766, 264688, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 264690, 264691, 264693, 20281069, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264566
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gi 3881810 emb CAA94856 - (Z70783) similar to EF-hand calcium binding protein: cDNA EST EMBL: C08700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 264909, 265006, 265008, 265009, 265010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811957, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	95314019 (3151, 3152)	Novel Protein sim. GBank gi 2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 265006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264638, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gi 2499130 sp P70315 WASP_MOUSE - WISKOTT - ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gi 2978255 db BAA25190 - (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35696286, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gi 4324682 gb AAD16986 - (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87169474, 265018, 264448, 265022, 264638, 55526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gi 2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906764, 55811957, 35695917, 264692, 55811576, 264637, 56182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gij5420387[emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		phosphatase	264259, 60432289, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gij5578958[emb CAB51351.1 - (AL050306) dJ475B7.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	60170831, 33657402, 264682, 21906766, 35695855, 264563
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gij5531815[gb AAD44482.1 - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	60424179, 52645842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432289, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52644045, 56182435, 264510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811386, 52644296, 87168474, 87168559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108374, 55810764, 55811576, 35696423, 65274781, 35695855, 56182323, 83373044, 18108387, 87168518, 60432113, 22279002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gij4240132[dbj BAA74846.1 - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	- phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 285006, 265007, 265008, 60433356, 33109954, 87168474, 265011, 265017, 264604, 264369, 264288, 264685, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108388, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gij3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			265017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gij3253159 (AF005355) - translation initiation factor eIF2C [Oryzotilus cuniculus]		UNCLASSIFIED	264907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 264567
1588	87802536 (3175, 3176)	Novel Protein sim. GBank gij1077573[pir S52680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)]	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170615, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gij2137756[pir I48746 - semaphorin C - mouse (fragment)]		UNCLASSIFIED	65274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27486265, 264639, 18108385, 56526486, 60432113

1590	95319825 (3179, 3180)			UNCLASSIFIED	264489, 22278996, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 60433356, 21906754, 265017, 265018, 265019, 264448, 264765, 264288, 52644229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 58526486, 60432113, 22279000, 22279002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank		MHC	
1592	87682533 (3183, 3184)	gi 4557749 ref NP_000237.1 pmHc2 - MHC class II transactivator			
1593	94991661 (3185, 3186)			UNCLASSIFIED	
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3877072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 60432049, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35696423, 22279000, 264565, 264567
1595	79919425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	UNCLASSIFIED	264488, 29331827, 264905, 264906, 264907, 264908, 264909, 264910, 264592, 264593, 264757, 264602, 264604, 264760, 264681, 264288, 264766, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264564, 264568
1596	79933928 (3191, 3192)			UNCLASSIFIED	29331826, 264908, 55811957
1597	86971857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - cytochrome P450	UNCLASSIFIED	29146498, 264758, 263967
1598	87662039 (3195, 3196)				264092, 29331824, 264508, 264682, 264569, 264686, 264630, 264563
1599	87649829 (3197, 3198)	Novel Protein sim. GBank gi 4506797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	264259, 264634
1600	80056002 (3199, 3200)				52645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1601	15023246 (3201, 3202)				29331826, 264603, 264691, 264563
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	264635
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken		struct	29146499, 264112, 264762, 18108351, 29148627, 263974
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4768831 gb AAD29633.1 AF11682 - (AF116827) unknown [Homo sapiens]	collagen		264490, 29331824, 264907, 264909, 264511, 265008, 264592, 265010, 265011, 264762, 264764, 264369, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
			ATPase associated		263977

1605	91221129 (3209, 3210)				264905, 264509, 264906, 264907, 264908, 264909, 264604, 264768, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gi 4505313 ref NP_003794.1 pMYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	- struct	22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21908767, 21906769, 52644150, 264691, 87168518, 264689
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gi 5174473 ref NP_005888.1 p PP - Intracisternal A particle- promoted polypeptide		Transcript factor	
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gi 2224629 db BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264909, 264910, 264591, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gi 4884073 emb CAB43213.1 - (AL049934) hypothetical protein [Homo sapiens]			52644507, 52645156, 52646365, 52646842, 56182575, 22278994, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 264508, 264509, 264907, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21906754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486261, 27486262, 35695763, 264628, 18108370, 18108376, 35696423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	85468200 (3219, 3220)	Novel Protein sim. GBank gi 263920 pir S27939 - tensin - chicken		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gi 107284 pir A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	- peroxidase	35696286, 21908765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gi 3874846 emb CAA94337 - (Z70307) Similarity to B subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL: C09951 comes from this gene; cDNA EST EMBL: C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	91228634 (3227, 3228)	Novel Protein sim. GBank gi 4680673 gb AAD27726.1 AF13285 - (AF132851) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - eRF 1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264566 22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1615	86121909 (3229, 3230)	Novel Protein sim. GBank gi 5689485 dbj BAA83026.1 - (AB028997) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3876260 emb CAB01696 - (Z78418) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk3992.3 comes from this gene; cDNA ...	UNCLASSIFIED	UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 35696970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644229, 21906764, 264689, 21906765, 21906766, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486262, 33657349, 27486265, 35695783, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 466053 sp P34879 YO41_CAEEL - HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264766, 264768, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		stfud	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptiactor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906768, 265021, 60170615, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486 264684
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	56182323, 56526486 264684

1621	87076708 (3241, 3242)	Novel Protein sim. GBank gij3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED	264910 18108392, 65274572, 18108398, 22278996, 22278997, 22278999, 29146498, 29148499, 264905, 264908, 264909, 264828, 52644045, 264592, 60433356, 21906754, 264602, 265017, 264369, 21906768, 55811957, 265021, 60170615, 264635, 264557, 60170394, 83373044, 18108385, 22279000, 22279002, 264566
1622	84741739 (3243, 3244)				
1623	87779106 (3245, 3246)	Novel Protein sim. GBank gij731086[sp]P40389[UV22_SCHPO - UV-INDUCED PROTEIN UV122]		ribosomalprot	18108398, 264259, 264909, 56182435, 87168474, 264448, 21906768, 35695917, 264691, 87168518, 264563
1624	87338178 (3247, 3248)	Novel Protein sim. GBank gij387566[emb]CAB054781 - (Z83104) cDNA EST EMBL: T00015 comes from this gene; cDNA EST EMBL: D33665 comes from this gene; cDNA EST EMBL: D36540 comes from this gene; cDNA EST yk2408.3 comes from this gene; cDNA EST yk387c8.3 comes from this gene; cDNA ES...		UNCLASSIFIED	66714117, 29331825, 264909, 265008, 264758
1625	95354748 (3249, 3250)	Novel Protein sim. GBank gij4589622[dbj]BAA76833.1 - (AB023206) KIAA0989 protein [Homo sapiens]		kinase	264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 264106, 264508, 33657084, 265017, 265018, 18108351, 264683, 264369, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 264691, 65274620, 18108368, 263972, 18108376, 35696423, 264631, 264634, 22279000, 22279002
1626	94734369 (3251, 3252)	Novel Protein sim. GBank gij5679070[gb]AAD46844.1 (AF160904) BcDNA HL05936 [Drosophila melanogaster]			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265009, 60432229, 60433356, 60433438, 21906754, 52646317, 52644296, 265011, 87168559, 264604, 265018, 264448, 264369, 264288, 264766, 52644229, 264689, 21906765, 21906768, 35695917, 265021, 265022, 52644150, 33657023, 65274620, 27486261, 27486262, 27486265, 35695763, 263972, 52644332, 60170394, 87168518, 60432113, 264567
1627	83368773 (3253, 3254)			UNCLASSIFIED	264288
1628	85708459 (3255, 3256)	Novel Protein sim. GBank gij3668087 (AC004667) - hypothetical protein [Arabidopsis thaliana]		eph	264288, 264686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gi 4240175 dbj BAA74866.1 - (AB020650) KIAA0843 protein [Homo sapiens]		struct	264555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 264693, 264634, 22279002
1631	87758454 (3261, 3262)	Novel Protein sim. GBank gi 1915892 emb CAA69955 - (Y08740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811957, 264259, 33657023, 264693, 29331824, 29331827, 29331828, 264906, 264908, 55811576, 264910, 264634, 264636, 264637, 56182323, 264559, 264758, 18108385, 264583, 264764, 264766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gi 2558501 dbj BAA22896 - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	264687, 264769, 264691, 264692, 29146499, 264509, 264905, 264907, 264511, 264512, 264482, 264681, 264763, 264682, 264683
1633	8773683 (3265, 3266)				264488, 264259, 264907, 264908, 264909, 264628, 264629, 264631
1634	85992817 (3267, 3268)	Novel Protein sim. GBank gi 4887229 gb AAD32244.1 AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	struct	265007, 264637, 22279002
1635	94232600 (3269, 3270)			UNCLASSIFIED	65274572, 22278998, 35696052, 52644045, 264511, 265008, 265009, 265010, 265011, 265018, 265019, 264448, 264369, 21906765, 21906768, 265021, 264690, 264482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gi 455751 ref NP_001339.1 pDAPK - death-associated protein kinase 3		UNCLASSIFIED	22278995, 264594, 264763, 265020
1637	80070435 (3273, 3274)		Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gi 3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21906765, 21906767, 22278996, 35696286, 22278998, 264259, 264692, 264693, 29331824, 33657109, 264508, 264906, 18108370, 264629, 265007, 33657402, 21906754, 264602, 264604, 264764, 264683, 264566, 264288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gi 5420389 emb CA46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 264908, 56182435, 264112, 265006, 265008, 264757, 264758, 55811386, 264603, 264760, 18108351, 264764, 264288, 264766, 264768, 21906767, 55811957, 264691, 33657023, 65274620, 18108370, 55810764, 55811576, 264558, 264639, 83373044, 18108385, 87168518

1640	94143185 (3278, 3280)	Novel Protein sim. GBank gi 2842469 emb CAA16847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35696286, 60432049, 60432289, 29331827, 35696052, 52644045, 56182435, 264510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21906765, 21906766, 21906768, 35695917, 265021, 60170615, 52644150, 33657023, 33657109, 33657349, 18108374, 35696423, 65274791, 35695855, 264632, 264555, 56182323, 22279000
1641	87625160 (3281, 3282)			UNCLASSIFIED	29146499, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gi 1575333 (U60416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278999, 29147620, 29331826, 29331828, 33656970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564
1643	94131766 (3285, 3286)				29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22279002, 264482
1644	88095125 (3287, 3288)			UNCLASSIFIED	264905, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1645	95013858 (3289, 3290)			UNCLASSIFIED	264685, 264693
1646	85362691 (3291, 3292)	Novel Protein sim. GBank gi 1076802 pir S49915 - extensin like protein - maize		UNCLASSIFIED	22278994, 56994075, 35696286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gi 5002573 emb CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264359, 21906768, 60170615, 264639, 22279000
1648	87642098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1649	95347628 (3297, 3298)	Novel Protein sim. GBank gij854065[emb CAA58337] - (X83413) U88 [Human herpesvirus 6]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 55811957, 35695917, 265021, 265022, 52644150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695855, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22279000, 22279002, 264482, 264565, 264566, 264487, 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418539 (3298, 3300)	Novel Protein sim. GBank gij3647335[emb CAA21059] - (AL031644) possible zinc-finger protein			
1651	91639773 (3301, 3302)	[Schizosaccharomyces pombe] Novel Protein sim. GBank gij4884278[emb CAB43247.1] - (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906766, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695855, 264556, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564
1652	86598622 (3303, 3304)	Novel Protein sim. GBank gij1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain	struct	22278997, 29146498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1653	94255993 (3305, 3306)	Novel Protein sim. GBank gij3776054[emb CAA06273] - (A1004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274791, 18108384, 60432113, 264567, 33657109, 264565
1654	79756471 (3307, 3308)			UNCLASSIFIED	

1655	86685346 (3309, 3310)	Novel Protein sim. GBank gij3355717[emb CAA73496] - (Y13053) seryl-RNA synthetase [Zea mays]		synthase	52644507, 35696286, 22278998, 22278999, 29331824, 29331825, 29331828, 33656970, 284908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 60432113
1656	79862287 (3311, 3312)	Novel Protein sim. GBank gij1890141[dbj BAA18947] - (D83206) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gij4557645[ref NP_001524.1 pHNRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - dna_rna_bind RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)		29331827, 265009, 21906766, 21906767, 265020, 265022, 33657109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gij3877072[emb CAA87060] - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal prokaryotic L21 protein	UNCLASSIFIED	52646355, 35696286, 22278998, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264369, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148629, 265021, 265022, 18108362, 263969, 263971, 18108374, 35696423, 18108383, 22279000, 264482
1659	88230101 (3317, 3318)	Novel Protein sim. GBank gij539218[pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87168518, 22278996, 265020, 22278999, 87168559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264635, 264565, 264488, 35696286, 264259, 35696052
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gij2497012[sp Q10010 YSV4_CAEEL - HYPOTHETICAL 26.8 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 21906766, 35695917, 264690, 33657023, 264693, 33657109, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108385, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331828, 29331827, 29331828, 264509, 66712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265019, 264448, 264766, 264768, 264769, 21906768, 21906769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730502 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108385
1663	94217146 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CAB43275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52645156, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22279000
1664	94234076 (3327, 3328)	Novel Protein sim. GBank gi 3043692 dbj BAA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696286, 29331824, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264766, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35695917, 265021, 264534, 60170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35696423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264566, 264486

1665	91226952 (3329, 3330)	Novel Protein sim. GBank gjl1083506[pir][S50065 - siabadesin - mouse]	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	264488, 29331826, 29331828, 264509, 264906, 264907, 264909, 264510, 264511, 264910, 264592, 264593, 264595, 264758, 264596, 264600, 264760, 264762, 264764, 264766, 264768, 264629, 264630, 264634, 264636, 83373044, 264564, 264566, 264567, 264488
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gjl3913431[spj042643]DDX8_SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29146498, 265009, 33109954, 87168559, 265019, 264288, 264688, 21906767, 21906769, 264691, 33857182, 18108370, 18108374, 18108385, 22279002
1667	91228655 (3333, 3334)	Novel Protein sim. GBank gjl5689535[gbjBAA83051.1] - (AB029022) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	264259, 29331822, 29331826, 264905, 264906, 264908, 264510, 265009, 264595, 264758, 265011, 87168559, 265017, 265018, 265019, 264448, 264766, 264686, 21906765, 21906767, 21906769, 265020, 265021, 60170615, 264690, 264692, 264693, 18108368, 18108370, 263972, 55810764, 264555, 83373044, 60432113, 22279000, 22279002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gjl2076894[gbjAAB53983.1] - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 264508, 264509, 264906, 264907, 264908, 264511, 264910, 264764, 264687, 264689, 33657109, 35696423, 35695855, 264632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gjl387537[lembjCAA85414.1] - (Z36946) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D64658 comes from this gene; cDNA EST EMBL:D66829 comes from this gene		UNCLASSIFIED	29331825, 33109954, 264369, 264767, 264689, 33657109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	264259, 29331824, 29331827, 60433438, 265022, 264636
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gjl462451[spjP34244]KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 22278997, 29331825, 264909, 21906754, 265017, 265018, 265019, 264682, 264683, 264768, 264688, 21906766, 21906767, 21906768, 21906769, 264691, 264555, 264556, 22279000, 264566, 264906, 264909, 264632, 18108381
1672	86291834 (3343, 3344)	Novel Protein sim. GBank gjl1814270 (U74586) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gjl2076894[gblAAB53983.1]- (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - kinase Phorbol esters/diacylglycerol binding domain (C1 domain)	264488, 264569, 18108394, 56994075, 22278996, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33657023, 264692, 264693, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264566, 264567, 264486
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gjl5262467[emb]CAB45693.1]- (AL080062) hypothetical protein [Homo sapiens]	kinase	29331822, 29331824, 264906, 52644045, 60433356, 87168559, 264448, 264288, 264686, 264691
1675	87606466 (3349, 3350)	Novel Protein sim. GBank gjl3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]	UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 66712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35696423, 35695855, 264637, 264639, 18108385, 264564
1676	95358086 (3351, 3352)	Novel Protein sim. GBank gjl4164085[gblAAD05327]- (AF111091) latrophilin 3 splice variant bbar [Bos taurus]	UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21906765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gjl3327046[dbj]BAA31591]- (AB014516) KIAA0616 protein [Homo sapiens]	UNCLASSIFIED	264908
1678	86866829 (3355, 3356)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	UNCLASSIFIED	29331824, 264102
1679	91214106 (3357, 3358)	Novel Protein sim. GBank gjl550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carboxyl-phosphate synthase (CPSase)	264488, 18108392, 18108394, 52646842, 18108397, 18108398, 35696286, 29331824, 265006, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21906765, 29148627, 29148629, 264690, 18108361, 18108362, 18108364, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	91005372 (3359, 3360)	Novel Protein sim. GBank gjl2394478 (AF024500) - No definition line found [Caenorhabditis elegans]	transport	65274572, 22278994, 22278999, 66714117, 29331827, 56182435, 21906754, 265018, 264288, 21906769
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gjl5689537[dbj]BAA83052.1]- (AB029023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	22278996, 29331822, 264908, 264593, 264604, 265019, 264683, 55811957, 264690, 33657023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)		UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - START domain	UNCLASSIFIED	263994, 35696286, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264760, 264761, 264762, 264763, 264764, 264369, 264766, 264768, 35695917, 264892, 33657109, 35698423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 264486
1684	80063409 (3367, 3368)			UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.5; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00625) - Kinase Guanylate kinase	UNCLASSIFIED	60424179, 52646842, 22278994, 35696286, 22278998, 264259, 52645080, 29331824, 29331826, 265007, 33657084, 265018, 264681, 264448, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27486262, 264635, 52644332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]		UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 264512, 265009, 264910, 264758, 265010, 265011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 264630, 264631, 264634, 264635, 264637, 264638, 264639, 264565, 264486, 264567
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	35695917, 264906, 264907, 264908, 264510, 265006, 265007, 264910, 264556, 18108381, 18108383, 265011
1688	82158442 (3375, 3376)			UNCLASSIFIED	264905, 264910, 264760, 264629, 264555
1688	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]		UNCLASSIFIED	264569, 35696286, 22278999, 264508, 264908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 264448, 264764, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274791, 83373044, 264089
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264369, 21906766, 264692, 264639, 87168518
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]			264768, 33657109, 29331827, 29148629, 264510, 264106, 264910, 264109, 264508, 60170831, 264563, 264905, 264564, 264691, 264637, 264628, 264907, 264908, 33657023, 264567, 264766, 263974
1692	86106709 (3383, 3384)				264106
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	UNCLASSIFIED	29331826, 264508, 264905, 264907, 264595, 265010, 265011, 21906768, 33657023, 264629, 263976, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_006225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	mapolymerase	35698286, 22278996, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29146499, 264905, 264908, 52644045, 264511, 265006, 265007, 265009, 264592, 60433358, 21906754, 265010, 265011, 18108351, 264763, 264682, 264448, 264683, 264288, 264768, 264689, 21906768, 60170815, 264691, 264692, 264693, 18108370, 18108374, 263978, 35696423, 35695855, 264558, 18108381, 18108385, 87168518, 264482, 264486 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22990 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21906766, 18108370
1697	85740963 (3393, 3394)	Novel Protein sim. GBank gi 505652 U10362 - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			56994075, 22278998, 22278999, 264509, 33657402, 264758, 87168474, 87168559, 265017, 265018, 264448, 264687, 29148627, 21906769, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002 35696286, 264635
1699	87424793 (3397, 3398)			UNCLASSIFIED	
1700	87859161 (3399, 3400)	Novel Protein sim. GBank gi 543344 pir S41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- nucl_rept	29331824, 52644045, 265008, 265009, 263969, 263971
1701	86570488 (3401, 3402)			UNCLASSIFIED	264092, 264110, 263977
1702	87795092 (3403, 3404)	Novel Protein sim. GBank gi 3877439 emb CAA96652 - (Z72510) similarity to yeast UTR3 protein (Swiss Prot accession number P21374); cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		MHC	22278995, 22278997, 264092, 29146498, 29146499, 264107, 264508, 264907, 264110, 264112, 265009, 60170831, 21906754, 265011, 265017, 264762, 18108351, 264288, 21906765, 35695917, 265021, 60170815, 263967, 33657109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 56526486, 87168518, 60432113 264909, 265017, 264628, 264629, 264638
1703	79568651 (3405, 3406)	Novel Protein sim. GBank gi 451544 U04267 - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	
1704	86622979 (3407, 3408)	Novel Protein sim. GBank gi 1263289 U47856 - fibron-4 [Araneus diadematus]		UNCLASSIFIED	264369
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 451962 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]			264569, 35696286, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264566
1706	87790987 (3411, 3412)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			22278998, 22278998, 264259, 264509, 265018, 264764, 264685, 264686, 21906768, 21906769, 265022, 264691, 264558, 22279000

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gi 4321664 gb AAD15797 - (AF055470) ZNF258 [Homo sapiens]		UNCLASSIFIED	18108396, 22278997, 264259, 29147620, 29331826, 29146498, 264905, 264906, 265008, 264593, 264595, 264758, 264596, 265018, 264760, 18108351, 264764, 264766, 264689, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gi 5174591 ref NP_005947.1 pMTHF - 5.10-methylenetetrahydrofolate dehydrogenase, 5.10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - Formate-tetrahydrofolate ligase	synthase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 265009, 60170831, 33657402, 33109954, 87168559, 265019, 18108351, 264448, 21906765, 21906767, 21906768, 29148627, 29148629, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563
1709	80222583 (3417, 3418)			UNCLASSIFIED	264107, 55811957, 263974, 263976, 263977, 263981
1710	20754572 (3419, 3420)			UNCLASSIFIED	264556
1711	91013729 (3421, 3422)	Novel Protein sim. GBank gi 5031735 ref NP_005760.1 pHEC - N-acetylglucosamine 6-O-sulfotransferase		sulfotransferase	65274572, 29331824, 29331826, 264768, 60431528, 35696423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gi 5454168 ref NP_006453.1 pXAP4 - HBV associated factor	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	kinase	56994075, 264093, 264259, 29331822, 264099, 29331824, 29331827, 264107, 264110, 264511, 264592, 265011, 265018, 264683, 264686, 264689, 265020, 33657023, 263967, 33657109, 263974, 35696423, 35695855, 264630, 264636, 264558, 264566
1713	94143453 (3425, 3426)	Novel Protein sim. GBank gi 160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED	22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1714	87420048 (3427, 3428)				22278997, 264757, 21906765, 265020, 265021, 264692, 56526486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gi 5689537 dbj BAA83052.1 - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	264509, 264905, 264908, 264907, 264908, 264909, 264910, 264591, 265011, 264766, 264768, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gi 4589468 dbj BAA76761.1 - (AB012808) mBOCT [Mus musculus]		transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264686, 265020, 264693, 55811576, 264558, 60432113, 22279002

1717	87563223 (3433, 3434)	Novel Protein sim. GBank gi 2765411 emb CAA74749 . (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264589, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264686, 18108357, 35695917, 264690, 264692, 264693, 264628, 264629, 35696423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108388, 18108391
1718	87032628 (3435, 3436)	Novel Protein sim. GBank gi 2833262 sp Q14999 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264688, 264689, 21906765, 265021, 264691, 33657023, 264693, 18108370, 35695855, 264632, 264634, 264636, 18108388, 22279002
1719	94315259 (3437, 3438)	Novel Protein sim. GBank gi 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 58182181, 66714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 58182435, 264592, 60431735, 60433438, 55812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35696423, 55811576, 35695855, 264631, 56182323, 264559, 264564, 264486, 56182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87168518
1720	94853063 (3439, 3440)	Novel Protein sim. GBank gi 2129478 pr S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gi 4886461 emb CAB43381.1 - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044
1722	94134549 (3443, 3444)	Novel Protein sim. GBank gi 5689375 dbj BAA82968.1 - (AB030644) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - Tudor domain	kinase	

1723	95358181 (3445, 3446)	Novel Protein sim. GBank gi 4426962 gb AAD20633 - (AF126062) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264769, 21906767, 21906768, 56182575, 55811957, 22278997, 22278998, 265020, 264259, 264692, 33657023, 29331822, 29331824, 29331825, 60432289, 33657182, 33656970, 33657349, 29146499, 264508, 264907, 18108370, 264629, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432229, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33109954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264567, 264486, 264369, 264766
1724	87713806 (3447, 3448)	Novel Protein sim. GBank gi 2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264636, 264555, 264558, 264559
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gi 3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	35696286, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264766, 264768, 21906769, 35695917, 264628, 35695423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264566
1726	85754255 (3451, 3452)	Novel Protein sim. GBank		UNCLASSIFIED	29146498, 264683, 264689
1727	85296362 (3453, 3454)	gi 4689348 gb AAD27861.1 AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264905, 265011, 264689, 21906768

1728	95348515 (3455, 3456)	Novel Protein sim. GBank gij4406549jgbjAAD20027j - (AF131738) Unknown [Homo sapiens]	UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 66712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264448, 264682, 264763, 264683, 264288, 264684, 264369, 264685, 264766, 264687, 264769, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56528486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gij854065jembjCAA58337j - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)		UNCLASSIFIED	264908, 264909, 265011, 264764, 264629
1731	88266068 (3461, 3462)	Novel Protein sim. GBank gij631600jirjjs47094 - hypothetical protein - rabbit	UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811578
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gij424023jdbjBAA74894.1j - (AB020678) KIAA0871 protein [Homo sapiens]	struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264638, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gij1575756 (U70674) - m-Numb [Mus musculus]	synthase	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264886, 264769, 264691, 264692, 264693, 264628, 264636, 264556
1734	87795261 (3467, 3468)			264693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi 4836807 gb AAD30566.1 AF14679 - (AF14679) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278998, 60432049, 264259, 29331822, 264908, 265008, 265007, 265008, 265009, 264591, 33657402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21906765, 21906768, 21906769, 29148629, 29148784, 265021, 265022, 52644150, 18108364, 18108365, 33657109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1736	95362884 (3471, 3472)	Novel Protein sim. GBank gi 4895647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 66714117, 66712502, 56182435, 265008, 265008, 264910, 60433356, 87168559, 265017, 265019, 18108351, 265020, 265022, 33657023, 33657109, 264555, 60431850, 264637, 60170394, 264558, 264639, 264584
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi 2143607 pir S68695 - BIK protein - rat	Contains protein domain (PF00168) - C2 domain	29331822, 29331830, 264591, 265011, 265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi 2225941 emb CAA69714 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)		Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	35696052, 264603, 264557
1740	83592939 (3479, 3480)	Novel Protein sim. GBank gi 4809 emb CAA44309 - (X62452) YCR601 [Saccharomyces cerevisiae]	traffic	264604, 21906764, 18108364, 264629, 35695855, 264636
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi 4883898 gb AAD31695.1 AF13042 - (AF13042) serine protease-like protein isoform [Homo sapiens]	UNCLASSIFIED	60432229, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21906769, 265020, 33657109
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi 4505193 ref NP_003667.1 pMLD - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264566
1743	86966475 (3485, 3486)			265017, 265020, 264692
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	22278998, 264508, 264907
1745	20290075 (3489, 3490)	Novel Protein sim. GBank	UNCLASSIFIED	264558
1746	84326110 (3491, 3492)	Novel Protein sim. GBank gi 731756 sp P38873 YHY6 YEAST - HYPOTHETICAL 175.8 KD PROTEIN IN GND1-IK1 INTERGENIC REGION [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	65274791, 264639, 264559
1747	94324333 (3493, 3494)		transcript factor	52646842, 29331824, 29331825, 52644045, 56182435, 265007, 52646317, 87168474, 265018, 18108351, 264369, 264769, 264689, 35695917, 60170615, 264691, 33657023, 65274791, 35695855, 60170394, 22279000, 264482

1748	88003580 (3495, 3496)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	(Contains protein domain (PF00684) - eph DnaJ central domain (4 repeats)	264489, 56182575, 29331824, 56182435, 264112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811576, 264635, 264555, 264556, 264557, 264559 264106
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi 5850780 gb AAD45948.1 AF15196 - (AF15196) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	
1750	94321664 (3499, 3500)	Novel Protein sim. GBank gi 4996894 gb AAC28444.2 - (AF065164) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]		33657402, 264288, 52644150, 263974, 83373044
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 db BAA24184 - (AB010054) outer arm dynein light chain 2 [Anthracidaris crassispina]	Contains protein domain (PF00560) - ATPase-associated Leucine Rich Repeat	265010, 264369
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3915482 sp P74346 YG29_SYN3 - HYPOTHETICAL 36.0 KD PROTEIN SLR1629	Contains protein domain (PF00849) - RNA pseudouridylylase synthase	264510, 264593, 264682, 21906765, 18108370
1753	94235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906766, 264692, 264693, 65274620, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39981 YE4_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION	transport	264488, 35696286, 264509, 264906, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264604, 264762, 264763, 264685, 264766, 264691, 264628, 35698423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567 264686
1755	79470282 (3509, 3510)	Novel Protein sim. GBank gi 1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED	
1756	92962614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]		52648842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 29331822, 60432289, 29331827, 33656970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21908768, 21906769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 emb CA46856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21906768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612971 (3515, 3518)	Novel Protein sim. GBank gjl3881040 emb CAA164031 - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33656970, 264508, 265006, 265007, 265009, 264591, 33657402, 33109954, 87168474, 264600, 265017, 265018, 21906769, 265020, 265021, 33657023, 33657109, 264629, 18108374, 35695855, 264632, 52644332, 22279002, 264563
1759	36984372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gjl5262748 emb CAB4588.1 - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432049, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264910, 60432229, 264592, 264595, 55812038, 264758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264628, 264629, 55811576, 35698423, 264632, 264634, 264636, 264557, 264639, 60432113, 264565, 264486
1761	87409586 (3521, 3522)	Novel Protein sim. GBank gjl12749 sp P10569 MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 264910, 264685, 264686
1762	95319887 (3523, 3524)	Novel Protein sim. GBank gjl3169158 (AC004770) - BC269730_2 [Homo sapiens]	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	desaturase	22278999, 264259, 264905, 264907, 60170831, 265010, 265011, 265017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 264690, 33657109, 18108374, 264558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gjl4809026 gb AAD30062.1 - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181686, 29331825, 35696052, 264905, 264906, 264909, 264763, 264682, 264769, 35695917, 265022, 33657023, 18108374, 35698423, 264634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gjl1360669 pir jCGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	22278998, 264259, 35696052, 29331828, 56182435, 265008, 265017, 265018, 264448, 264288, 21906766, 21906767, 29148627, 35695917, 264691, 33657023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gjl486806 pir jS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 264259, 264104, 264508, 264905, 264907, 264511, 265007, 265008, 264910, 265009, 21906754, 265010, 265017, 264603, 265018, 265019, 18108351, 264682, 264448, 264369, 264288, 264766, 18108359, 21906766, 21906767, 29148627, 29148629, 35695917, 265020, 265021, 264692, 264628, 264629, 18108374, 263976, 264636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 2499087 sp Q09332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 60170615, 33657023, 264693, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1 - (AL022239) dJ1042K10.4 [novel protein] [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264591, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	95413144 (3539, 3540)	Novel Protein sim. GBank gi 15204 sp P00736 C1R_HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	- complement	264488, 264768, 264769, 56182575, 55811957, 264690, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264684, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914191 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	- transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22279000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AAD34351.1 AF12136 - (AF121360) DNZDHH/NEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHC zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264764, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424269, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265006, 265007, 265008, 60170831, 60433438, 264758, 55811386, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495699 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22279002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gij1469199[dbj]BAA094871 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278997, 29331822, 29331826, 60432289, 29331828, 35696052, 29331830, 66712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 60433438, 55812038, 21906754, 85658542, 87188559, 264601, 265017, 265018, 265019, 264762, 264448, 264288, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 265021, 265022, 264691, 33657023, 264692, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56526486, 87188518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gij4589676[dbj]BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gij3219939[sp]P87115]YDK9_SCHPO - HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME I		nucl_recl	56984075, 29331826, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gij3875648[emb]CAA01454.1] - (Z66561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL.M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9...		UNCLASSIFIED	29331826, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gij4589676[dbj]BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265006, 265007, 265008, 18108385, 65274727, 264482, 264369, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264906, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gij729225[sp]P41237[CTXN_RAT] - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264638, 264637, 264639, 264563
1783	85717805 (3565, 3566)	Novel Protein sim. GBank gij2257543[dbj]BAA21436] - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gij1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - PH domain	struct	35696286, 264259, 35696052, 264508, 264905, 264906, 264907, 66712502, 264908, 264909, 265007, 265008, 265009, 264910, 264591, 264594, 264757, 264758, 264759, 265010, 265011, 264601, 264602, 264604, 264605, 18108351, 264762, 264763, 264764, 264369, 264766, 264687, 264768, 264688, 21906768, 35695917, 264690, 264691, 264692, 264693, 264628, 18108374, 35696423, 264631, 264632, 264635, 264637, 264638, 264639, 18108385, 22279000, 22279002, 264565, 264566, 264486
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gij459552[jdbj(BAA76798.1) - (AB023171) KIAA0954 protein (Homo sapiens)]		UNCLASSIFIED	65274572, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 264905, 264906, 264908, 66712502, 56182435, 264511, 265007, 60433356, 55811150, 264683, 264369, 264687, 52644229, 21906767, 52644150, 33657023, 65274620, 33657182, 65274791, 35695855, 264555, 65274727, 22279002
1786	85296465 (3571, 3572)	Novel Protein sim. GBank gij117789[splP26770(CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)		UNCLASSIFIED	264908, 35696423, 264636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gij3877175[embj(CAA90338.1) - (Z50028) cDNA EST yk321h8.5 comes from this gene; cDNA EST EMBL.D68896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264905, 264908, 264909, 264595, 264764, 264766, 264692, 60431528, 264629, 264636, 264564, 264566
1788	91228779 (3575, 3576)			UNCLASSIFIED	264488, 83373044
1789	88094529 (3577, 3578)	Novel Protein sim. GBank gij2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 29331828, 264909, 18108351, 264288, 265021, 264555, 264636
1790	82489734 (3579, 3580)				35696052, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 264758, 265011, 265019, 264764, 264766, 264769, 264628, 264635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gij2114321[dbj][BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33657023, 264693, 264509, 264905, 264628, 264907, 264629, 264908, 264909, 264510, 265006, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264566, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87792690 (3583, 3584)	Novel Protein sim. GBank gij4337106[gb][AAD18082] - (AF129756) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33657402, 87168559, 264369, 33657023, 35695855, 20281071, 264559, 18108387, 87168518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gij5579331[gb][AAD45504.1][AF14573] - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - Glycosyl hydrolase family 47	ATPase-associated	65274572, 22278995, 22278996, 22278997, 22278999, 264093, 264259, 29331824, 66714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21906754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 52644150, 33657023, 33657109, 18108370, 18108374, 65274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gij4914604[emb][CAB43677.1] - (AL050369) hypothetical protein [Homo sapiens]	Contains protein domain (PF01798) - Putative snoRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87168474, 265011, 265017, 18108351, 264763, 264448, 264683, 264369, 21906765, 21906766, 21906767, 21906768, 29148784, 35695917, 60170615, 33657023, 264629, 18108374, 18108376, 35696423, 35695855, 264556, 264557, 264638, 264558, 18108385, 264584
1795	79747856 (3589, 3590)			UNCLASSIFIED	264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1796	86599486 (3591, 3592)	Novel Protein sim. GBank gij585084[sp][Q07803]IEFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)		glycoprotein	264488, 264907, 264909, 264594, 264595, 264766, 264687, 21906765, 21906767, 264628, 264630, 264559

1797	91223219 (3593, 3594)	Novel Protein sim. GBank gi 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906768, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1798	91221276 (3595, 3596)	Novel Protein sim. GBank gi 2832906 dbj BAA24608.1 - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 60433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108385, 87168518, 22279000, 264486
1799	86321713 (3597, 3598)	Novel Protein sim. GBank gi 5689541 dbj BAA83054.1 - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	264691, 264556, 264566 52644045, 265007, 264632
1801	95060723 (3601, 3602)	Novel Protein sim. GBank gi 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)			35696286, 66714117, 264508, 264509, 56182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gi 4680679 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264769, 264689, 21906769, 35696286, 35695917, 264259, 264691, 264692, 264693, 20281099, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 66712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264598, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264683, 264764, 264566, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gij3879914[emb]CAA98538.1] - (Z74043) predicted using GeneFinder; cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21906754, 264766, 21908765, 21908768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gij5453644[ref]NP_006461.1]pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35696423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gij4589676[dbj]BAA76857.1] - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35696423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gij4884079[emb]CAB43235.1] - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264488, 35696052, 66714117, 35696052, 66712502, 264592, 60433438, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264563, 264564, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gij1916927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264586, 29148629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88096316 (3619, 3620)	Novel Protein sim. GBank gij1352944[sp]P47179]JRP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264488, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264686, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gij2134984[pir]j137275 - death-associated protein kinase (EC 2.7.1.-) - human	Contains protein domain (PF00023) - kinase Ank repeat		264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264766, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265019, 18108351, 21906769

1813	88090972 (3625, 3626)	Novel Protein sim. GBank gi 5051636 gb AAD38326.1 AF07372 - (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 264259, 29331824, 66714117, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 265007, 264910, 264591, 264593, 55812038, 265011, 265018, 264760, 264682, 264764, 264683, 264369, 264766, 264768, 264769, 21906766, 21906768, 264691, 264693, 18108374, 35695855, 264634, 264635, 264637, 264639, 264559, 22279000, 22279002, 264566
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	264488, 35696286, 22278998, 264092, 264094, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264107, 52644045, 56182435, 265009, 60432229, 60433356, 87168474, 87168559, 264369, 264288, 21906765, 35695917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 264638, 56526486, 264482
1815	85296473 (3629, 3630)	Novel Protein sim. GBank gi 117780 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		sluc1	22278999, 264508, 264509, 264907, 264908, 264910, 265011, 264760, 264766, 264634, 264636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176623 sp P41846 YO96_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 264509, 264907, 264908, 264909, 265009, 264591, 265011, 265017, 264687, 264689, 265022, 264691, 18108362, 18108368, 18108370, 18108374, 18108379, 264635, 264557, 264564, 264567
1817	88095268 (3633, 3634)	Novel Protein sim. GBank gi 3766377 emb CAA21429 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	histone	264488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27486262, 18108370, 18108374, 60170394, 56182323, 22279002
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 387912 emb CAA94370 - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL: T01923 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcript factor	35696286, 60433356, 264758, 264369, 264686, 21906769, 264693, 264632
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HMGIC fusion partner		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331826, 264908, 265007, 265008, 265009, 60432229, 265017, 265018, 265019, 264448, 264288, 21906768, 21906769, 265020, 18108381, 18108384, 22279000, 22279002, 264567

1820	87769455 (3639, 3640)				264905, 264907, 264594
1821	80431510 (3641, 3642)				264907, 264768, 263978
1822	91221523 (3643, 3644)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1 - (AL050101) hypothetical protein (Homo sapiens)			22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 35696052, 29331828, 264908, 29331830, 60170831, 264591, 264593, 60433356, 264596, 265017, 265019, 18108351, 264763, 264683, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 18108364, 18108370, 35695855, 22279000, 22279002
1823	85522330 (3645, 3646)			UNCLASSIFIED	264488, 264259, 264511, 264288, 264768, 264693, 35696423, 264634, 18108385, 264486
1824	86612025 (3647, 3648)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	264907, 264908, 264909, 264511, 264631, 264634, 264635, 264637, 264638, 264639, 264758, 264568
1825	87430125 (3649, 3650)	Novel Protein sim. GBank gi 3036803 emb CAA18493 - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60432049, 264910, 264487
1826	91723612 (3651, 3652)	Novel Protein sim. GBank gi 4680685 gb AAD27732.1 AF13295 - (AF132957) CGI-23 protein [Homo sapiens]		ATPase-associated	52644507, 52645156, 52646842, 22278994, 22278996, 56994075, 264259, 60432049, 52645080, 35696052, 66712502, 52644045, 265008, 265009, 60432229, 60433356, 60433438, 52646317, 52644296, 265011, 87168559, 264448, 264288, 264369, 264688, 52644229, 264689, 21906765, 21906768, 265020, 60170815, 52644150, 33657023, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 264404, 22279002
1827	81647212 (3653, 3654)				264758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank gil4503571ref NP_001419.1 pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52646842, 56182575, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52644045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33109954, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 265021, 60170615, 33657023, 33657349, 263972, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264565, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 29331827, 264908, 265009, 264910
1830	94312942 (3659, 3660)	Novel Protein sim. GBank gil2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644296, 87168559, 265019, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695763, 263974, 35696423, 35695855, 52644332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791
1832	84521663 (3663, 3664)	Novel Protein sim. GBank gil1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8.....			264602

1833	95314184 (3665, 3666)	Novel Protein sim. GBank gij5174413[ref]NP_006026.1pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29148499, 264508, 264509, 264908, 264907, 68712502, 264908, 52844045, 264909, 264512, 265008, 264591, 264593, 60433356, 21906754, 33657084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27486264, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56526486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)				264259, 264907, 264689, 22279000, 22279002
1835	94135718 (3669, 3670)			UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21908768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gij4759286[ref]NP_004268.1pUCP4 - uncoupling protein 4	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	29331825, 264908, 265019, 264764, 264686, 21906765, 264635
1837	94234297 (3673, 3674)	Novel Protein sim. GBank gij3334400[sp]Q24574UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	94324369 (3675, 3676)	Novel Protein sim. GBank gij1362599[pir]A56154 - Abi substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain		29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gij2117310[emb]CAB09116.11 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264601, 21906765, 21906766, 265021, 33657109, 264556
1840	87391708 (3679, 3680)	Novel Protein sim. GBank gij127560[sp]P23249[MV10_MOUSE - PROTEIN MOV-10		UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gij4572464[gb]AAD23834.1 AF12365 - (AF123653) FEZ1 [Homo sapiens]			56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	90992645 (3683, 3684)	Novel Protein sim. GBank gi 1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108364, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264563, 264564
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264567, 264595, 264766
1844	87444764 (3687, 3688)	Novel Protein sim. GBank gi 2496887 (sp Q09232) YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gi 1175494 (sp Q09819) YAC5_SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21906765, 52644150, 33657109, 264555, 264556, 264557, 56182323, 18108382, 83373044, 18108385, 264564
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gi 3881080 (emb CAA21739) - (AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h6.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk467g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87821497 (3693, 3694)	Novel Protein sim. GBank gi 5059323 (gb AAD38967.1) AF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22278997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gi 5701854 (emb CAB52191.1) - (AJ245417) G5b protein [Homo sapiens]		tm7	29331825, 29331826, 29331827, 265017, 264683, 264288, 264766, 264768, 21906767, 21906768, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gi 4503665 (ref NP_001989.1) pFBLN - fibulin 2 precursor	Contains protein domain (PF00008) - EGF-like domain	ATPase_associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gi 4589582 (dbj BAA76813.1) - (AB023186) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gi 220637 (dbj BAA01477) - (D10627) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35696052, 264910, 60433438, 264688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174629 ref NP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35696286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432229, 60433358, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 284448, 264688, 264687, 21906765, 21906767, 21906769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22279002, 264563 264687, 264768, 52644507, 264769, 21906765, 21906767, 21906768, 22278995, 56994075, 22278999, 52644150, 264259, 264692, 29331822, 29331824, 52645129, 29331827, 33656970, 33657349, 35695763, 264508, 264908, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265006, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644296, 87168518, 87168559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264567, 264288, 264369, 264766
1853	91222267 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264592
1854	86038152 (3707, 3708)	Novel Protein sim. GBank gi 2072964 (U93569) - putative p150 [Homo sapiens]		nuclease	18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21906754, 87168474, 265011, 87168559, 264681, 264288, 264768, 18108359, 21906764, 21906768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264636, 18108381, 264482
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CAB39994.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - nucl_rept Kelch motif		
1856	84231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA06945 - (AJ006278) acetylglucosaminyltransferase-like protein [Mus musculus]		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	84324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120 - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase_associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gil4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomal prot	264757
1859	84407464 (3717, 3718)	Novel Protein sim. GBank gil4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			22278996, 29331824, 265007, 33109954, 265019, 264369, 21906768, 29148784, 27486261, 52644332, 22279002 265019
1860	17829308 (3719, 3720)	Novel Protein sim. GBank gil4009522 (AF099731) - connexin 31.1 [Homo sapiens]			
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gil2143637 pir J84505 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase		264887, 264259, 29331822, 29331824, 29331825, 265007, 265009, 264591, 33109954, 265010, 265019, 264369, 264288, 264886, 264691, 264693, 27486264, 18108370, 18108374, 263977, 55811576, 56182323, 264639, 22279000, 22279002, 264482
1862	87372923 (3723, 3724)	Novel Protein sim. GBank gil125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35696286, 264259, 87168474, 264369, 21906766, 264558, 264563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gil3820909 emb CAA09299 - (AJ010642) Dof protein [Drosophila melanogaster]		UNCLASSIFIED	264601, 264766, 29148627, 29148629, 264692, 264629, 264635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gil4322263 gb AAD15985 - (AF077736) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/8 type C domain	synthase	22278999, 264259, 264907, 265018, 18108370, 264634, 264635, 264555, 264556, 264638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gil2495727 sp Q93073 Y256_HUMAN - HYPOTHETICAL PROTEIN KIAA0256			22278999, 264490, 29331822, 66714117, 66712502, 265006, 265007, 265008, 265009, 264591, 60433438, 265010, 265019, 264760, 264448, 264768, 29148627, 29148629, 265020, 265022, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gil5262617 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]		kinase	18108374, 264769, 18108377, 21906765, 21906766, 35696423, 56182575, 21906769, 29148629, 35696286, 35695917, 265021, 264510, 264511, 264512, 264534, 264535, 60170831, 52644150, 264555, 264691, 264259, 264556, 264692, 264557, 33657023, 60433356, 29331822, 264559, 264595, 29331824, 18108385, 21906754, 33657182, 29331827, 35696052, 33656970, 87168518, 265017, 60431602, 22279000, 264508, 264509, 18108351, 264907, 264682, 264567, 18108372, 264765, 264486
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gil3859330 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]		UNCLASSIFIED	264094

1868	87357459 (3735, 3738)	Novel Protein sim. GBank gi 3881525 emb CAA3884 - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk35710.5 comes from this gene [Caenorhabditis elegans]		nuclease	264489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33657402, 87168474, 18108351, 21906768, 21906769, 265020, 265021, 60170615, 27486284, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264568, 264567
1869	86977292 (3737, 3738)	Novel Protein sim. GBank gi 4826772 ref NP_004961.1 p[GFA - insulin-like growth factor binding protein, acid labile subunit]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264508, 264509, 264906, 264908, 264909, 264910, 264591, 264600, 18108351, 264683, 264766, 264769, 35695855, 264634, 264558, 264639, 18108385, 264563, 264486
1870	95349488 (3739, 3740)	Novel Protein sim. GBank gi 1669859 emb CAB06722 - (Z86099) very large tegument protein [human herpesvirus 2]		UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695917, 60170615, 264692, 18108368, 35695763, 35696423, 65274791, 264638, 264639, 56526486
1871	80234464 (3741, 3742)			UNCLASSIFIED	264509, 264905, 264595, 264768, 264635, 264636, 264583, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]		protease	264510, 264594, 264565
1873	80213890 (3745, 3746)				264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)		Contains protein domain (PF00293) - Bacterial mutT protein	UNCLASSIFIED	264488, 35695917, 264259, 264905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264567, 264768
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gi 4589520 dbj BAA76782.1 - (AB023155) KIAA0938 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264828, 264592, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi 263810 bbs 122920 - collagen alpha chain [Riftia pachyptila=lube worms, Peptide, 1027 aa]		UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264556, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi 3983355 gb AAC83924.1 - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]		UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gij4510345jgb AAD21434.1 - (AC006921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264569, 264488, 35696286, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 29146498, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264369, 264288, 264766, 264687, 264768, 264769, 21906766, 35695917, 265021, 60170615, 33657023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264564, 264566, 264488, 264567
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gij4929643jgb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264908, 265007, 264565, 264566
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gij1550765jemb CAA69283 - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214949 (3761, 3762)	Novel Protein sim. GBank gij93144 pir IB40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhouser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gij2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gij1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264638

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 56181686, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265009, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87168559, 264600, 265017, 264604, 265019, 264605, 264760, 55811150, 264761, 264682, 264763, 264683, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810764, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264486, 264567
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	56182575, 264259, 264905, 264909, 265008, 264596, 264766, 265020, 264628, 60431528, 264634, 56526486, 264080, 264563
1886	86674062 (3771, 3772)	Novel Protein sim. GBank gi 2854158 gb AAC02577.1 - (AF045641) No definition line found [Caenorhabditis elegans]			22278998, 22278999, 60432049, 264910, 265018, 264766, 21906768, 29148629, 264690, 264693, 264628, 264555, 264488
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 pCPNE - copine VI (neurofil) [Homo sapiens]	Contains protein domain (PF00168) - C2 domain	ATPase-associated	29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 264681, 264768, 29148627, 264693, 18108364, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264563
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gi 3319931 emb CAB10841 - (Z98046) dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		263978
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir A56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21906765, 21906768, 21908769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240195 dbj BAAT4876.1 - (AB020660) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108398, 29147620, 264907, 265009, 264600, 265018, 18108351, 264288, 264689, 21906765, 21906768, 21906769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264909, 18108379, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gij5689535jdbj BAA83051.1 - (AB029022) KIAA1099 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533826 (3785, 3786)			laminin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331828, 264906, 265006, 265008, 265009, 264592, 265018, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264766, 264687, 264689, 21906768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631881 (3789, 3790)	Novel Protein sim. GBank gij5282574 embj CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264905, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764, 18108379, 264634, 58182323, 56526486
1896	85673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	264907, 265008, 264682, 264686, 21906768, 264629, 264631, 264634, 264555, 264259
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gij728836 sp P39193 ALU6_HUMAN - III ALU SUBFAMILY SP WARNING ENTRY III		cadherin	
1898	87617637 (3795, 3796)	Novel Protein sim. GBank gij127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase	22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 55810764, 22279000
1899	86673097 (3797, 3798)	Novel Protein sim. GBank gij2909819 (AF031548) - erythrocyte membrane glycoprotein Rh50 [Homo sapiens]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21906765, 21906769
1900	87641858 (3799, 3800)	Novel Protein sim. GBank gij4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]		UNCLASSIFIED	264683

1801	95186647 (3801, 3802)	Novel Protein sim. GBank gij585959 sp P38378 S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52645156, 18108396, 52646365, 52646842, 18108397, 58182575, 22278994, 22278995, 58994075, 35696286, 22278997, 22278998, 264490, 60432049, 264259, 29331822, 52645080, 29331824, 29331825, 68714117, 29331826, 60432289, 29331827, 29331828, 35696052, 33656970, 29146498, 264906, 264907, 29331830, 264908, 52644045, 264909, 264112, 265006, 264512, 265008, 264910, 265009, 60170831, 60432229, 60433356, 33657402, 60433438, 55812038, 264758, 33109954, 21908754, 33657084, 52644296, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 52644229, 21908765, 21906766, 21908767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108382, 33657023, 264693, 336967, 33657109, 33657182, 27486264, 33657349, 35695763, 18108370, 18108376, 55811576, 35696423, 35695855, 60431850, 264636, 263981, 52644332, 60170394, 83373044, 18108385, 87168518, 60432113, 264564 264107, 263976
1802	80202013 (3803, 3804)	Novel Protein sim. GBank gij4426613 gb AAD20451 - (AF098796) SLM-1 [Mus musculus]		dna_rna_bind	
1803	8778554 (3805, 3806)	Novel Protein sim. GBank gij3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 29331825, 29331827, 264508, 264907, 265008, 60170831, 60433356, 60433438, 264759, 21906754, 264448, 264288, 265021, 265022, 33657023, 264693, 55811576, 264555, 264556, 22279000
1804	80434213 (3807, 3808)	Novel Protein sim. GBank gij1352911 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264905, 264906, 264907, 264908, 265007, 264910, 264686, 264768, 264687, 264769, 264693, 264628, 18108374, 264634, 264636, 264637, 264585
1805	95351140 (3809, 3810)	Novel Protein sim. GBank gij3043714 dbj BAA25521 - (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00293) - Bacterial mutT protein		264488, 264768, 264769, 264689, 29148629, 35695917, 35696286, 264259, 264692, 18108362, 33657023, 29331824, 33657109, 29146499, 264508, 264509, 264905, 264906, 264907, 66712502, 264908, 264909, 35696423, 35695855, 264510, 264511, 264512, 264910, 264634, 264635, 264637, 264638, 33657402, 264758, 85658542, 264602, 264760, 264761, 264482, 264563, 264762, 264483, 264764, 264566, 264288, 264766
1806	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	85351144 (3813, 3814)	Novel Protein sim. GBank gi 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21906754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21906765, 21906766, 21906768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313641 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109906) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264905, 264906, 264907, 264908, 66712502, 264909, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264596, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264688, 264688, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2224653 db BAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264704, 264766, 18108370, 264634, 264637, 264486
1910	94216821 (3819, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486

1911	91725345 (3821, 3822)	Novel Protein sim. GBank gi 4803339 gb AAD30184.1 AC006530) hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33656970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21906765, 21906768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413519 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA83003.1 - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264905, 264906, 264907, 264908, 52644045, 56182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 65274791, 264637, 56182323, 83373044, 56526486, 22279002, 264563, 264568
1913	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265006, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21906765, 21906766, 21906768, 21906769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA82991.1 - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565
1916	79640761 (3831, 3832)				264693, 264639

1917	87821680 (3833, 3834)	Novel Protein sim. GBank gj1568391[gbj BAAB2979.1] - (AB028950) KIAA1027 protein [Homo sapiens]		struct	284769, 284689, 21906765, 21906768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 284905, 264906, 264628, 264907, 264908, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264566, 264764, 264766
1918	95302795 (3835, 3836)	Novel Protein sim. GBank gj15281517[gbj AAD41524.1 AF15483 - (AF154831) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35696286, 35695917, 22278996, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52645129, 35696052, 29331828, 27486262, 27486264, 35695763, 264508, 264905, 264509, 264906, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644298, 56526486, 97168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264584, 18108351, 264762, 264682, 264565, 264448, 264764, 264566, 264486, 264567, 264369, 264288, 264766, 264487, 264685
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gj13878584[embj CAB01237] - (Z77667) cDNA EST EMBL.C08125 comes from this gene; cDNA EST EMBL.C09753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 28331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gj1809231 (AC000115) - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	264510, 264511, 264512, 264566
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gj14580997[gbj AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641863 (3843, 3844)	Novel Protein sim. GBank gi 138595 sp P02845 VIT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	94323589 (3845, 3846)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278995, 264094, 264259, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264681, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21906766, 264691, 33657023, 264693, 65274620, 33657109, 18108370, 264628, 264629, 35698423, 264630, 264631, 264632, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87188518, 264563, 264564, 264585, 264586, 264567
1924	87338925 (3847, 3848)	Novel Protein sim. GBank gi 3877655 emb CAA96657 - (Z72511) possible zinc finger protein; cDNA EST EMBL:M89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1...	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		28331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi 4981903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278995, 22278996, 22278997, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	88094739 (3851, 3852)	Novel Protein sim. GBank gi 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		strud	264905, 264906, 264907, 264910, 264593, 265018, 264760, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264563
1927	85654857 (3853, 3854)	Novel Protein sim. GBank gi 3043632 dbj BAA25480 - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87799054 (3855, 3856)	Novel Protein sim. GBank gi 1665761 dbj BAA13377 - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Extracellular link domain	Inf	264489, 264259, 265017, 265021, 264692
1929	86997236 (3857, 3858)	Novel Protein sim. GBank gi 5001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/trypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gij1709230[sp]P52963[NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35686286, 29331828, 264905, 264907, 264908, 264909, 264511, 264910, 264758, 264601, 265017, 265019, 264605, 264760, 264764, 264766, 264686, 264769, 265022, 35698423, 264638, 60432113
1931	87797279 (3861, 3862)	Novel Protein sim. GBank gij404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264906, 264908, 60432229, 264758, 264764, 264288, 265020, 264692, 264634, 264637
1932	15030972 (3863, 3864)				264684, 264691, 264635
1933	11613668 (3865, 3866)			UNCLASSIFIED	264595
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gij4115748[djb]BAA36494] - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		struct	56182575, 56182435, 264510, 264757, 264758, 55812038, 55811386, 265018, 55811150, 21906765, 264691, 264631, 264635, 264637
1935	87752511 (3869, 3870)			UNCLASSIFIED	264686, 265011, 264511, 264905, 18108351, 264564, 264681, 264259, 18108370, 264566, 264764, 264369, 264595
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gij4827040[ref]NP_005110.1[ptTRAP - lthyroid hormone receptor-associated protein, 150 kDa subunit			60432289, 265007, 265010, 265011, 265019, 33657109, 18108374
1937	94847141 (3873, 3874)	Novel Protein sim. GBank gij543187[pil]S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85658542, 21906767, 35685917, 60170615, 264693, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gij4544431[gbl]AAD22340.1[AC006955 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	264488, 29146498, 264905, 264559
1939	91004978 (3877, 3878)	Novel Protein sim. GBank gij500858[djb]BAA03210] - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 265017, 21906765, 21906768, 21906768, 55811957, 27486264, 35698423, 60432113, 264564
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gij1946300[emb]CAA73132] - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	264488, 29331822, 264448, 264683, 264288, 265020, 33657023, 264631
1941	94147177 (3881, 3882)	Novel Protein sim. GBank gij4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 264259, 29331824, 29331827, 264905, 265008, 33657084, 265017, 265018, 264288, 264687, 21906765, 21906766, 21906767, 265020, 52644150, 27486264, 83373044, 18108387, 60432113, 22279002, 264565
1942	87641670 (3883, 3884)	Novel Protein sim. GBank gij4927204[gbl]AAD33049.1[AF133911] ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	264488, 18108398, 29331825, 27486261, 264509, 18108370, 18108374, 264482
1943	94325298 (3885, 3886)	Novel Protein sim. GBank gij3122952[sp]O15736[TIPD_DICD1 - TIPD PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 264511, 265008, 264592, 60432228, 265017, 265018, 265019, 264684, 264692, 33657109, 65274791, 264636

1944	94232958 (3887, 3888)	Novel Protein sim. GBank gij1799570[dbj BAA13432] - (D87671) TIP120 [Rattus norvegicus]	UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52645080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432229, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170615, 264692, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264563
1945	87641872 (3888, 3890)	Novel Protein sim. GBank gij4927204[gb AAD33049.1 AF13391 - (AF133911) ARL-6 interacting protein-4 [Mus musculus]	UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264486, 264567
1946	87443990 (3891, 3892)	Novel Protein sim. GBank gij2498104[sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN	UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21906767, 52644150, 264693, 27486264, 264637, 87168518, 264563
1947	86438862 (3893, 3894)	Novel Protein sim. GBank gij3914801[sp O54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)	mapolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264764, 264288, 264768, 264688, 21906768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gij5420387[emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	struct	264909, 60170831, 264591, 264594, 265010, 265011, 264764, 264369, 264689, 264631, 264638
1949	7640129 (3897, 3898)	Novel Protein sim. GBank gij3876766[emb CAA93466.1 - (Z69637) predicted using GeneFinder; Similarity to E. coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	264369
1950	87788531 (3899, 3900)	Novel Protein sim. GBank gij3876766[emb CAA93466.1 - (Z69637) predicted using GeneFinder; Similarity to E. coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gij2626753[dbj BAA23424] - (AB008782) sulfate transporter [Arabidopsis thaliana]	transport	56182575, 22278997, 52645080, 29331824, 29331825, 29331827, 55812038, 52646317, 265018, 265019, 264369, 21906765, 21906767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gij4928633[gb AAD34077.1 AF15184 - (AF151840) CGI-82 protein [Homo sapiens]	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264565

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gij1168715isp P31721C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gij4240271 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263394, 18108394, 35696286, 22278998, 29331822, 66714117, 29331826, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 265007, 265008, 264910, 265009, 60170831, 60432229, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264766, 264769, 35695917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264564, 264566, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	58182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35696052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906766, 21906767, 55811957, 265020, 265021, 52645129, 33657109, 27486264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gij1665821 dbj BAA13407 - (D87469) Similar to D.melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278996, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21906769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264563, 264564

1957	94326510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA76856.1 - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52646842, 56182575, 22278997, 22278998, 22278999, 29331824, 66714117, 29331827, 29146498, 264593, 33657402, 33109954, 87168474, 265018, 264448, 264369, 264288, 264766, 21906766, 21908767, 21906768, 21906769, 265020, 265021, 264692, 65274620, 27486264, 33657349, 27486265, 35959555, 22279002, 264482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264092, 264094, 264259, 60432049, 29331824, 56182181, 66714117, 264107, 264109, 264909, 264511, 60170831, 60432229, 21906754, 265010, 21906769, 35959517, 265022, 65274620, 263967, 263976, 35696423, 264631, 264632, 264634, 264635, 18108365, 22279000, 22279002, 264593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860 - (Z98056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3918, 3920)	Novel Protein sim. GBank gi 227485 dbj BAA21515 - (D64159) 3-7 gene product [Homo sapiens]		strudt	264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264595, 265017, 264604, 265018, 18108351, 264764, 264369, 264766, 264768, 21906765, 18108368, 264629, 18108379, 264635, 264636, 264637, 264638, 264486
1961	16292607 (3921, 3922)				264635
1962	91008385 (3923, 3924)			UNCLASSIFIED	65274572, 264592, 264593, 265019, 264691
1963	90936017 (3925, 3926)	Novel Protein sim. GBank gi 3721653 dbj BAA33581 - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		eph	65274572, 18108398, 35696286, 29331825, 60432289, 29331827, 264828, 265006, 265009, 60433356, 60433438, 21906754, 265020, 265021, 33657023, 33657109, 27486265, 35695855, 264555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1 - (AL080169) hypothetical protein [Homo sapiens]		cadherin	264488, 264092, 264259, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265007, 265009, 264910, 264592, 264593, 264594, 264595, 264758, 264600, 264603, 264604, 264605, 264760, 264762, 264448, 264764, 264288, 264685, 264766, 264768, 264769, 21906766, 264691, 264692, 264693, 18108370, 264628, 264629, 18108374, 264630, 264631, 264634, 264636, 264637, 264638, 18108382, 83373044, 18108385, 264483, 264584, 264565, 264566, 264486, 264567
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294 - (AB001773) PEM-6 [Ciona savignyi]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264488, 264510, 264760, 264768, 264486

1866	94192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264567
1867	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044576) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 56526486
1868	86095641 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264564, 264565, 264566, 264567
1869	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1870	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1871	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134206 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264488, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21906765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278000, 264583, 264584, 264565, 264566, 264486
1872	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 dbj BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278998, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644296, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1873	86395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264555, 264556, 264557, 264558, 264559
1874	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	94316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 56182435, 265006, 264757, 55812038, 265010, 265017, 264369, 55811957, 65274791, 35695855, 56182323, 60432113
1976	95358614 (3951, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852664 (3953, 3954)	Novel Protein sim. GBank gi 2499526 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSporter (NA(+)/SULFATE COTRANSporter)		homeobox	264908, 264596, 265021, 264566
1978	87447645 (3955, 3956)	Novel Protein sim. GBank gi 103421 pir A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcription factor	60170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gi 2244815 emb CAB10238.1 - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	29331826, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21906768, 35695917, 265020, 60170615, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264565
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gi 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl- terminal hydrolase, X-linked		ubiquitin	264489
1981	87606974 (3961, 3962)	Novel Protein sim. GBank gi 4406693 gb AAD20060 - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264906, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21906767, 33657023, 27486264, 18108370, 18108374, 18108376, 264630, 264631, 264635, 18108385, 87168518, 22279000, 264482, 264564
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gi 5689523 db BA483045.1 - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gi 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	22278996, 35696286, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 264509, 264905, 264906, 264907, 66712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 264758, 265010, 264600, 264603, 264604, 264760, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21906765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35696423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1984	85760989 (3967, 3968)	Novel Protein sim. GBank gij2896695[emb]CAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264888, 21906766, 55811957, 56994075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33657182, 29146499, 264628, 18108370, 264908, 264629, 55811576, 35695855, 265006, 265007, 264591, 21906754, 33657084, 265010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131[gb]AAD47379.1[AF12049] DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264584
1986	80200507 (3971, 3972)			UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443[gb]AAD31319.1[AF14457] Mx-Interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain		22278999, 29331830, 265007, 265018, 21906768, 33657023, 264692, 264693, 18108377, 264635, 60170394, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264886, 264768, 265021, 284692, 264628, 264629, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc97 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52644045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85699888 (3979, 3980)	Novel Protein sim. GBank gij5701727[dbj]BAA83074.1] - (AB024729) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287[dbj]BAA74922.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01602) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35696286, 56994075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264685, 264766, 264687, 264769, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264584, 264486
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	29331827, 264906, 264807, 264909, 265007, 264603, 264766, 264686, 264768, 21906768, 264628, 264635, 264636, 18108385, 56526486, 264566, 264567
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG26 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35696423

1994	94329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC006017 similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	mapolymerase	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 264908, 265006, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 264684, 264369, 264685, 264686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 18108362, 264693, 65274620, 18108370, 264635, 264555, 264556, 264557, 56182323, 83373044, 56526486, 22279000, 22279002, 264564
1995	95414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit		UNCLASSIFIED	264488, 18108396, 22278994, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331826, 29331827, 35696052, 29146499, 264905, 264907, 66712502, 56182435, 265006, 265007, 265008, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 264448, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 264693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264631, 264634, 264635, 264555, 264636, 60431850, 264557, 264558, 264559, 83373044, 20798451, 87168518, 264404, 60432113, 264567 264564
1996	80254186 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020 - (X86028) extensin-like protein [Vigna unguiculata]		UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	phosphatase	264908, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 dbj BAA76839.1 - (AB023212) KIAA0995 protein [Homo sapiens]		UNCLASSIFIED	264113, 264685, 264555, 264567

1899	84324903 (3997, 3998)	Novel Protein sim. GBank gi 5225312 gb AAD40846.1 AF072441 - (AF072441) calciuretin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424269, 29331827, 29331828, 35696052, 265006, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264682, 264369, 284685, 284686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3999, 4000)	Novel Protein sim. GBank gi 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C1D4.10 IN CHROMOSOME I		UNCLASSIFIED	57646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21906754, 52644296, 265017, 265018, 265019, 264761, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 65274620, 52645129, 27486261, 27486262, 27486264, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526486, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi 107560 pir I B38637 - Ras inhibitor (clone JC265) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21906768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236368 (4003, 4004)	Novel Protein sim. GBank gi 729433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSOMAL PROTEIN) (P58)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264910, 264603, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gi 86388 pir I A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1 - (AL049996) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35686286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331824, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264908, 264592, 60433356, 33657402, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264763, 264683, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486282, 33657349, 27486285, 35695763, 18108374, 18108376, 18108377, 35696423, 35695855, 264631, 52644332, 264558, 18108385, 58526486, 87168518, 60432113, 264483
2005	87400864 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33366 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this gene...		ubiquitin	264488, 264906
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613 - (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 264259, 56182181, 60424269, 68714117, 35696052, 264906, 66712502, 264909, 264510, 60433356, 85658542, 265010, 265018, 265019, 264682, 264448, 264288, 264768, 29148627, 21906769, 29148784, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 55810764, 55811576, 35695855, 87168518, 60432113, 264563, 264482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007900) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265007, 264910, 264592, 264595, 264758, 265011, 264760, 264762, 264764, 264766, 264685, 264767, 264768, 264769, 55811957, 35695917, 265020, 264691, 264693, 264628, 264629, 65274791, 35695855, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 264566
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	264909, 264768, 35695855

2009	85749240 (4017, 4018)	Novel Protein sim. GBank gi 3882305 dbj BAA34512.1 - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	2227899, 264259, 264910, 264591, 265017, 264681, 264683, 21906768, 264691, 33657182, 33657349, 264631, 87168518, 264404, 22279002, 264563
2010	85422458 (4019, 4020)	Novel Protein sim. GBank gi 5262629 emb CAB45753.1 - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF000057) - Low-density lipoprotein receptor domain class A	eph	52644507, 52645156, 52646365, 52646842, 18108397, 65274572, 22278994, 56994075, 35698286, 22278996, 22278997, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432229, 60433356, 21906754, 52646317, 33109954, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 264691, 264692, 33657023, 263967, 52645129, 35695763, 18108376, 35698423, 65274791, 35695855, 264631, 264634, 60431850, 264637, 264638, 52644332, 60170394, 18108385, 87168518, 22279002, 264564, 264565, 264566, 264567
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gi 3347953 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35696052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265019, 264681, 264448, 264683, 264369, 264288, 264685, 264766, 264687, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 65274620, 33657109, 264629, 264557, 264559, 83373044, 87168518, 60432113, 22279002
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gi 1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29146498, 87168559, 265019, 264682, 264288, 264686, 21906764, 265020, 265022, 33657023, 264693, 33657109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264567
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gi 4507985 ref NP_003427.1 pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21906767, 265020, 264692
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gi 127720 sp P20938 MYPO_HETFR - MYELIN PO PROTEIN PRECURSOR		UNCLASSIFIED	264488, 29331826, 264907, 264636, 264555, 264639, 264558

2015	88094922 (4029, 4030)	Novel Protein sim. GBank gi 81286 pir S22697 - extensin - Volvox carteri (fragment)		UNCLASSIFIED	56182575, 35696286, 264259, 35696052, 264508, 264906, 264907, 264510, 264512, 87188474, 265010, 264681, 264288, 264689, 264628, 35696423, 35695855, 264639, 264563, 264584
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gi 285046 pir S26413 - t-complex protein Tc-10 - mouse		struct	264102, 264508, 264110, 265009, 33109954, 21906768, 265021, 33657109, 27486282, 263972, 18108374, 263976, 264555, 264564
2017	79464293 (4033, 4034)			UNCLASSIFIED	264685, 264636
2018	79637067 (4035, 4036)	Novel Protein sim. GBank gi 124735 sp P18175 INVO_PIG - INVOLUCRIN			264693
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gi 2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat		phosphatase	264107, 264110, 264112, 265017, 263976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gi 2078483 (U43200) - antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	264259, 264508, 264591, 265018, 264682, 264288, 264688, 22279002
2021	86718818 (4041, 4042)	Novel Protein sim. GBank gi 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 264593, 33109954, 21906754, 21906768, 33657023, 33657109, 27486261, 87188518
2022	95295665 (4043, 4044)	Novel Protein sim. GBank gi 4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			264757, 264767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gi 5410230 gb AAD42992.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	18108394, 22278999, 264259, 264905, 264906, 264908, 264595, 264762, 264769, 264634, 264636, 87188518, 60432113, 22279000, 264482, 264565
2024	87896443 (4047, 4048)				60433438, 265017, 264686, 264692, 264693, 264636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gi 475518 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 264509, 264906, 264909, 55812038, 265017, 265021, 265022, 60170615, 264556
2026	94122114 (4051, 4052)	Novel Protein sim. GBank gi 165569 emb CAA69032 - (Y07752) pterophorin-S [Volvox carteri]		UNCLASSIFIED	56994075, 60432049, 264508, 66712502, 264112, 60170831, 87188559, 264288, 264688, 264689, 21906766, 33657109, 18108370, 264638, 18108385, 60432113, 22279000, 22279002, 264564, 264566, 264567
2027	80249001 (4053, 4054)			UNCLASSIFIED	263978, 264634, 264486

2028	94699884 (4055, 4056)	Novel Protein sim. GBank gji1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - HECT-domain (ubiquitin-transferase).	ubiquitin	52644507, 52645156, 52646842, 56182575, 56994075, 35696286, 22278997, 22278998, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264906, 264907, 264908, 29331830, 52644045, 56182435, 265006, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264658, 83373044, 56526486, 22279000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank gji3599940 (AF017368) - facio-genital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED	18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432228, 29331826, 264108, 66712502, 264628, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264585
2030	91213734 (4059, 4060)	Novel Protein sim. GBank gji5630080 [gbjAAD5825.1] AC004890 similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	264591, 55811957, 18108365, 264557, 264558, 18108382, 18108384
2031	80245281 (4061, 4062)				65274572, 35696286, 29331824, 264908, 265009, 264593, 265018, 264288, 264686, 264769, 21906766, 21906767, 29148627, 264628, 35696423, 264634, 264556, 18108381, 60170394, 264559, 83373044, 18108385, 264482, 264484
2032	91232607 (4063, 4064)	Novel Protein sim. GBank gji5689491 [dbj] BAA83029.1 - (AB029000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase	56181562, 264628, 264632, 264555, 264556
2033	95000809 (4065, 4066)	Novel Protein sim. GBank gji2494828 [sp] Q64686 [CAG7 RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2,6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)]		synthase	
2034	91232529 (4067, 4068)	Novel Protein sim. GBank gji4826984 [ref] NP_005147.1 [PROD1 - UNKNOWN]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_mn_bind	22278996, 22278999, 264907, 29331830, 265008, 265018, 264681, 264682, 264684, 21906767, 21906768, 21906769, 33657109, 83373044, 56526486

2035	83553451 (4069, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gij2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331826, 29331828, 35696052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264594, 55812038, 33109954, 21906754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264563
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gij3880625[emb]CAB07858] - (Z93785) predicted using GeneFinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35696052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35696423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264564, 264566
2039	95514626 (4077, 4078)	Novel Protein sim. GBank gij224653[dbj]BAA20813] - (AB002354) KIAA0356 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35696423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gij2500625[sp]P70700[RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	rnapolymrase	UNCLASSIFIED	264488, 22278998, 35696052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21906766, 265021, 265022, 264692, 33657109, 264628, 264629, 35696423, 35695855, 264637, 264638, 264563, 264564, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gij440659[gb AAD20040] - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 264509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433356, 264595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21908765, 35695917, 264535, 52644150, 264691, 264692, 18108365, 27486261, 27486262, 27486265, 18108374, 35696423, 65274791, 35695855, 264555, 264558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gij5052554[gb AAD38607.1 AF145632] BcDNA GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264498, 52644507, 52646365, 56994075, 22278997, 22278999, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 29146498, 264509, 264908, 52644045, 56182435, 265006, 33657402, 21906754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264093, 29331827, 264905, 66712502, 264592, 264689, 21906765, 21906769, 265020, 264692, 264482, 264566
2045	79635532 (4089, 4090)				264892
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gij4406698[gb AAD20062] - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22279002
2047	84578601 (4093, 4094)	Novel Protein sim. GBank gij4101720 (AF006466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29146498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148628, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2048	84606378 (4095, 4096)			UNCLASSIFIED	264909
2049	88094690 (4097, 4098)	Novel Protein sim. GBank gij4589556[dbj BAA76850.1] - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21906767, 21906768, 264629, 264634, 264637, 22279002, 264584, 264565, 264566, 264567

2050	79633835 (409, 4100)			UNCLASSIFIED	264893
2051	87780168 (4101, 4102)			UNCLASSIFIED	264488, 264259, 264509, 264906, 264907, 264769, 18108374, 35696423, 264563, 264566, 264486
2052	88096393 (4103, 4104)	Novel Protein sim. GBank gi 4529889 gb AAD21812.1 - (AF134726) G9A [Homo sapiens]	Contains protein domain (PF00856) - SET domain	kinase	264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567, 264488, 263994, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264113, 264511, 265009, 264910, 60170831, 264592, 264758, 265010, 265011, 264605, 264760, 264682, 264764, 264369, 264766, 264686, 264768, 264769, 52644229, 264689, 35695917, 33657023, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264556, 264638, 264639, 18108385, 56526486, 60432113, 264563, 264564, 264566, 264486, 264567
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gi 2995449 emb CAA75113 - (Y14848) midline 1 protein [Mus musculus]		UNCLASSIFIED	22278996, 22278997, 264259, 29331822, 264102, 264508, 35695917, 263972, 264482
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gi 3876326 emb CAB02090 - (Z79754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain		60424179, 264094, 264259, 29331825, 60424269, 264906, 60432229, 60433356, 87168559, 265019, 264760, 264288, 264686, 21906769, 33657023, 264693, 55810764, 55811576, 264635, 56182323, 60432113
2055	88259449 (4109, 4110)	Novel Protein sim. GBank gi 5353746 gb AAD42226.1 AF159133 - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED	264488, 29331826, 60432289, 29331828, 60433356, 265019, 264683, 264684, 265021, 33657109, 18108374, 264637, 18108385, 87168518, 60432113, 22279000, 264564

2056	86177396 (4111, 4112)	Novel Protein sim. GBank gi 4826980 ref NP_005042.1 pQARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	- synthase	264486, 52645156, 56182575, 22278994, 35696286, 56994075, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 60432289, 29331827, 29331828, 33656970, 264104, 264908, 264908, 265006, 265008, 60170831, 264591, 60432228, 60433438, 18108348, 21906754, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 264760, 18108351, 264681, 264682, 264448, 264683, 264368, 264288, 264685, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108368, 33657182, 27486261, 27486264, 27486265, 33657349, 264628, 18108370, 264629, 18108374, 18108377, 18108379, 35696423, 55811576, 20281152, 264636, 264952, 18108385, 18108386, 87168518, 264482, 264565, 264566, 264567, 52646842, 52646365, 56182575, 35696286, 22278996, 22278997, 22278998, 264093, 52645080, 35696052, 29331828, 33656970, 265009, 52646317, 55811386, 52644296, 52644229, 21906769, 35695917, 265021, 60170615, 52644150, 33657109, 33657182, 27486261, 27486262, 35695763, 35696423, 35695855, 52644332
2057	87877905 (4113, 4114)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	
2058	86276896 (4115, 4116)				265007, 265008, 264591
2059	79866684 (4117, 4118)	Novel Protein sim. GBank gi 119714 sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 264682, 264686, 264691, 264693, 22279002
2060	83050800 (4119, 4120)	Novel Protein sim. GBank gi 2811122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331826, 264910, 55811957, 18108370, 55811576

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2496947 sp Q09298 YQ09_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29331828, 264906, 66712502, 29331830, 264908, 264909, 264112, 264511, 265007, 265009, 264910, 264591, 33657402, 21906754, 85658542, 265017, 265019, 264448, 264683, 264288, 264684, 264369, 264686, 264687, 18108358, 264689, 21906765, 21906767, 21906768, 21906769, 265020, 265022, 264691, 33657023, 33657109, 20281149, 18108379, 35695855, 264634, 264556, 264557, 264558, 18108382, 264559, 83373044, 18108384, 56528486, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - struct Ank repeat	264905, 264628, 264907, 264629, 264908, 264909, 18108374, 263978, 35695855, 264512, 264635, 60431850, 264636, 264760, 264563, 18108351, 264762, 264565, 264764, 264487, 264766
2063	87601272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 dbj BAA76803.1 - (AB023176) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - oncogene RasGEF domain	22278994, 22278999, 264259, 29331827, 264906, 264909, 52644045, 264686, 21906767, 55811957, 264692, 18108365, 263972, 55811576, 18108384, 22279002, 264482, 264563, 264564, 264484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 dbj BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]	hydrolase	264488, 52646365, 56994075, 35696286, 22278997, 22278998, 264259, 29331826, 60432289, 29331827, 29331828, 35696052, 264509, 265007, 265008, 60432229, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264761, 18108351, 264682, 264369, 264288, 52644229, 21906765, 21906767, 21906768, 35695917, 33657109, 18108388, 18108374, 35696423, 35695855, 52644332, 264559, 60432113, 22279000, 22279002, 264566, 264486
2065	95092238 (4128, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN	kinase	264569, 18108394, 56182181, 60432289, 29331826, 264905, 264906, 264908, 60431735, 60433356, 55811386, 85658542, 265018, 55811150, 264681, 264766, 264692, 60431528, 263974, 55810764, 35695855, 264631, 264634, 264635, 60431850, 264557, 83373044, 18108388, 22279000, 22279002
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein [Plasmodium yoelii]	Contains protein domain (PF00096) - UNCLASSIFIED Zinc finger, C2H2 type	56182575, 264259, 264906, 264764, 264288, 56182323, 264567

2067	95303892 (4133, 4134)				35696286, 22278997, 22278998, 60432049, 264259, 60432289, 60433438, 264682, 264448, 264369, 264288, 18108355, 21906765, 21906768, 265022, 33657109, 35696423, 35695855, 264558, 264404, 264553, 264486
2068	84344754 (4135, 4136)		UNCLASSIFIED		264687
2069	94319177 (4137, 4138)	Novel Protein sim. GBank gi 3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat		60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35696052, 29331828, 33656970, 264509, 264905, 56182435, 265009, 60433356, 87168559, 265017, 265018, 264604, 265019, 264448, 264764, 264766, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 33657109, 263976, 264555, 264557, 56182323, 83373044, 87168518, 60432113, 22279000, 22279002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gi 5712131 gb AAD47379.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	UNCLASSIFIED		35695917, 264905, 264628, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gi 3551531 dbj BAA33016 - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265006, 265007, 265008, 265009, 264594, 265010, 265011, 18108351, 18108354, 18108364, 18108365, 18108368, 264634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophysial hormones, C-terminal Domain		22278995, 35696286, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 265008, 33657402, 21906754, 265011, 265019, 18108351, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264690, 264692, 35696423, 264555, 264556, 264558, 22279000
2073	27925664 (4145, 4146)	Novel Protein sim. GBank gi 1504026 dbj BAA13212 - (D86976) similar to C.elegans protein (Z37093) [Homo sapiens]	UNCLASSIFIED		264556
2074	94324767 (4147, 4148)	Novel Protein sim. GBank gi 4240317 dbj BAA74937.1 - (AB020721) KIAA0914 protein [Homo sapiens]			29331822, 264909, 264511, 265009, 264594, 264595, 265010, 265011, 265017, 265018, 265019, 264448, 264683, 265020, 265021, 18108370, 264632, 83373044, 264567

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gij5138930jgb AAD40382.1 - (AF093880) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35696052, 29331828, 284905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264689, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 33657023, 27486262, 27486265, 35696423, 35695855, 264631, 264634, 264639, 87168518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331826, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)		UNCLASSIFIED	ubiquitin	264592
2078	87539364 (4155, 4156)	Novel Protein sim. GBank gij4220590jdbj BAA74579 - (D87908) nuclear protein np95 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger		29331825, 265017, 265018, 264288, 265020, 265021, 264634, 56528486
2079	88085916 (4157, 4158)	Novel Protein sim. GBank gij4240255jdbj BAA74906.1 - (AB020690) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264906, 264907, 264628, 20281069, 264909, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264563, 264564, 264448, 264684, 264567, 264685
2080	94136689 (4159, 4160)	Novel Protein sim. GBank gij2408021jemb CAB16219.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gij5524734jgb AAD44360.1 AF16635 - (AF166350) ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - eph CUB domain		22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85658542, 265011, 265018, 265019, 21906787, 21906768, 264693, 18108385, 22279000, 22279002
2082	87628629 (4163, 4164)	Novel Protein sim. GBank gij3880558jemb CAA94234 - (Z70271) predicted using Genefinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264907, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264509, 264112, 265009, 264593, 21908754, 265018, 265019, 264448, 264288, 264685, 21906769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264563
2084	95189298 (4167, 4168)	Novel Protein sim. GBank gij728836jsp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	94989476 (4169, 4170)	Novel Protein sim. GBank gi 165569 emb CAA69032 - (Y07752) perophorin-S [Volvox carter]		UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264763, 264369, 264686, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gi 3875032 emb CAA88936 - (Z49125) similarity to Trichostrongylus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 come...		UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35696423, 35695855, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)			UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gi 3880930 emb CAA16334.1 - (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080....		UNCLASSIFIED	264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35696423, 35695855, 83373044, 87168518, 22279000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gi 4758118 ref NP_004623.1 pDAP3 - Death associated protein 3	cadherin		18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278996, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29146498, 29146499, 264102, 264106, 264107, 264109, 264508, 264905, 264509, 264906, 264907, 264908, 66712502, 264828, 52644045, 264909, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21908754, 33657084, 55811386, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108358, 56181562, 264769, 18108359, 264689, 21908765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 29148629, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690

2080	88222470 (4179, 4180)				22278995, 22278998, 22278999, 264259, 29331826, 35696052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265022, 60170615, 33657023, 35696423, 35695855, 264952, 18108387, 22279000
2091	95309161 (4181, 4182)	Novel Protein sim. GBank gij4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	263994, 264905, 264908, 264511, 264512, 265008, 264910, 55611386, 264288, 264768, 56181562, 21906765, 21906768, 21906769, 265022, 264628, 264563, 264567
2092	88223605 (4183, 4184)			homeobox	22278997, 22278999, 66712502, 87168559, 264683, 265021, 264486
2093	87406073 (4185, 4186)	Novel Protein sim. GBank gij2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus cuniculus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264905, 264906, 264907, 264908, 264510, 265006, 265007, 265009, 264910, 264596, 21906754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21906767, 21906768, 21906769, 265021, 264690, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264584
2094	91230929 (4187, 4188)	Novel Protein sim. GBank gij4929551 gb AAD34036.1 AF15179 - (AF151799) CGI-40 protein [Homo sapiens]		MHC	35696286, 265017, 265018, 265019, 18108388
2095	95351526 (4189, 4190)	Novel Protein sim. GBank gij1363238 pir A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_rna_bind	35696286, 52644045, 265006, 265007, 265008, 87168559, 18108351, 21908769, 29148784, 265020, 33657023, 27486262, 18108374, 18108388
2096	94119760 (4191, 4192)	Novel Protein sim. GBank gij3834423 (AF070689) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182575, 22278996, 22278997, 22278999, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 52644045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21906754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 52644150, 264691, 264692, 33657023, 264693, 27486261, 35695763, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264638, 264639, 264563, 264483, 264565, 264566, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi 5174501 ref NP_006051.1 p YF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170615, 264892, 33657109, 18108370, 264635, 264483
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi 4758208 ref NP_004081.1 p DUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	56994075, 264259, 264288, 265020, 264563
2099	95412927 (4197, 4198)	Novel Protein sim. GBank gi 2685659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDPr [Bos taurus]		phosphatase	65274572, 264905, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi 3881189 emb CAB16514 (Z98281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nucl_rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 29146498, 264909, 265008, 265009, 264910, 264591, 60432229, 60433356, 33657402, 264758, 21906754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21906765, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108374, 35696423, 264558, 83373044, 87168518, 60432113, 22279000, 22279002, 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87762604 (4201, 4202)	Novel Protein sim. GBank gi 4589468 db BAA76761.1 (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	264088, 264489, 35696286, 264259
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi 3874149 emb CAA97423.1 (Z73103) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	35696052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433356, 264758, 264601, 264605, 264760, 18108351, 264448, 264764, 264288, 264767, 264768, 21906769, 35695917, 18108374, 264634, 264555, 264559, 264563, 264482, 264488
2103	95413576 (4205, 4206)	Novel Protein sim. GBank gi 4240159 db BAA74858.1 (AB020642) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278999, 264259, 29331824, 29331825, 35696052, 29331828, 66712502, 265009, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21906765, 21906768, 265022, 33657023, 27486262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	94848080 (4209, 4210)	Novel Protein sim. GBank gi 1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g6.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....		UNCLASSIFIED	264488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264508, 264905, 264509, 264907, 29331830, 52644045, 264510, 264511, 265007, 264512, 265009, 60170831, 60432229, 33657402, 60433356, 264595, 60433438, 264758, 33657084, 87168474, 265010, 87168559, 265017, 265018, 265019, 264762, 18108351, 264684, 18108354, 264288, 264686, 52644229, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 52644150, 264692, 33657023, 264693, 33657109, 60431528, 18108374, 65274791, 35695855, 264635, 60170394, 264639, 264558, 18108385, 18108387, 56526486, 87168518, 60432113, 264564, 264566, 264567
2106	83365475 (4211, 4212)				265006, 265019
2107	79822662 (4213, 4214)	Novel Protein sim. GBank gi 3881524[emb CAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]			264906, 264639
2108	94233976 (4215, 4216)	Novel Protein sim. GBank gi 3176689 (AC003671) - Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]		UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264758, 265011, 264600, 264601, 264764, 264766, 264767, 264768, 264769, 264693, 264629, 35695855, 264632, 264634, 264635, 264638, 264639, 83373044, 264486
2109	80478719 (4217, 4218)			UNCLASSIFIED	18108348, 264769, 18108370, 18108374, 264555, 264556, 264557, 264558
2110	87729075 (4219, 4220)	Novel Protein sim. GBank gi 481043 pir S37671 - bat2 protein - human		UNCLASSIFIED	264564
2111	87818419 (4221, 4222)			UNCLASSIFIED	264766, 35695917, 264630, 264567, 264486
2112	87293783 (4223, 4224)	Novel Protein sim. GBank gi 2143639 pir S56542 - calmodulin-binding protein - rat	Contains protein domain (PF00069) - struct	UNCLASSIFIED	264508, 264906, 264591, 264682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gi 426629 gb AAD20459 - (AF100960) protocadherin [Rattus norvegicus]	Eukaryotic protein kinase domain		265006
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gi 3327184 dbj BAA31660 - (AB014585) KIAA0685 protein [Homo sapiens]	Contains protein domain (PF00028) - cadherin		66714117, 29331826, 29331827, 60433438, 55812038, 265017, 265019, 264689, 21906769, 55811857, 265020, 265021, 33657109, 60170394, 264558
2115	90993785 (4229, 4230)	Novel Protein sim. GBank gi 4757890 ref NP_004328.1 pc8OR - chromosome 8 open reading frame 1		UNCLASSIFIED	65274572, 264689, 264691, 264692, 60432113

2116	88250387 (4231, 4232)	Novel Protein sim. GBank gjl2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	3569286, 22278999, 56182181, 29331824, 29331825, 29331827, 35696052, 264907, 56182435, 265008, 264591, 55812038, 55811386, 87168559, 264288, 264369, 21906769, 29148629, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788904 (4233, 4234)	Novel Protein sim. GBank gjl2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	29331824, 264511, 265009, 33109954, 265017, 265018, 264288, 264689, 265020, 264692, 56526486, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gjl1078307 [pir]B56573 - nuclear pore complex glycoprotein p62 - African clawed frog		glycoprotein	264259, 264905, 264907, 264908, 264510, 264511, 265009, 264910, 265010, 264602, 264288, 264768, 264693, 263967, 263972, 264638, 264559
2119	8699317 (4237, 4238)	Novel Protein sim. GBank gjl4321407 [gb]AAD15748 - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	264693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gjl4885527 [ref]NP_005480.1 [pNSP3 - novel SH2-containing protein 3]	Contains protein domain (PF00017) - Src homology domain 2	eph	264091, 264259, 29331826, 29331828, 265017, 264604, 264288, 264685, 265020, 264691, 18108370, 55810764, 264555, 264636, 60432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gjl475728 [ref]NP_004886.1 [pAGTA - angiotensin/vasopressin receptor AII/AVP-like]		UNCLASSIFIED	264601, 264766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gjl4929551 [gb]AAD34036.1 [AF151799] CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 264907, 56182435, 265007, 264910, 265010, 265018, 264686, 265020, 55811576, 264555, 264637, 18108382, 83373044, 18108383, 18108384, 56528486, 264565, 264567
2123	86787988 (4245, 4246)	Novel Protein sim. GBank gjl2224551 [dbj]BAA20764 - (AB002303) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYVE zinc finger	struct	18108396, 264757, 265011, 18108351, 264691, 264634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gjl5609455 [dbj]BAA83011.1 - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 264906, 264907, 264591, 264639, 264563
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gjl28831 [sp]P39188 [ALU1_HUMAN - III] ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	264259, 264509, 264907, 264511, 85658542, 264763, 21906765, 35695917, 264636, 264486
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gjl4539264 [emb]CAB39853.1 - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	264488, 264489, 29331827, 35696052, 264905, 264509, 264908, 264909, 264510, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264596, 264758, 264601, 264603, 265018, 264604, 264605, 264760, 264681, 264762, 264683, 264764, 264684, 264288, 264685, 264689, 60170615, 33657023, 33657109, 55810764, 264635, 264636, 264637, 264638, 264639, 83373044, 264564, 264566

2127	81118652 (4253, 4254)	Novel Protein sim. GBank gij4868435gb AAD31315.1 AF14323 - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35696286, 29331826, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 264512, 265007, 265009, 264910, 264758, 265011, 264600, 264601, 264604, 264762, 264763, 264766, 264687, 264768, 264769, 264689, 35695917, 264690, 264691, 264692, 264693, 264629, 18108374, 35695855, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264553, 264554, 264567, 56182575, 35696286, 56182181, 29331824, 60432289, 35696052, 264905, 264907, 66712502, 264908, 264909, 264510, 264512, 265009, 264910, 264591, 55812038, 265018, 264764, 264288, 264369, 264687, 264768, 55811957, 264692, 18108388, 264628, 264632, 264634, 264635, 264637, 56182323, 264639, 18108384, 18108388, 264563, 264567
2128	87414262 (4255, 4256)				66714117, 264828, 264595, 55812038, 55811150, 55811957, 264693, 18108374, 263978, 65274791, 18108381, 83373044, 22279000
2129	95102089 (4257, 4258)		UNCLASSIFIED		263981
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gjl2649255 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gjl1086886 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]	potassium_channel	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	35696052, 264909, 264768, 35695917
2132	95361096 (4263, 4264)	Novel Protein sim. GBank gjl5689373dbj BAA82973.1 - (AB028944) KIAA1021 protein [Homo sapiens]	ATPase_associated	Contains protein domain (PF00122) - E1-E2 ATPase	264488, 22278999, 264259, 29331827, 29331828, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264910, 264591, 264592, 264595, 264758, 21906754, 33109954, 87168474, 265011, 264600, 264601, 264605, 265019, 264760, 18108351, 264681, 264762, 264764, 264288, 264684, 264766, 264686, 264687, 264768, 264769, 264688, 21908769, 264690, 52644150, 264691, 264693, 18108370, 264628, 264629, 18108372, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264636, 264555, 264637, 18108380, 264639, 264558, 56182323, 56526486, 264564, 264565, 264566, 264567

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gi 4220489 (AC006069) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	60424179, 52646365, 52646842, 56994075, 35696286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21906754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264369, 264288, 52644229, 56181562, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657109, 60431528, 18108374, 35696423, 65274791, 35695855, 264634, 60431850, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264566
2134	95412687 (4267, 4268)	Novel Protein sim. GBank gi 3875351[emb]CAB09415] - (Z96047) DY3.6 [Caenorhabditis elegans]			56181686, 35696286, 21906754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21906768, 35695917, 265020, 33657023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gi 5689559[dbj]BAA83063.1] - (AB029034) KIAA1111 protein [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264758, 52646317, 265011, 87168559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33657023, 264692, 35695763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84346478 (4271, 4272)	Novel Protein sim. GBank gi 2662167[dbj]BAA23715] - (AB007903) KIAA0443 [Homo sapiens]		UNCLASSIFIED	264639
2137	87637716 (4273, 4274)	Novel Protein sim. GBank gi 4884110[emb]CAB43262.1] - (AL050090) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264569, 264909, 33109954, 264763, 21906768, 60170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gi 5174779[gb]AAD40696.1] - (U87804) 50 kDa protein [Caulobacter crescentus]		ATPase-associated	264259, 29331828, 35696052, 264909, 265006, 265017, 265018, 18108351, 264288, 21906768, 33657023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843882 (4277, 4278)	Novel Protein sim. GBank gi 3850821[emb]CAA77135] - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]			264905, 264910, 264591, 55812038, 55811386, 85658542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33657023, 18108364, 55811576, 83373044, 18108385, 56526486, 264482

2140	87645655 (4278, 4280)	Novel Protein sim. GBank gi 4417293 gb A020418 - (AC007018) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265006, 264769, 265018, 264448, 264288, 21908768, 55811957, 265021, 33657023, 27488265, 35696423, 264636, 264556, 264557, 264559, 264566
2141	79623986 (4281, 4282)		UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank gi 2135766 pir S53362 - mucin 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank gi 2078483 (U43200) - antilfreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida]	UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264906, 264908, 264591, 265011, 87168559, 264600, 265019, 264288, 264768, 21908765, 21906767, 55811576, 35696423, 65274791, 22279002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank gi 1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264909, 60433356, 264686
2147	80432911 (4293, 4294)	Novel Protein sim. GBank gi 3080398 emb CAA18718.1 - (AL022603) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264907, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III	UNCLASSIFIED	264593
2149	87362022 (4297, 4298)	Novel Protein sim. GBank gi 119863 sp P20693 FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	29331824, 29331826, 35696052, 264758, 87168474, 265018, 52644150, 33657109
2150	84140059 (4299, 4300)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21906766, 264486
2151	95353241 (4301, 4302)	Novel Protein sim. GBank gi 5689407 dbj BAA82987.1 - (AB028958) KIAA1035 protein [Homo sapiens]		22278996, 56994075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 29331828, 264508, 264511, 60433356, 264758, 264596, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264688, 21906765, 21906766, 21908768, 265020, 60170615, 33657109, 33657182, 33657349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	88313371 (4305, 4306)	Novel Protein sim. GBank gij4758704[ref]NP_004216.1lpMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263394, 52646842, 22278996, 22278998, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265019, 264760, 264288, 264368, 264766, 264687, 264769, 52644229, 21906768, 21906768, 35695917, 33657023, 33657109, 35695855, 264631, 264632, 264635, 264636, 264639, 18108385, 264483, 264594, 264486
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gij225150[prf]1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56994075, 264094, 265009, 265019, 264288, 21908767, 35695917
2155	87424072 (4309, 4310)			UNCLASSIFIED	18108392, 18108398, 22278996, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84295205 (4311, 4312)	Novel Protein sim. GBank gij3970966 (AC004974) - spa-1- like, similar to AF026504 (PID:g2555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gij1076211[prf]S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gij4650844[dbj]BAA77027.1 - (AB026190) Ketch motif containing protein [Homo sapiens]			264596
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gij2879925[dbj]BAA24826 - (AB007897) KIAA0437 [Homo sapiens]	Contains protein domain (PF00551) - BTB/POZ domain	dna_rna_bind	29331822, 264112, 265009, 264691, 33657023, 264634
2160	16283674 (4319, 4320)				264634
2161	87739131 (4321, 4322)	Novel Protein sim. GBank gij1504006[dbj]BAA13202 - (D86966) similarto human ZFY protein. [Homo sapiens]		UNCLASSIFIED	265008
2162	94319526 (4323, 4324)			UNCLASSIFIED	65274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264688, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264566, 264567
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gij3876537[emb]CAA98270 - (Z73974) cDNA EST yk291f5.3 comes from this gene; cDNA EST yk291f5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278996, 264093, 264683, 33657023, 65274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01006) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264565

2165	94329169 (4329, 4330)	Novel Protein sim. GBank gij1086794 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 29331830, 58182435, 265009, 21906754, 33657084, 265011, 265019, 264448, 264288, 264389, 21906765, 21906768, 21906769, 265020, 265021, 264691, 264692, 33657023, 65274620, 35695855, 264556, 60170394, 83373044, 60432113, 22279002, 264567
2166	87618934 (4331, 4332)	Novel Protein sim. GBank gij2706522[emb]CAA75816] - (Y15895) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		52645156, 22278994, 22278998, 66714117, 29331828, 52644045, 265018, 265019, 264369, 21906765, 21906767, 21906768, 21906769, 265021, 265022, 264693, 27486262, 35695763, 18108376, 56526486, 87168518, 264567
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gij2224713[dbj]BAA20840] - (AB002384) KIAA0386 [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 29146498, 58182435, 265008, 265009, 264592, 264593, 33657402, 33109954, 265011, 265017, 265018, 18108351, 264369, 21906764, 21906765, 21906768, 29148627, 21906769, 52644150, 33657109, 35696423, 18108381, 18108384, 18108385, 60432113, 264567
2168	86999334 (4335, 4336)	Novel Protein sim. GBank gij4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	Contains protein domain (PF00664) - ABC transporter transmembrane region.	transport	66714117, 29331827, 264907, 264511, 264591, 265018, 264764, 264683, 264766, 264768, 264568
2169	87868937 (4337, 4338)				264629, 264555, 264559
2170	94141033 (4339, 4340)	Novel Protein sim. GBank gij5106521[gb]AAD39741.1[AF10536] - (AF105365) K-CI cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	63274572, 56182575, 22278997, 22278998, 264259, 29331825, 264509, 264906, 56182435, 60433436, 55812038, 264596, 55811386, 265019, 264762, 264763, 264448, 264764, 264684, 264288, 264766, 264685, 56181562, 264689, 55811957, 265020, 264535, 264691, 33657109, 60431528, 18108374, 35696423, 55811576, 65274791, 264634, 264639, 264558, 87168518, 60432113, 264564
2171	80194050 (4341, 4342)			UNCLASSIFIED	264369, 265020, 264558
2172	85452460 (4343, 4344)			UNCLASSIFIED	264259, 264558
2173	87036740 (4345, 4346)	Novel Protein sim. GBank gij4309681[gb]AAD15478] - (AC006930) R33423.1 [Homo sapiens]		UNCLASSIFIED	264369
2174	95003288 (4347, 4348)	Novel Protein sim. GBank gij2493778[sp]Q09456[YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5]			264906, 35695855, 264555, 264557

2175	94325850 (4349, 4350)	Novel Protein sim. GBank gij1263287 (U47855) - fibrin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35696052, 264109, 284508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264600, 264603, 264760, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21906768, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264486, 264567
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gij728837ispj39194/ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!	Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 264910, 33657402, 264758, 52644296, 87168559, 265018, 264689, 21908785, 21906767, 21906769, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108376, 18108377, 35695855, 87168518, 60432113, 264404, 22279000, 264486 18108392, 22278997, 22278999, 264093, 33657402, 265019, 264448, 264766, 264689, 21906767, 21906768, 21906769, 265021, 33657023, 18108370, 18108374, 60432113, 22279002
2177	94128942 (4353, 4354)	Novel Protein sim. GBank gij5454072refjNP_006416.1pSLU7 - step II splicing factor SLU7		kinase	
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gij473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644296, 87168474, 18108370, 35695855, 22279002, 60424269, 264760, 264628, 264632
2179	87316275 (4357, 4358)			UNCLASSIFIED	

2180	95351397 (4359, 4360)	Novel Protein sim. GBank gi 3122317 sp P90648 KMH_B_DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21906765, 21906766, 21906769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27486265, 33657349, 18108374, 35696423, 35695855, 263981, 60170394, 18108385, 56526486, 87168518, 60432113, 22279000, 264482, 264566, 264567, 264486 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gi 3024689 sp Q15542 T2D4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIID 100 KD SUBUNIT (TAFII-100) (TAFII100)		kinase	
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (A)243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	22278986, 22278997, 22278999, 264259, 29331822, 56182435, 264112, 264764, 264288, 21906767, 21906768, 21906769, 33657109, 18108376, 60170394, 22279000, 22279002 264760
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gi 3873406 gb AAC77482.1 - (U17129) unknown [Rhodococcus erythropolis]		Inf	29331822, 29331825, 29331826, 56182435, 265011, 264685, 264686, 21906768, 18108370, 264629, 264631, 264636, 264557 29331824, 264907, 66712502, 264757, 265019, 264288, 264692, 56526486
2184	87760690 (4367, 4368)	Novel Protein sim. GBank gi 3114713 (AF061346) - Edp1 protein [Mus musculus]			
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF113615) - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]			
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gi 2864625 emb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]		ATPase-associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264760, 264768, 55811957, 33657023, 55811576, 56182323, 264563
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264566, 264486 18108398, 56994075, 264259, 29331824, 29331825, 66714117, 29331827, 264906, 29331830, 265018, 265020, 265021, 56182323, 264559, 22279000, 22279002
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gi 5107816 gb AAD40129.1 AF14941 - (AF14941) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gi 3452357 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01596) - O-methyltransferase		22278996, 264259, 29331826, 21906754, 264369, 264288, 263987

2190	87639197 (4379, 4380)	Novel Protein sim. GBank gij132575 spP29315 IRINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278996, 22278999, 29331822, 29331824, 29331826, 265008, 264910, 60170831, 55812038, 52644296, 265010, 265018, 264685, 264688, 56181562, 21906769, 35695917, 265022, 60170394, 22279000
2191	95198928 (4381, 4382)	Novel Protein sim. GBank gij5327002 emb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			29331825, 29331826, 29331830, 264510, 264511, 264910, 264593, 264594, 264556, 264559
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462600 spP34400 MI10_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		264558
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181686, 29331825, 29331827, 264508, 264909, 265008, 264592, 60432229, 264288, 264684, 264766, 35695917, 33657023, 60431602, 60431528, 55810764, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			264592
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763 emb CAA15685.1 - (AL009191) /prediction=(method:; /prediction=(method:; /match=(desc:; /match=(desc:; /molif=(desc: [Drosophila melanogaster]		UNCLASSIFIED	22278996, 22278999, 35696052, 265006, 21906754, 265017, 35695917, 265021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gij5262487 emb CAB45699.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 264259, 29331822, 66714117, 60432289, 29331827, 35696052, 29331828, 264508, 52644045, 56182435, 264510, 265007, 265008, 265009, 60433438, 55812038, 265010, 265011, 264448, 264288, 264686, 264687, 52644229, 21906765, 21906766, 21906767, 35695917, 265022, 264691, 33657023, 264693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 264636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929567 gb AAD34044.1 AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			264768, 264769, 21906765, 21906766, 21906767, 29148627, 55811957, 35696286, 265020, 22278998, 265021, 264259, 33657023, 264693, 29331824, 35696052, 29331828, 18108370, 35695855, 264113, 265008, 264910, 60432229, 56182323, 33657402, 264758, 83373044, 21906754, 265018, 265019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88060914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953_1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gjl2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]			264105, 264110, 264112, 264688, 55811957, 33657023, 264692, 263967, 20281071, 56526486
2200	87405385 (4399, 4400)	Novel Protein sim. GBank gjl3043634[dbj][BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct		29331824, 264763, 264768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gjl3913470[sp][O57314][DHBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2	Contains protein domain (PF00106) - short chain dehydrogenase		29331824, 35696052, 264905, 264907, 33657402, 55811386, 265017, 265018, 265019, 264288, 21906768, 35695917, 265020, 265022, 33657023, 33657109, 27486261, 18108370, 35696423, 35695855, 264555, 264556, 83373044, 87168518, 60432113
2202	91672385 (4403, 4404)	Novel Protein sim. GBank gjl5262665[emb][CAB45767.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264489, 264259, 29331824, 60432289, 35696052, 264905, 264909, 264592, 265017, 265018, 265019, 18108351, 264762, 264448, 264369, 264288, 264766, 21906765, 21906766, 264690, 264691, 264692, 33657109, 264634, 264636, 264555, 264639, 264558, 264559, 83373044, 18108385, 264404, 22279002, 264482
2203	87761832 (4405, 4406)	Novel Protein sim. GBank gjl1172845[sp][P46629][R25_RABIT - RAS-RELATED PROTEIN RAB-25	Contains protein domain (PF00071) - Ras family	glycoprotein	57646365, 56994075, 264259, 29331822, 29331826, 29331827, 29331828, 264910, 265010, 265011, 87168559, 265018, 265019, 264605, 264288, 21906769, 35695917, 33657023, 264692, 33657109, 35695763, 18108376, 264638, 22279000, 264566, 264567
2204	88086671 (4407, 4408)	Novel Protein sim. GBank gjl121036[sp][P29348][GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN G(T), ALPHA-3 SUBUNIT (GUSTOCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED	
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gjl4589480[dbj][BAA76768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_na_bind	18108394, 18108397, 56182575, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 264906, 265007, 265008, 265009, 60432229, 265010, 265011, 265018, 264683, 264288, 264369, 264686, 21906766, 21906768, 21906769, 264690, 264691, 264693, 18108368, 55811576, 65274791, 264634, 18108381, 18108384, 60432113, 22279002, 264563, 264566, 264591
2206	20620008 (4411, 4412)		UNCLASSIFIED		264591
2207	87787970 (4413, 4414)	Novel Protein sim. GBank gjl4557753[ref][NP_000372.1pMID1 - midline 1 protein	Contains protein domain (PF00622) - SPRY domain		29331822, 56182181, 29331827, 35696052, 52644045, 265006, 265019, 56181562, 55811957, 265021, 33657023, 35695763, 35695855, 60170394, 60432113, 264566
2208	86100830 (4415, 4416)				264906, 265019, 18108351, 21906769
2209	87800420 (4417, 4418)	Novel Protein sim. GBank gjl3986746 (AF105228) - lufelin [Bos taurus]	struct		264112, 265009, 264691, 18108365, 18108374, 264634, 20281166

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	264685, 264686, 18108365, 22279002, 264482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA09214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278999, 264092, 264094, 29331822, 66714117, 29331826, 29331828, 264907, 52644045, 265009, 60170831, 21906754, 87168559, 265017, 265019, 18108351, 264683, 18108354, 264369, 264766, 264887, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 33657109, 18108370, 18108374, 264638, 56182323, 18108384, 18108387, 87168518, 264565
2213	91219309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			56182575, 22278996, 22278997, 35696052, 264905, 66712502, 264908, 264828, 56182435, 264112, 265008, 60431735, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 18108351, 264765, 21906765, 21906768, 21906769, 265020, 265021, 264693, 264629, 263974, 263976, 18108379, 55811576, 264556, 264637, 264558, 83373044, 22279002, 264482, 264483

2214	95361453 (4427, 4428)	Novel Protein sim. GBank gi 4504325 ref NP_000173.1 pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52644507, 18108394, 56182575, 22278994, 22278995, 35696286, 56994075, 22278997, 22278998, 22278999, 264490, 60432049, 264259, 52645080, 29331822, 29147620, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 20281100, 264509, 264907, 66712502, 264908, 29331830, 52644045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433356, 60433438, 33109954, 33657084, 52644298, 87168474, 285010, 265011, 87168559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 264532, 60170615, 264690, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 33657182, 27486262, 27486264, 27486265, 35695763, 18108370, 264629, 60431528, 18108374, 18108376, 55810764, 35696423, 35695855, 264634, 264636, 52644332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264566, 264909, 265006, 264555, 264558, 87168518
2215	95419206 (4428, 4430)	Novel Protein sim. GBank gi 1947160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614046 (4431, 4432)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	UNCLASSIFIED	264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gi 5031707 ref NP_005503.1 pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264556
2218	85518254 (4435, 4436)	Novel Protein sim. GBank gi 3878636 emb CAA88953 - (Z49128) similar to cAMP-dependant protein kinase; cDNA EST EMBL: T00719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk492i4.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35696423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gi 1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388268) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108378

2220	95354165 (4439, 4440)	Novel Protein sim. GBank gil4507261[ref]NP_003145.1[pSTAT - staltherin			264488, 18108394, 18108395, 35696286, 264259, 264097, 60432289, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264510, 264511, 265007, 264512, 264910, 265009, 264593, 264594, 60433356, 264595, 55812038, 264758, 85658542, 265010, 264601, 264603, 265019, 264605, 264760, 264762, 264448, 264764, 264369, 264766, 18108357, 264768, 264687, 18108358, 264769, 55811957, 264690, 264691, 33657023, 264692, 18108362, 18108368, 264628, 264629, 18108374, 263978, 264634, 264635, 264636, 264637, 264638, 18108385, 264483, 264566, 264486, 264567
2221	88060927 (4441, 4442)	Novel Protein sim. GBank gil3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	264908, 265020, 35695855
2223	95091649 (4445, 4446)			UNCLASSIFIED	265010, 264685, 264690, 264693, 264628, 263974, 263976, 55811576, 264555, 264638, 83373044, 264483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank gil3876005[emb]CAA84799] - (Z35719) cDNA EST EMBL:D67419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES...	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	264259, 264509, 56182435, 265006, 265008, 265009, 264757, 21906754, 18108351, 264693, 18108374, 18108385
2225	85748484 (4449, 4450)	Novel Protein sim. GBank gil1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans]	transport		22278994, 22278995, 22278999, 52644045, 264600, 265019, 21908765, 21908769
2226	86978953 (4451, 4452)	Novel Protein sim. GBank gil4826524[emb]CAB42852.1] - (AL049848) hypothetical protein [Homo sapiens]			264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265007, 264691, 264634, 264486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 265006, 265008, 18108354, 29148629, 29148784, 27486261, 18108374, 264637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank gil606976 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	264091, 264092, 264094, 29331822, 29331825, 66714117, 264693, 263972, 264639, 83373044, 264563
2229	88060931 (4457, 4458)	Novel Protein sim. GBank gil3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342815 (4459, 4460)	Novel Protein sim. GBank gij26154 prfj 1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264488, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 29331827, 264508, 264509, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	88060937 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328_1 [Homo sapiens]		UNCLASSIFIED	
2232	87762581 (4463, 4464)	Novel Protein sim. GBank gij5281316 gb AAD41476.1 AF133124) transcription factor IIC63 [Homo sapiens]		transcription factor	18108394, 56182575, 22278995, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264758, 55812038, 264603, 265018, 265019, 18108351, 264682, 264764, 264683, 264369, 264288, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264690, 52644150, 264691, 33657023, 264693, 18108370, 18108374, 55811576, 35695855, 264639, 18108385, 264564, 264906, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385
2233	87755292 (4465, 4466)	Novel Protein sim. GBank gij4249733 gb AAD13780 - (AF109377) IdIBp [Mus musculus]			kinase
2234	87771817 (4467, 4468)	Novel Protein sim. GBank gij1706559 sp P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)			
2235	91012316 (4469, 4470)	Novel Protein sim. GBank gij4972734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278997, 264563
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675 prfj B53814 - p20 protein - human	Contains protein domain (PF00011) - Hsp20/alpha crystallin family	eph	264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734 gb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22279000, 265019, 22279002, 264482, 18108351, 264288

2238	94998857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein		264509, 264907, 264629, 264634, 264564
2239	87798688 (4477, 4478)				29331825, 265009, 264369, 33657109, 18108370, 18108374, 264557, 264559
2240	94121471 (4479, 4480)	Novel Protein sim. GBank gi 2982311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Ubiquitin-conjugating enzyme	ubiquitin	264488, 65274572, 56182575, 35696286, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 52644045, 56182435, 264511, 265007, 265008, 265009, 60433356, 60433438, 55812038, 21906754, 33657084, 55811386, 265018, 265019, 18108351, 264683, 264288, 264768, 264687, 264688, 264769, 21906765, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695763, 18108370, 35696423, 35695855, 87168518, 22279000
2241	80091951 (4481, 4482)			UNCLASSIFIED	264693, 264629
2242	91228075 (4483, 4484)	Novel Protein sim. GBank gi 2494312 sp P70541 E2BG_RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)		synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264369, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 27486264, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87168518, 264564
2243	78902026 (4485, 4486)			UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gi 2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]		UNCLASSIFIED	264604
2245	95318545 (4489, 4490)	Novel Protein sim. GBank gi 470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 60433438, 264758, 21906754, 265011, 264603, 264764, 264687, 21906767, 21906768, 21906769, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 60432113, 22279000, 22279002, 264566

2246	94848710 (4491, 4492)	Novel Protein sim. GBank gi 4996096 dbj BAA78326.1 - (AB028069) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 35696052, 264108, 264905, 264907, 265006, 265007, 265008, 60433438, 33109954, 87168559, 265018, 265019, 264288, 21906765, 21906767, 21906768, 21906769, 55811957, 35695917, 285020, 265022, 27486264, 18108370, 18108374, 65274791, 35695855, 60432113
2247	87662542 (4493, 4494)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	UNCLASSIFIED	52645156, 52646365, 52645080, 35696052, 33656970, 52646317, 33657084, 265017, 21906768, 21906769, 35695917, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 27486265, 18108387
2248	95412986 (4495, 4496)	Novel Protein sim. GBank gi 4758502 ref NP_004123.1 pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	264488, 264259, 264907, 29331830, 264909, 265007, 265009, 264595, 21906754, 65274444, 264603, 265019, 264762, 264448, 264288, 264689, 21906766, 55811957, 265021, 264691, 18108374, 264634, 264635, 264636, 264555, 264638, 264557, 264558, 264559, 18108383, 83373044, 18108385, 264488
2249	94685662 (4497, 4498)	Novel Protein sim. GBank gi 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	264766, 264628, 264636, 264637
2250	79827508 (4499, 4500)	Novel Protein sim. GBank gi 3738140 emb CAA21241 - (AL031852) vavl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	UNCLASSIFIED	264908, 18108374
2251	87385863 (4501, 4502)	Novel Protein sim. GBank gi 3218467 emb CAA07090.1 - (AJ006529) putative phosphatase [Gallus gallus]	UNCLASSIFIED	UNCLASSIFIED	264259, 35696052, 264508, 56182435, 265009, 264592, 264593, 264760, 264448, 264884, 264288, 264690, 264628, 55811576, 264555, 264556, 264557, 264558, 264559, 264566
2252	87735867 (4503, 4504)	Novel Protein sim. GBank gi 4929325 gb AAD33953.1 AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	264092, 264094, 264259, 29331822, 66714117, 29331828, 264102, 264103, 264104, 264105, 264109, 264112, 264511, 265007, 60433356, 265010, 18108351, 21906767, 21906768, 264691, 263974, 263977, 264486, 264567
2253	91010703 (4505, 4506)		UNCLASSIFIED	UNCLASSIFIED	65274572, 265019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gi 4502847 ref NP_001271.1 pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264569, 18108394, 18108398, 56182575, 56994075, 35696286, 22278999, 264094, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 35696052, 264106, 264508, 264509, 264906, 264907, 29331830, 66712502, 264908, 264909, 264510, 265006, 264511, 265007, 265008, 265009, 60170831, 60432229, 60433358, 60433438, 264758, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264764, 264288, 264369, 264766, 264686, 264768, 264769, 21906765, 21906767, 55811957, 264691, 33657023, 264692, 18108362, 65274620, 263969, 264628, 18108370, 60431528, 263972, 264629, 18108372, 18108377, 18108379, 55811576, 35696423, 35695855, 264630, 264634, 264635, 264636, 264558, 263981, 264638, 56182323, 60170394, 264558, 18108381, 18108382, 83373044, 18108385, 87168518, 60432113, 22279002, 264482, 264564, 264565, 264486, 264567, 18108391
2255	91010546 (4508, 4510)	Novel Protein sim. GBank gi 5541865 emb CAB51072.1 - (AL098658) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264508, 264905, 264906, 264907, 66712502, 264908, 56182435, 264510, 264511, 265008, 264593, 264595, 21906754, 33109954, 87168474, 265011, 265017, 265019, 264682, 264764, 264369, 264288, 264766, 264685, 264686, 264768, 21906765, 21906766, 21906768, 21906769, 265020, 60170615, 52644150, 264690, 264692, 264693, 33657109, 33657349, 264632, 264636, 52644332, 56182323, 22279000, 22279002 264768, 264689, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gi 3327174 dbj BAA31655 - (AB014580) KIAA0680 protein [Homo sapiens]		UNCLASSIFIED	
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278996, 22278999, 264681, 21906765, 21906766, 264567
2258	88090516 (4515, 4516)	Novel Protein sim. GBank gi 3025446 (AC004528) - R32184_2 [Homo sapiens]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264908, 264592, 264764

2259	95364155 (4517, 4518)	Novel Protein sim. GBank gi 4884140 emb CAB43278.1 - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108395, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87188559, 18108351, 264448, 264683, 264288, 264369, 56181562, 265021, 60170615, 264690, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22279000, 22279002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gi 3080663 (AC004614) - similar to f-spondin proteins AB006086 (PID:g3529225) [Homo sapiens]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264906, 264908, 35696423, 264511, 264635, 55812038, 264758, 265018, 265019, 264605, 264760, 264583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gi 3334526 emb CAA16138 - (AL021306) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639292 (4523, 4524)	Novel Protein sim. GBank gi 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278999, 29331822, 29331825, 60432289, 29331827, 35696052, 264508, 66712502, 52644045, 56182435, 265006, 265008, 265009, 60433356, 55812038, 265010, 265017, 265019, 264288, 264369, 21906765, 21906767, 55811957, 35695917, 52644150, 33657023, 33657109, 55811576, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gi 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52644150, 18108381, 264693, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gi 1657601 (U66220) - unknown [Nannocystis exedens]		UNCLASSIFIED	264686, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 35695855, 264510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264584, 264565, 264764, 264566, 264486, 264766
2265	86918663 (4529, 4530)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264910, 264764
2266	8773458 (4531, 4532)	Novel Protein sim. GBank gi 3150479 (AF067212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21906754, 265010, 265011, 265017, 264448, 264683, 264288, 264689, 21908765, 21906768, 35695917, 265021, 18108374, 264638, 22279000, 22279002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gij3560229[emb]CAA20697.1] - (AL031530) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 35696052, 29331828, 264905, 284509, 264907, 264908, 264909, 264512, 265009, 264910, 264593, 33657402, 265010, 265018, 264762, 264448, 264288, 264369, 264768, 52644229, 35695917, 264691, 33657023, 18108382, 33657109, 35698423, 264634, 18108381, 87168518, 264566
2268	85693867 (4535, 4536)	Novel Protein sim. GBank gij728832[sp]P39189/ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	cadherin		264488, 264259, 264509, 264595, 265010, 265017, 264766, 18108385, 264486
2269	88177877 (4537, 4538)	Novel Protein sim. GBank gij103418[pr]S17885 - TcD37 protein - fruit fly [Drosophila melanogaster]	UNCLASSIFIED		56182575, 60432049, 265007, 265009, 264591, 87168559, 264605, 18108351, 21906764, 265020, 264629, 60431528, 264638, 18108385, 18108387, 60432113, 264763
2270	80410327 (4539, 4540)				264909, 56182435, 265008, 55812038, 55811957, 33657023, 264693, 33657109, 55810764, 55811576, 56182323
2271	91010392 (4541, 4542)		cyl450		264905, 264908
2272	84208220 (4543, 4544)		UNCLASSIFIED		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264688, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gij4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin		52645156, 22278996, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264909, 265006, 264593, 60433438, 21906754, 265018, 264688, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486264, 18108376, 35696423, 35695855, 264630, 52644332, 264558, 56182323, 22279002
2274	91640217 (4547, 4548)	Novel Protein sim. GBank gij1480112[emb]CAA67961] - (X98642) HP1-BP74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	histone	52645156, 22278997, 22278999, 52645080, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 52644045, 264511, 265008, 265009, 60170831, 264591, 21906754, 33109954, 265011, 265018, 18108351, 264448, 264288, 264684, 264766, 21906765, 21906766, 21906767, 21906768, 52644150, 264693, 18108384, 35695763, 18108374, 35698423, 264634, 264557, 264638, 52644332, 83373044, 18108385, 56526486, 87168518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gij3165406 (AC004755) - fos37502.2 [Homo sapiens]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	
2276	11287447 (4551, 4552)		UNCLASSIFIED		264555, 264556

2277	88084123 (4553, 4554)	Novel Protein sim. GBank gi 2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369906) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278999, 35696052, 265008, 265019, 264369, 265020, 265022, 55810764, 264404, 22278002
2278	94133078 (4555, 4556)	Novel Protein sim. GBank gi 2618702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 29331826, 60433356, 60433438, 21906754, 285018, 33857023, 264639, 83373044, 264565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gi 119714 (sp P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	264766, 264565
2280	94239723 (4559, 4560)	Novel Protein sim. GBank gi 4240299 (dbj BAA74928.1) - (AB020712) KIAA0905 protein [Homo sapiens]			265008, 33109954, 265010, 265019, 265020
2281	95293048 (4561, 4562)		Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	264092, 264259, 29331822, 29331824, 29331826, 35696052, 264107, 264906, 264909, 52644045, 265006, 33657402, 60433356, 264758, 265011, 265019, 264681, 264683, 264684, 264686, 21906765, 21906767, 21906768, 21906769, 60170615, 264690, 52644150, 18108362, 264692, 18108368, 18108374, 263978, 264631, 18108381, 264559, 18108385, 56526486, 22279000, 264566, 264567
2282	87602829 (4563, 4564)	Novel Protein sim. GBank gi 1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	264488, 264259, 29331822, 29331824, 29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21906767, 21906769, 55811957, 33657023, 52645129, 33657109, 33657182, 27486262, 263972, 55811576, 87168518, 20281169
2283	95362386 (4565, 4566)	Novel Protein sim. GBank gi 2495729 (sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	60424179, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 56182181, 29331825, 29331827, 35696052, 29146499, 264905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811386, 87168474, 265010, 265011, 265018, 265019, 55811150, 264683, 264369, 264288, 264688, 21906765, 21906767, 21906768, 29148827, 21906769, 55811957, 265020, 265022, 33657182, 27486261, 18108370, 264628, 18108374, 55810764, 18108379, 55811576, 35696423, 35695855, 264630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22279000, 264482, 264587

2284	95414955 (4567, 4586)	Novel Protein sim. GBank gi 2498797 sp O64311 PNAD_MOUSE - PROTEIN N- TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN- AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAA)			60424179, 52644507, 18108394, 52646842, 22278994, 35696286, 22278996, 22278997, 22278998, 264259, 60432049, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331830, 52644045, 56182435, 33657402, 60433438, 33109954, 21906754, 85658542, 87168559, 265018, 265019, 55811150, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 33657023, 33657182, 27486262, 27486264, 27486265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 60432113, 264482, 264564
2285	87781484 (4568, 4570)	Novel Protein sim. GBank gi 3342234 (U93909) - nuclear antigen EBNA-1 [Cercopithecine herpesvirus 15]	collagen		35696052, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264595, 264760, 18108351, 264682, 264763, 264685, 264766, 264686, 264768, 264693, 264629, 35695855, 264631, 264634
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gi 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]	kinase		35696286, 56182435, 60170831, 264591, 60432229, 264592, 264593, 264594, 264595, 55812038, 264596, 87168474, 35695917, 264592, 55811576, 264555, 264557
2287	82986696 (4573, 4574)	Novel Protein sim. GBank gi 630905 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	UNCLASSIFIED	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	264682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gi 726832 sp P39189 ALU2_HUMAN - !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!	tm7		22278995, 56994075, 22278997, 22278999, 264259, 60432289, 264508, 264512, 265008, 33657402, 265017, 265018, 265019, 18108351, 264448, 21906765, 21906766, 21906767, 21906768, 33657023, 264557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	kinase	Contains protein domain (PF00400) - WD domain, G-beta repeat	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	Contains protein domain (PF00400) - WD domain, G-beta repeat	264683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gi 3253120 (AC005175) - R31449_3 [Homo sapiens]	srcf		18108394, 264907, 265006, 265009, 33109954, 52646317, 265010, 18108351, 264681, 264686, 264692, 18108370, 18108374, 18108385

2292	94328634 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133769) nuclear transport receptor [Homo sapiens]	UNCLASSIFIED	56182575, 35696286, 56994075, 29331824, 29331825, 35696052, 56182435, 60433438, 55812038, 33109954, 87168474, 87168559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181562, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27486264, 264629, 55810764, 55811576, 35695855, 56182323, 56526486, 87168518, 22279000, 264567
2283	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - struct Leucine Rich Repeat	264488, 18108397, 35696286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264910, 18108351, 264764, 264369, 264288, 264685, 264766, 265020, 265022, 264534, 35696423, 264631, 284637, 18108381, 56182323, 264639, 18108385, 264404, 264563, 264565
2284	86693580 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88964) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - nuclease Exonuclease	22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35696052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35696423, 35695855, 264634, 22279000, 22279002, 264563, 264486
2285	95312200 (4589, 4590)		UNCLASSIFIED	22278996, 60432289, 264682, 264683, 264689, 18108374
2296	80030781 (4591, 4592)			263974, 263978
2287	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 dbj BAA83034.1 - (AB029005) KIAA1082 protein [Homo sapiens]	transcriptfactor	264488, 55274572, 56182575, 22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 35696052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264766, 21906765, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 60170394, 83373044, 18108385, 56526486, 264564, 264486

2298	95312207 (4595, 4596)	Novel Protein sim. GBank gi 3675051 emb CAB02849 - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65564 comes from this gene; cDNA EST EMBL:D69046 comes from this gene; cDNA EST yk366b12.3 comes from this gene; cDNA EST yk366b12.5 comes from this gene ...		collagen	60424178, 56181686, 22278995, 35696286, 22278996, 22278998, 22278999, 264490, 264259, 28331822, 29331824, 66714117, 60424269, 35696052, 29331828, 68712502, 56182435, 264510, 265006, 60433438, 21906754, 33109954, 55811386, 265010, 265018, 55811150, 264762, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21906766, 21906767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264567, 264486
2299	80193720 (4597, 4598)			UNCLASSIFIED	264369
2300	94124346 (4599, 4600)	Novel Protein sim. GBank gi 2443886 (AC002294) - Unknown protein [Arabidopsis thaliana]			264488, 22278996, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168559, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21906766, 21906767, 35695917, 265021, 264691, 33657023, 35695763, 18108370, 18108374, 35696423, 35695855, 264631, 264636, 264638, 18108385, 22278002, 264563
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gi 2143637 pir I84505 - calcium-dependent actin-binding protein - rat		struct	264908, 264758, 265017, 21906765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gi 2887497 (AC004144) - R34001_1 [Homo sapiens]		UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gi 4884194 emb CAB43220.1 - (AL049946) hypothetical protein [Homo sapiens]		struct	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264762, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gi 2494162 sp Q10005 VRY1_CAEEL - HYPOTHETICAL 39.8 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR		UNCLASSIFIED	264259, 29331824, 21906767, 33657182, 33657349
2305	90935911 (4609, 4610)	Novel Protein sim. GBank gi 492666 gb AAD34738.1 - (AF132150) unknown [Drosophila melanogaster]			55274572, 22278996, 264908, 265006, 21906769, 264691, 264486

2306	95334940 (4611, 4612)	Novel Protein sim. GBank gi 4929565 gb AAD34043.1 AF15180 - (AF151806) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 284508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 85658542, 265010, 265011, 264601, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264768, 264769, 21906765, 21906766, 21906767, 21906768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486
2307	78415283 (4613, 4614)			UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCS - molybdenum cofactor synthesis 2		synthase	35696286, 264259, 29331822, 29331824, 264112, 264512, 264757, 21906754, 264288, 264690, 27486264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070 - (Z99942) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72944 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432049, 29331822, 29331826, 60432289, 66712502, 60432229, 60433356, 60433438, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21906766, 21906768, 265020, 264681, 264692, 264693, 65274620, 65274791
2310	78601668 (4619, 4620)			UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir 48281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	transcriptfactor	18108397, 56182575, 22278996, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265006, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264688, 33657023, 20281149, 20281069, 264628, 263972, 55811578, 35696423, 20281071, 264632, 264636, 18108385, 18108387, 87168518, 22279000, 264563, 264486

2312	87549681 (4623, 4624)	Novel Protein sim. GBank gij2911264 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52644045, 60432229, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 255022, 60170815, 33657023, 27486261, 27486264, 35696423, 35695855, 18108385, 22279000, 22279002
2313	80042533 (4625, 4626)	Novel Protein sim. GBank gij3043626(dbj BAA25477) - (AB011123) KIAA0551 protein [Homo sapiens]			263981
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gij5596714(emb CAB51401.1) - (AL035398) dJ796117.2 (CGI-51) [Homo sapiens]		UNCLASSIFIED	52644507, 52646365, 52646842, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 60432229, 29331826, 29331827, 29331828, 35696052, 33656970, 52644045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906766, 21906768, 35695917, 52644150, 33657023, 33657109, 52645129, 33657349, 35695763, 18108374, 35696423, 35695855, 52644332, 22279000, 22279002, 264553, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385
2316	94312191 (4631, 4632)	Novel Protein sim. GBank gij5531827(gb AAD4488.1) - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	glycoprotein	52644507, 52645156, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 52645080, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264906, 264907, 29331830, 52644045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906754, 52646317, 33109954, 33657084, 52644296, 87168474, 265010, 87168559, 265017, 265018, 265019, 264681, 264763, 264448, 264683, 264369, 52644229, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 33657023, 18108362, 52645129, 33657182, 33657349, 35695763, 18108370, 18108376, 35696423, 35695855, 264631, 264556, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 264910, 60432228, 264686, 264687, 264688, 264689, 264558, 18108385
2318	79959879 (4635, 4636)			UNCLASSIFIED	265006, 264910
2319	95101781 (4637, 4638)	Novel Protein sim. GBank gij5262613[emb]CAB45746.1] - (AL080155) hypothetical protein [Homo sapiens]			264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 264259, 52645080, 29331825, 29331826, 29331827, 29331828, 29331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21906754, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 27486264, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 83373044, 18108385, 56526486, 87168518, 264564, 264565, 264566
2320	91622426 (4639, 4640)	Novel Protein sim. GBank gij728837[sp]P39194[ALU7_HUMAN - IIII] ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	22278994, 60432049, 60432289, 29331827, 264511, 265008, 52646317, 265017, 265019, 21906765, 18108372, 18108387, 22279002
2321	94320377 (4641, 4642)	Novel Protein sim. GBank gij3873837[emb]CAB02700] - (Z81029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154); cDNA EST EMBL: T00543 comes from this gene; cDNA EST EMBL: T01062 comes from this gene; cDNA EST EMBL: T01321 comes from this gene; cDNA EST EMBL: T02288 com...		UNCLASSIFIED	264488, 264687, 18108394, 264689, 21906765, 18108397, 18108398, 21906767, 21906768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170615, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 29331824, 18108365, 18108348, 18108384, 29331825, 18108385, 33109954, 29331827, 56526486, 29146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87803165 (4643, 4644)	Novel Protein sim. GBank gij5678957[emb]CAB51685.1] - (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00105) - short chain dehydrogenase	dehydrogenase	22278996, 264907, 264511, 264757, 18108351, 264768, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi 2494162 sp Q10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00226) - eph DnaI domain	22278994, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 56182435, 264511, 265008, 60433356, 60433438, 55812038, 33109954, 21906754, 85658542, 87168474, 265011, 87168559, 265017, 265019, 264760, 264681, 18108351, 264369, 264288, 18108355, 264687, 264688, 21906765, 21906767, 21906768, 55811957, 35695917, 265021, 33657023, 18108362, 27486262, 55811576, 264631, 264555, 83373044, 87168518, 60432113, 22279002 264592, 264593, 265020
2324	86533607 (4647, 4648)	Novel Protein sim. GBank gi 5419865 emb CAB46377.1 - (AL096732) hypothetical protein [Homo sapiens]	ATPase-associated	265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00067) - cyto450 Cytochrome P450	265006, 264759, 35695855, 56182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi 231885 sp P29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020676) KIAA0869 protein [Homo sapiens]	UNCLASSIFIED	264259, 264508, 264905, 264906, 264907, 264908, 265007, 264512, 264910, 264758, 265010, 264766, 264768, 264769, 33657023, 264693, 264628, 264631, 264634, 264638, 264639, 264488
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi 1245105 U46463 - glutamine repeat protein-1 [Mus musculus]	UNCLASSIFIED	60433438, 264595, 265017, 264766, 264692, 264629, 264635, 264636, 264638, 56182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	UNCLASSIFIED	265017, 264685, 60432113, 264088
2330	87335396 (4659, 4660)	Novel Protein sim. GBank gi 1169343 sp P42209 DIF6_MOUSE - DIFF6 PROTEIN	transport	265009
2331	86990463 (4661, 4662)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]	ATPase-associated	35686286, 22278998, 29331824, 60424269, 265006, 265008, 265018, 264448, 264764, 21906765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi 2104452 emb CAB08779 - (Z95397) unknown [Schizosaccharomyces pombe]	UNCLASSIFIED	56182575, 56994075, 29331826, 29331828, 264107, 33657402, 87168559, 264683, 35695917, 265021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi 3879895 emb CAA92691.1 - (Z68318) cDNA EST CEMSD62F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C08493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST ...	UNCLASSIFIED	
2334	94319788 (4667, 4668)	Novel Protein sim. GBank gi 4966270 gb AA052261.2 - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - dehydrogenase Acyl-CoA dehydrogenase	56182575, 29331825, 21906768, 264636, 83373044

2335	80046103 (4668, 4670)	Novel Protein sim. GBank gij3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00612) - struct IQ calmodulin-binding motif	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gij1929056[embjCAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	kinase	264907, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gij4495063[embjCAB39181.1] - (Z85986) dJ108K1.1.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424269, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906768, 35695917, 264691, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gij2224689[dbjBAA20829] - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	18108394, 29331822, 66714117, 60432289, 284908, 56182435, 265009, 60433438, 264596, 265010, 265019, 18108354, 264288, 264369, 55811957, 265021, 33657023, 263976, 55811576, 264632, 56182323, 264639
2339	85663318 (4677, 4678)	Novel Protein sim. GBank gij3873550[embjCAA22127] - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35696286, 284592, 264369, 264691, 264558
2340	90937716 (4679, 4680)			65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331826, 29331830, 265009, 33657402, 33109954, 265017, 265018, 264766, 264685, 21906769, 35695917, 264691, 264692, 35696423, 87168518, 22279000
2341	87775281 (4681, 4682)			264259, 264908, 264909, 264682, 22279000
2342	95334968 (4683, 4684)	Novel Protein sim. GBank gij3874563[embjCAB02797] - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - kinase W/D domain, G-beta repeat	264488, 65274572, 22278995, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 35696052, 264905, 264509, 29331830, 265006, 60170831, 60432229, 60433358, 87168474, 265017, 265018, 265019, 264448, 264369, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810764, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264563, 264564, 264565, 264566, 264567, 264907, 264512, 265011, 264683
2343	87775448 (4685, 4686)	Novel Protein sim. GBank gij4929741[gb AAD34131.1]AF15189 - (AF151894) CGI-136 protein [Homo sapiens]	UNCLASSIFIED	
2344	79953198 (4687, 4688)		UNCLASSIFIED	264758
2345	94319799 (4689, 4690)	Novel Protein sim. GBank gij2506307[sp P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)]	Contains protein domain (PF00092) - collagen von Willebrand factor type A domain	264488, 264259, 66712502, 264759, 83373044, 264566

2346	94131820 (4691, 4692)	Novel Protein sim. GBank gji1255411 (U53153) - one short region of weak similarity to <i>S. cerevisiae</i> protease A inhibitor 3 (SP:P01094) and another short region of weak similarity to <i>S. cerevisiae</i> glucose repression mediator protein (SP:P14922) [<i>Caenorhabditis elegans</i>]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35696286, 22278998, 264259, 35696052, 29331828, 33657402, 60433356, 33109954, 87168559, 264603, 265019, 18108351, 264681, 264685, 21906766, 265021, 33657109, 55811576, 35695855, 264637, 52644332, 264557, 83373044, 22279000, 22279002
2347	85330367 (4693, 4694)				22278997, 264511, 264683, 264684, 264766, 264687, 264688, 264691, 264692, 55811576, 18108394, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265011, 264601, 264762, 18108351, 264764, 264288, 264766, 264768, 264689, 35695917, 264693, 264628, 18108370, 264629, 18108374, 35696423, 264631, 264635, 264636, 264637, 264638, 264639, 83373044, 18108385, 264567, 264486
2349	87776502 (4697, 4698)	Novel Protein sim. GBank gji4884108[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35696052, 29146499, 264909, 264369
2350	88260594 (4699, 4700)				22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 33109954, 21906754, 265010, 87168559, 265018, 265019, 264761, 264681, 264288, 18108357, 21906766, 21906767, 264691, 264692, 35695855, 87168518, 22279000, 22279002, 264482
2351	86968042 (4701, 4702)	Novel Protein sim. GBank gji728832[sp]P39189[ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII]		kinase	56182575, 264909, 265006, 264558
2352	87337196 (4703, 4704)	Novel Protein sim. GBank gji731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264259, 264448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gji1346955[sp]P48809[R827_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 264692, 264636
2354	87337199 (4707, 4708)	Novel Protein sim. GBank gji731637[sp]P38760[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 264908, 265006, 265008

2355	91638786 (4709, 4710)	Novel Protein sim. GBank gjl4938503jemb CAB43861.1 - (AL078465) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	5694075, 22278996, 35696286, 22278999, 264259, 29331825, 29331826, 29331828, 29146498, 264905, 264908, 265006, 264758, 87168474, 265010, 265017, 264687, 21906765, 21906767, 21906769, 264691, 264692, 263967, 18108370, 87168518, 22279000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gjl5138920jgb AAD40377.1 - (AF092135) PTD014 [Homo sapiens]			52644507, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35696052, 29331828, 264908, 66712502, 264512, 265007, 265008, 60170831, 60432229, 60433356, 60433438, 264758, 52646317, 33109954, 21906754, 55811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264369, 264288, 264686, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 33657109, 27486264, 35695763, 55810764, 18108379, 35696423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526486, 264404, 60432113, 22279000, 264482, 264563, 264566, 264486, 264567
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gjl4929741jgb AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]		UNCLASSIFIED	264488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264566, 264369, 18108354
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gjl4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755859 (4717, 4718)	Novel Protein sim. GBank gjl1086830 (U41264) - coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk2018.5; coded for by C. elegans cDNA yk16g12....		UNCLASSIFIED	35696286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21906769, 265020, 264692, 35695855, 264558, 56526486, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gjl3881545jemb CAA93779 - (Z69904) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	22278997, 29331826, 263981, 22279000
2361	94232191 (4721, 4722)	Novel Protein sim. GBank gjl746487 (U23514) - No definition line found [Caenorhabditis elegans]			22278995, 22278999, 264512, 265009, 264757, 21906765, 65274620, 18108370, 60431528, 18108374, 264635, 60170394, 264482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank gil1171093 sp P19706 MYSB_ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)		UNCLASSIFIED	22278999, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264682, 264683, 264369, 21906765, 21906768, 21906769, 60432113, 22279000, 22279002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank gil854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264907, 264628, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank gil5638830 gb AAD45886.1 AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	reductase	264488, 18108394, 264887, 18108398, 22278998, 56994075, 35696286, 22278997, 22278998, 264259, 66714117, 29331825, 35696052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 265006, 264512, 265007, 265008, 33657402, 264758, 21906754, 87168474, 265010, 87168559, 264603, 265017, 265018, 265019, 264760, 264762, 18108351, 264448, 264764, 264683, 264684, 264288, 18108355, 264766, 18108358, 264689, 18108359, 21906765, 21906766, 21906767, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264691, 33657023, 264692, 18108364, 33657109, 18108368, 18108370, 18108374, 35696423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56528486, 264482, 264564, 264486
2365	94140746 (4729, 4730)	Novel Protein sim. GBank gil1840045 (U49082) - transporter protein [Homo sapiens]		transport	22278996, 22278998, 22278999, 264907, 264909, 264910, 33657402, 264758, 264600, 264766, 264687, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 83373044, 264566
2366	94312388 (4731, 4732)			UNCLASSIFIED	52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 265008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264766, 264689, 21906766, 21906769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264564, 264568
2367	94140910 (4733, 4734)	Novel Protein sim. GBank gil1065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	35696286, 21906768, 55810764, 65274791, 264567
2368	94322190 (4735, 4736)				264628

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gjl5360901[dbj BAA02158.1] - (AB029343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52644507, 52646842, 35696286, 264092, 264094, 52645080, 35696052, 264107, 29331830, 52644045, 265006, 265007, 265009, 52644296, 52644229, 264689, 21906765, 21906766, 35695917, 265020, 52644150, 263967, 33657109, 27486265, 35695763, 18108370, 263974, 18108374, 18108376, 52644332, 263981, 18108385, 264508, 264909, 264596, 264369
2370	79804120 (4738, 4740)			UNCLASSIFIED	
2371	57280406 (4741, 4742)			UNCLASSIFIED	
2372	87642413 (4743, 4744)			UNCLASSIFIED	
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gjl4589582[dbj BAA76813.1] - (AB023186) KIAA0969 protein [Homo sapiens]		UNCLASSIFIED	263967, 263981
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gjl5105131[dbj BAA0445.1] - (AP000061) 246aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exonuclease family	UNCLASSIFIED	264634, 60432113
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gjl1351115[sp P47758]SRPB_MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)		UNCLASSIFIED	265006, 265007, 265008, 265009, 265011, 264766, 35695917, 35695855, 263981, 264557, 264565
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gjl2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	60432049, 29331824, 264907, 52644045, 264512, 60433356, 21906754, 52644296, 87168559, 264448, 21906765, 21906768, 21906769, 33657023, 18108368, 55811576, 52644332
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gjl5257005[gb AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	264259, 29331830, 264909, 264910, 265009, 60433438, 21906754, 265017, 265018, 265019, 264682, 264288, 264685, 21906767, 263972, 35695855, 87168518, 60432113, 18108394, 65274572, 22278997, 22278999, 264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33656970, 29146498, 29146499, 264509, 265006, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 264764, 264288, 21906767, 21906768, 29148627, 29148629, 265021, 33657023, 33657109, 18108370, 18108374, 18108379, 35696423, 264556, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gjl1072198 (U40942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35696286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 60432289, 28331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21906765, 33657023, 264557, 56182323, 83373044, 18108385, 22279002, 264482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gjl3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	265017, 264288, 21906768

2380	86923062 (4759, 4760)	Novel Protein sim. GBank gi4502939 ref NP_001845.1 pCOL1 - collagen, type XI, alpha 1	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	264908, 264910, 265011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gi4455609 emb CAB36555 - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00395) - 'chromo' (CHRromalin Organization Modifier) domain	helicase	56182575, 264091, 264093, 264259, 29331825, 264105, 264906, 60433356, 21906754, 265017, 265019, 264883, 264288, 264685, 264686, 264687, 264691, 264692, 264693, 55811576, 264636, 264567 29331824, 60432289, 264905, 264596, 21906754, 264769, 265022, 264893, 263967, 33657109, 264629, 264631, 264658, 83373044, 60432113, 264482
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gi4325130 gb AAD17276 - (AF119716) dMi-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	264488, 52644507, 52645156, 52646365, 35696286, 22278999, 52645080, 29331824, 29331826, 35696052, 29331828, 264906, 264828, 52644045, 265006, 265008, 265009, 33109954, 33657084, 52644296, 265011, 265017, 265018, 264683, 52644229, 21906765, 21906767, 21906768, 265020, 52644150, 33657023, 264693, 65274620, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108374, 35695855, 264634, 264555, 264556, 264557, 52644332, 264558, 264559, 18108385, 22279000, 22279002
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gi1902982 dbj BAA19005 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2384	95354766 (4767, 4768)	Novel Protein sim. GBank gi2462851 (AF016252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	struct	UNCLASSIFIED
2385	95419485 (4769, 4770)				264488, 52644507, 52645156, 264887, 52646365, 22278995, 22278996, 22278997, 22278999, 264259, 52645080, 29331822, 29331826, 35696052, 52644045, 265006, 265007, 265008, 265009, 264910, 60432229, 60433356, 52646317, 21906754, 265019, 264448, 264683, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 55811957, 265021, 265022, 264690, 264691, 264692, 65274620, 33657109, 18108370, 264631, 52644332, 22279000, 22279002, 264563, 264565, 264567
2386	94742649 (4771, 4772)	Novel Protein sim. GBank gi492989 gb AAD34110.1 AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	264488, 22278995, 22278996, 22278997, 264259, 29146498, 264112, 264511, 60170831, 60432229, 264595, 60433438, 87168474, 87168559, 264682, 21906765, 21906766, 21906767, 21906769, 29148829, 35695917, 265021, 264690, 33657109, 264628, 18108376, 83373044, 60432113, 22279000, 264564, 264566, 264487

2387	14997890 (4773, 4774)			UNCLASSIFIED	264634
2388	11424604 (4775, 4776)			UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gi 4758058 ref NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED - dna_rna_bind	284488, 22278998, 22278999, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264511, 264512, 264910, 264591, 21908754, 264601, 264604, 264761, 18108351, 264764, 264288, 264766, 264768, 264769, 21906765, 21906768, 264692, 264693, 35696423, 264635, 264636, 264555, 83373044, 22279000, 264486
2390	94320912 (4779, 4780)	Novel Protein sim. GBank gi 1644239 dbj BAA12223 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	UNCLASSIFIED - polymerase	52644507, 56182575, 22278995, 35696286, 22278996, 22278997, 22278999, 29331822, 29331825, 29331826, 35696052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 265011, 265017, 265018, 264605, 52644229, 21906765, 21906767, 21906768, 21906769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35696423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56526486
2391	80036194 (4781, 4782)			UNCLASSIFIED	263976
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gi 4240169 dbj BAA74863.1 - (AB020647) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED - nuclease	35696286, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264600, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264769, 264689, 35695917, 264629, 18108374, 263978, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486

2383	95302633 (4785, 4786)	Novel Protein sim. GBank gi4506667 ref NP_000993.1 pRPLP - ribosomal protein, large, P0	Contains protein domain (PF00466) - Ribosomal protein L10	ribosomalprot	18108392, 60424179, 264489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278999, 264093, 60432049, 264259, 29331822, 29147620, 20281099, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146499, 264508, 264509, 264905, 264907, 264908, 66712502, 52644045, 264828, 264909, 56182435, 264112, 264113, 264510, 265006, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52646317, 33109954, 21906754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264369, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 29148629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108368, 27486261, 27486262, 33657349, 35695763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810764, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264558, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265006, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21906765, 21906768, 21906769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264584, 264566, 264567
2384	94323266 (4787, 4788)	Novel Protein sim. GBank gi4159888 (AC004908) - zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gi5712756 gb AAD47636.1 AF16079 - (AF160798) calcium transporter CaT1 [Rattus norvegicus]		dna_rna_bind	264259, 29331824, 264910, 264288, 265021, 83373044, 18108387, 264563, 264566

2396	95096700 (4791, 4792)	Novel Protein sim. GBank gi 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - Leucine Rich Repeat	nuclease	52646365, 18108397, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264106, 264907, 29331830, 66712502, 264110, 60170831, 264591, 33657402, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 265017, 265018, 265019, 264760, 264448, 264288, 264766, 52644229, 21906766, 21906767, 265020, 265021, 60170615, 264692, 33657023, 65274620, 52645129, 33657182, 27486262, 27486264, 27486265, 264629, 18108374, 35696423, 35695855, 264631, 264556, 52644332, 264558, 83373044, 18108388, 87168518, 22279002, 264482
2397	87280854 (4793, 4794)				52644507, 52645156, 56182575, 264259, 29147620, 264905, 264907, 264908, 264909, 264910, 264758, 52644296, 264603, 264604, 264762, 264681, 264764, 18108357, 264769, 21906768, 264693, 264628, 264635, 264638, 264639, 264584
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258609 (AC005178) - H53_GS1 [Homo sapiens]		UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 60432289, 264906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87168474, 264600, 265017, 265018, 265019, 264764, 264785, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265022, 60170615, 33657023, 18108370, 18108374, 264556, 60170394, 264558, 87168518, 22279000, 22279002, 264564, 264566, 264487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1 - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	21906766, 52646842, 56994075, 33657182, 27486262, 52644296, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gi 2352822 gb AAB69285.1 - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]		phosphatase	52644507, 52645156, 52644229, 264688, 21906764, 21906785, 52646385, 52646842, 21906766, 21906767, 21906768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 265020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 29331824, 33657109, 52645129, 29331826, 33657182, 29331827, 35696052, 27486261, 27486262, 33656970, 33657349, 27486265, 35695763, 264106, 264905, 35696423, 35695855, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644296, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]			
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gi 4929575 gb AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF000062) - C-type lysozyme/alpha-lactalbumin family		22278999, 35696052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gi 2315796 (AF016685) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	35696286, 29331826, 35696052, 265008, 265018, 21906769, 264564
2405	94311851 (4808, 4810)	Novel Protein sim. GBank gi 464178 dbj BAA03581 - (D14853) polypeptide [Hepatitis C virus]		UNCLASSIFIED	35696286, 29331822, 265007, 21906754, 265017, 265018, 265019, 264763, 264369, 21906765, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	88094501 (4811, 4812)	Novel Protein sim. GBank gi 2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - CAP-Gly domain	struct	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264102, 264106, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264369, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563, 264685, 264686
2407	79465005 (4813, 4814)	Novel Protein sim. GBank gi 423442 pir S33513 - gene F1f protein - mouse		UNCLASSIFIED	264910, 265010, 264448, 264557
2408	87391503 (4815, 4816)			UNCLASSIFIED	

2409	94741770 (4817, 4818)	Novel Protein sim. GBank gij1176801 sp P45966 YNZ6 CAEL - HYPOTHETICAL 20.8 KD PROTEIN T09A5.6 IN CHROMOSOME III		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29146498, 52644045, 60433438, 33657084, 87168474, 264760, 21906767, 29148627, 29148629, 52644150, 33657023, 263967, 20281089, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gij1176801 sp P45966 YNZ6 CAEL - HYPOTHETICAL (U64849) Contains similarity to Pfam domain: PF00646 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gij3114713 (AF061346) - Edp1 protein [Mus musculus]		Inf	29331824, 29331827, 29331828, 264764, 264369, 33657109, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gij5410336 gb AAD43038.1 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278998, 29331827, 264907, 265011, 265017, 265018, 265019, 18108351, 21906766, 265020, 33657109, 264559, 18108385
2413	94133820 (4825, 4826)	Novel Protein sim. GBank gij5262705 emb CAB45778.1 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	264488, 264259, 29331826, 264508, 264905, 264509, 264908, 264907, 264908, 264510, 264511, 264512, 265008, 265009, 264910, 265011, 264682, 264764, 264766, 264686, 264768, 264689, 265021, 33657023, 18108370, 264628, 35695855, 264632, 264634, 264635, 264636, 83373044, 264563, 264584, 264585, 264586, 264587, 264486
2414	94312590 (4827, 4828)	Novel Protein sim. GBank gij1082340 pir S52863 - DNA- binding protein R kappa B - human		ubiquitin	52645156, 52646842, 52646365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 29331830, 264909, 60433356, 33657402, 264594, 52646317, 21906754, 33657084, 265010, 87168559, 265017, 265018, 265019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906765, 21906766, 21906767, 29148627, 21906769, 265020, 265021, 60170615, 33657023, 264693, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52644332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22279002

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gi 423915 pir A45439 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21906754, 265018, 264687, 264689, 21906769, 55811957, 265021, 264690, 264691, 33657023, 264693, 35696423, 56182323, 56526486
2416	94118356 (4831, 4832)	Novel Protein sim. GBank gi 3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gi 1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gi 1176572 sp P45895 YNA4 CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432289, 29331828, 264905, 264907, 264511, 265009, 60432229, 21906754, 87168559, 265019, 264682, 21906768, 21906769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264566
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gi 284006 pir S18732 - autoantigen, 64K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gi 1076211 pir S07955 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)			UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	transport	18108392, 18108394, 18108398, 264906, 265006, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gi 4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase Kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	Kinase	264259, 60432049, 29331822, 29331826, 60432289, 29331828, 265008, 265009, 60433356, 21906754, 265017, 265018, 265019, 21906766, 21906768, 21906769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gi 2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278997, 60432049, 264259, 29331826, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264766, 21906768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22279000
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gi 2077932 dbj BAA19879 (D85558) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	Kinase	264634
2426	87613945 (4851, 4852)	Novel Protein sim. GBank gi 2039368 gb AAB53003.1 (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21906767, 18108370, 18108374, 263976

2427	87622693 (4853, 4854)	Novel Protein sim. GBank gi1468095 gb AAD27737.1 AF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	ribosomalprot	264259, 20281099, 35696052, 265008, 264594, 265011, 264760, 18108351, 264682, 264683, 264369, 264684, 264686, 264687, 264689, 21906766, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gi1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278999, 35696052, 21906754, 264288, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22279002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gi1601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264906, 264909, 264511, 265009, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86948827 (4859, 4860)	Novel Protein sim. GBank gi1366072 emb CAA14630 - (AJ235270) CELL DIVISION PROTEIN FTSJ (fts-J)	Contains protein domain (PF01728) - FtsJ cell division protein	UNCLASSIFIED	264112, 264691
2431	87649884 (4861, 4862)	Novel Protein sim. GBank gi13876367 emb CAA93287 - (Z69360) Weak similarity to Eimeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89266 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	29331826, 29331827, 35696052, 29146499, 264905, 264906, 264681, 264288, 264689, 21906765, 264692, 35696423
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gi12224593 dbj BAA20784 - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264569, 264905, 265018, 264762, 264683, 264691, 264558, 264557, 264639, 264558
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gi12224593 dbj BAA20784 - (AB002324) KIAA0326 [Homo sapiens]			264563
2434	19520148 (4867, 4868)	Novel Protein sim. GBank gi1263289 (U47856) - fibroin-4		UNCLASSIFIED	264555
2435	20759044 (4869, 4870)	[Araneus diadematus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gi13641352 (AF091234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gi13660014 (AF091088) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331826, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 265006, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264558, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850850 (4877, 4878)	Novel Protein sim. GBank gij4263519lgb/AAD15345j - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424179, 18108397, 56182575, 56181686, 56994075, 22278996, 35696286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264509, 264905, 264906, 52644045, 60431735, 33109954, 21906754, 33657084, 55811386, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 60431528, 263977, 55810764, 35696423, 65274791, 35695855, 60431850, 56182323, 60432113, 22279000, 22279002, 264567
2440	87641733 (4879, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 265019, 264448, 264369, 265020, 265021, 56182323, 264539, 22279002
2441	87623914 (4881, 4882)	Novel Protein sim. GBank gij3024889sp/P56524IY288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 18108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gij4506013ref/NP_002703.1pPPP1 - protein phosphatase 1, regulatory subunit 7			
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gij1170658sp/Q02975KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278996, 22278999, 29331822, 264768, 264693
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gij4758824ref/NP_004280.1pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF01352) - KRAB box	transcription factor	264906
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gij2135950pirj/S58222 - PQ-rich protein - human	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	264259, 18108382, 18108383, 18108385, 22279000
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gij4753887embjCAA05409.2j - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00095) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	protease inhibitor	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gij4885613ref/NP_005409.1pST5j - suppression of tumorigenicity 5		cadherin	56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 265018, 264692, 65274620, 60431528, 65274791, 56182323

2448	87749680 (4895, 4896)				UNCLASSIFIED	22278996, 22278997, 22278999, 29331826, 35698052, 264107, 264110, 87168474, 87168559, 18108351, 21906767, 21906769, 27486262, 263976
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gij728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII			cadherin	264259, 264828, 265007, 264595, 265021, 56528486
2450	86597784 (4899, 4900)				UNCLASSIFIED	264906
2451	91014563 (4901, 4902)	Novel Protein sim. GBank gij1710021 sp P35290 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)		Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 66714117, 29331826, 29331828, 35696052, 264907, 66712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21906767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	91230509 (4903, 4904)	Novel Protein sim. GBank gij1504034 dbj BAA13216 - (D86980) KIA0227 [Homo sapiens]			isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264563
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gij2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369908) [Homo sapiens]		Contains protein domain (PF00560) - Leucine Rich Repeat	ngf receptor	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gij1076802 pir S49915 - extensin like protein - maize		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 66714117, 29331827, 264508, 264509, 284905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264592, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264688, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264563, 264564, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gij543817 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)		Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264488, 22278996, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21908768, 21908767, 21908769, 29148629, 35695917, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264563, 264564, 264566, 264567
2456	88166700 (4911, 4912)	Novel Protein sim. GBank gij2588630 (AC003079) - Ankyrin- like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]		Contains protein domain (PF00023) - Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gij3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	56181686, 264905, 264907, 264511, 264596, 55811386, 264682, 264684, 264685, 264687, 264691, 33657023, 264693, 35695855, 264636, 264555, 56182323, 264558, 56526486, 264563
2458	85675304 (4915, 4916)	Novel Protein sim. GBank gij2384942 (AF022985) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264691, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gij5441942 [AAD43187.1] (AC004997) supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gij4929701 [gbjAAD34111.1] (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35696286, 22278996, 22278997, 60432049, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 29146499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21908765, 21906766, 21906769, 35695917, 265020, 264691, 33657023, 27486261, 18108374, 35695855, 87168518, 60432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gij4426962 [gbjAAD20633] - (AF126062) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	284259, 29331828, 264910, 18108351, 18108370, 18108374
2462	8698002 (4923, 4924)	Novel Protein sim. GBank gij5420387 [embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			264909, 264758, 264684, 18108374, 264637, 18108385
2463	84388543 (4925, 4926)	Novel Protein sim. GBank gij5052516 [gbjAAD38588.1] (AF14561) - (AF145613) BcDNA GH03108 [Drosophila melanogaster]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264566
2464	91219957 (4927, 4928)	Novel Protein sim. GBank gij5410300 [gbjAAD43021.1] - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01399) - PCI domain	protease	264489, 52646842, 22278995, 35696286, 22278996, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52646317, 33109954, 33657084, 265017, 265018, 265019, 264762, 264448, 264764, 264288, 264766, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264486

2465	95357483 (4928, 4930)	Novel Protein sim. GBank gi4506401 ref NP_002871.1 pRAF1 - v-raf-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	oncogene	18108392, 52644507, 52645156, 52646365, 22278994, 22278995, 35696286, 22278996, 22278998, 264259, 29331822, 29331824, 29331825, 60424269, 60432289, 29331827, 35696052, 29331828, 264907, 29331830, 52644045, 264909, 56182435, 264511, 265007, 265008, 265009, 264910, 33657402, 60433438, 55812038, 21906754, 33109954, 265010, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264369, 264288, 264685, 264767, 21906765, 21906767, 21906768, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 52645129, 33657109, 27486261, 27486264, 35695763, 264628, 263972, 18108374, 35695855, 264636, 264637, 60170394, 56526486, 87168518, 60432113, 264563, 264564, 264566, 264487 264369
2466	85681386 (4931, 4932)	Novel Protein sim. GBank gi4321619 gb AAD15788.1 - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]			
2467	88059465 (4933, 4934)	Novel Protein sim. GBank gi13513300 (AC005595) - F16601_1, partial CDS [Homo sapiens]		UNCLASSIFIED	56994075, 264908, 21906768, 33657023
2468	87614696 (4935, 4936)	Novel Protein sim. GBank gi12143455 pir 58106 - gene DMR-N9 protein - mouse (fragment)	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	29331824, 52644045, 265008, 264910, 265019, 21906765, 21906769, 265021 264288, 264628
2469	86294397 (4937, 4938)	Novel Protein sim. GBank gi15420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264592, 264692, 264555, 264556, 264557, 264558, 264559, 18108385, 264482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi15419882 emb CAB46424.1 - (AL086749) DKFZp434G153 [Homo sapiens]		UNCLASSIFIED	65274572, 35696286, 29331827, 265007, 264592, 33109954, 265018, 265019, 264288, 55811957, 265020, 264693, 55811576, 56182323
2472	95060811 (4943, 4944)	Novel Protein sim. GBank gi4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]		UNCLASSIFIED	264092, 60432049, 29331825, 60433356, 265010, 265011, 18108351, 264764, 264288, 264692, 65274620, 18108370, 18108372, 18108374, 264634, 18108385
2473	95421509 (4945, 4946)	Novel Protein sim. GBank gi4539009 emb CAB39630.1 - (AL049481) putative protein [Arabidopsis thaliana]			60424179, 65274572, 22278999, 60424269, 29331826, 265008, 60433356, 60433438, 265010, 18108351, 264448, 264288, 264687, 264689, 265021, 264692, 65274620, 60431528, 65274791, 264556, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi13252827 (AC004382) - Unknown gene product [Homo sapiens]			65274572, 56994075, 264259, 29331826, 60170831, 265017, 265018, 265019, 264683, 264369, 265020, 264693, 264563, 264564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gij1216486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - Igf EGF-like domain	264259, 29331822, 265006, 265007, 265010, 265011, 264448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108382, 264693, 18108370, 18108374, 18108379, 35698423, 83373044, 18108383, 18108385, 264564, 264565, 264567
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gij3252827 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED	264259, 60424269, 66714117, 264905, 265006, 264511, 265008, 265009, 264758, 265010, 265011, 18108351, 264681, 264369, 264288, 264689, 21906767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)		UNCLASSIFIED	263978
2478	17659165 (4955, 4956)		UNCLASSIFIED	265017
2479	94314569 (4957, 4958)	Novel Protein sim. GBank gij1644232 [dbj BAA11082] - (D67066) N-WASP [Bos taurus]	Im7	56994075, 22278999, 21906754, 264682, 21906765
2480	95295605 (4959, 4960)		UNCLASSIFIED	264905, 264907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gij5689469 [dbj BAA83018.1] - (AB028989) KIAA1066 protein [Homo sapiens]	collagen	65274572, 56182575, 22278997, 264094, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 56182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 265011, 265017, 265018, 264760, 264762, 18108351, 264764, 264288, 264766, 264686, 264768, 21906768, 55811957, 265020, 264691, 264692, 264693, 264629, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22279002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gij321249 [pir S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse	UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264563
2483	87731583 (4965, 4966)		UNCLASSIFIED	264488, 22278995, 264093, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108388, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gij728831 [sp P39188] ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	kinase	264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gij1185397 (U25281) - SH3 domain binding protein [Rattus norvegicus]	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265019, 264448, 264288, 264685, 264686, 264769, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gi 2662167 dbj BAA23715 - (AB007903) KIAA0443 [Homo sapiens]	Contains protein domain (PF00071) - Ras family		265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gi 464559 sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14		glycoprotein	22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 28331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265006, 264511, 265008, 265009, 60433438, 21906754, 33109954, 87168559, 265018, 264681, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35696423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264563, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gi 4886439 emb CAB43355.1 - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264686, 264693, 55811576, 22279002
2490	88069609 (4979, 4980)	Novel Protein sim. GBank gi 2598624 (AC003083) - Rap2 interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	91242116 (4981, 4982)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - !!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!		Im7	264259, 29331826, 265008, 264762, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gi 3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21906764, 21906768, 264692, 60431528, 87168518, 60432113, 22279000

2493	95422415 (4985, 4986)	Novel Protein sim. GBank gi 4240307 dbj BAA74932.1 - (AB020716) KIAA0909 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264887, 65274572, 56182575, 22278995, 56994075, 60432049, 29331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264509, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21906754, 265011, 264600, 265017, 265018, 264604, 264605, 265019, 55811150, 264762, 18108351, 264681, 264448, 264683, 264369, 264288, 18108355, 18108357, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264691, 264692, 33657023, 33657349, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264566, 264486
2494	30703118 (4987, 4988)			UNCLASSIFIED
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	collagen	263994, 22278997, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264766, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264564, 264567, 264486
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gi 4808220 emb CAB42832.1 - (AL022315) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2497	91723554 (4993, 4994)			UNCLASSIFIED
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gi 1200503 (U47924) - B [Homo sapiens]		52644507, 22278996, 22278999, 29331824, 29331828, 33657402, 21906754, 87168474, 265019, 264369, 264689, 21906765, 21906766, 21906767, 21906768, 265020, 33657023, 18108376, 18108387
2499	94665125 (4997, 4998)	Novel Protein sim. GBank gi 3510234 (AC005581) - R31237_1, partial CDS [Homo sapiens]	kinase	29331827, 264512, 264910, 264288, 18108374, 35695855
			Contains protein domain (PF00069) - Eukaryotic protein kinase domain	264909, 55812038, 264631, 264637, 264558

2500	94648324 (4998, 5000)	Novel Protein sim. GBank gi 3881275 emb CAA21725 - (AL032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255e11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	5284507, 52645156, 22278995, 56994075, 35696286, 22278998, 264259, 52645080, 29331824, 29331825, 66714117, 60432289, 29331828, 29331827, 35696052, 29331828, 264508, 264509, 264510, 264512, 33657402, 60433438, 21906754, 52644296, 87168474, 87168559, 264603, 264681, 264448, 264683, 264288, 264369, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 33657182, 35695763, 35696423, 35695855, 52644332, 83373044, 18108387, 87168518, 22279002
2501	94303896 (5001, 5002)	Novel Protein sim. GBank gi 4929615 gb AAD34068.1 AF15183 - (AF151831) CGI-73 protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	65274572, 56182575, 35696286, 22278998, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264910, 264591, 60432229, 33657402, 60433356, 264595, 55812038, 264758, 264596, 87168474, 87168559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264369, 264288, 264766, 18108357, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264692, 33657023, 264629, 35696423, 55811576, 35695855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87168518, 60432113, 22279002, 264566
2502	90993716 (5003, 5004)	Novel Protein sim. GBank gi 3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g129308) [Homo sapiens]	Contains protein domain (PF01237) - Oxysterol-binding protein	UNCLASSIFIED	65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33657109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87168518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gi 2196874 emb CAA72638 - (Y11896) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868706 (5007, 5008)	Novel Protein sim. GBank gij550420[emb]CAA48220] - (X68101) tg [Rattus norvegicus]			264488, 52644507, 52645156, 52646842, 22278994, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264906, 264908, 52644045, 265009, 60433356, 33657402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52644229, 21906765, 21906766, 21906767, 21906768, 52644150, 264692, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52644332, 56182323, 18108387, 87168518, 60432113, 22279002, 264564
2505	8760559 (5009, 5010)			UNCLASSIFIED	264605
2506	91232326 (5011, 5012)	Novel Protein sim. GBank gij2137562[pri]49635 - mouse Dhml protein - mouse		nuclease	264488, 52644507, 52645156, 52646365, 65274572, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331826, 29331828, 264509, 56182435, 264112, 264593, 60433356, 55812038, 21906754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 33657023, 27486264, 18108379, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264565
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[ref]NP_006035.1[pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		264488, 263994, 264592, 264595, 264369, 264866, 264768, 35695917, 35696423, 264563
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[emb]CAB42889.1] - (AL031447) dJ126A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	22278995, 22278999, 60432049, 264259, 29331828, 265006, 265007, 60433438, 33657084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21906765, 21906769, 55811957, 265020, 265022, 27486261, 33657349, 18108377, 35695855, 60432113, 22279002, 264563, 264565
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264556, 264567

2510	95421379 (5019, 5020)	Novel Protein sim. GBank gi 3293537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]			dna_ma_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21906754, 87168474, 265017, 265018, 264448, 264288, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265022, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486262, 33657349, 18108370, 35695855, 264555, 56182323, 83373044, 60432113, 22279002, 265017, 21906764, 265020, 264692
2511	87384281 (5021, 5022)	Novel Protein sim. GBank gi 4323152 gb AAD16228.1 - (AF098863) Ets-protein Spi-C [Mus musculus]				
2512	88084771 (5023, 5024)	Novel Protein sim. GBank gi 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor		Contains protein domain (PF000097) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 264259, 29331825, 29331826, 29146499, 264907, 264909, 265006, 265008, 264591, 60432229, 21906754, 264763, 264683, 264766, 18108357, 264689, 21906769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gi 3004657 (AF017777) - bobby sox [Drosophila melanogaster]			UNCLASSIFIED	60424179, 52645156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424269, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264369, 56181562, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 33657023, 18108366, 33657109, 27486261, 27486262, 33657349, 18108374, 55810764, 35696423, 56182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gi 2258437 (AF008197) - syncollin [Rattus norvegicus]			UNCLASSIFIED	264510
2515	87994509 (5029, 5030)	Novel Protein sim. GBank gi 3757727 emb CAA18783 - (AL022727) dJ80119.7 (olfactory receptor-like protein (hs6M1-3)) (Homo sapiens)		Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
2516	87786908 (5031, 5032)				UNCLASSIFIED	264259, 29146498, 264905, 264288, 29148629, 35695917, 27486261, 264634
2517	87784966 (5033, 5034)	Novel Protein sim. GBank gi 4220527 emb CAA23000 - (AL035356) putative protein [Arabidopsis thaliana]			UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33109954, 265017, 265018, 264605, 264760, 264762, 264763, 264766, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264564

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gil4929591 gb AAD34056.1 AF15181 - (AF151819) CGI-61 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 264907, 264909, 264511, 265007, 60432229, 60433356, 60433438, 55812038, 265010, 265017, 264448, 264288, 264689, 21906768, 21906769, 265022, 52644150, 264693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088
2519	94326180 (5037, 5038)	Novel Protein sim. GBank gil4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4 (AC004883) similar to KIAA0766; similar to PID.g3882253 [Homo sapiens]	kinase		264259, 66714117, 29331826, 29331827, 29331828, 264907, 66712502, 265006, 265008, 264594, 265010, 265011, 265018, 264288, 21906769, 265020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22279002, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gil4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		264259, 264908, 264910, 264682, 21906769, 265020, 264563
2521	95316244 (5041, 5042)	Novel Protein sim. GBank gil5174489 ref NP_006035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 264489, 263394, 65274572, 22278995, 22278998, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 264907, 66712502, 264511, 265006, 265007, 264591, 264592, 264593, 264594, 264595, 264596, 264681, 264448, 264763, 264682, 264764, 264684, 264369, 264288, 264685, 264686, 21906768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264565, 264566, 264567
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gil4580011 gb AAD24201.1 U81002_ - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21906754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank gil1809327 (U76374) - skm- BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 264512, 265008, 60170831, 33657402, 265010, 87168559, 265019, 264288, 21906765, 21906769, 35695917, 265020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486261, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gjl2073564 (U00223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278999, 60432049, 60432289, 29331828, 264905, 265008, 55812038, 21906754, 265019, 264369, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22279002, 264565
2526	95289404 (5051, 5052)	Novel Protein sim. GBank gjl4589628dbj BAA76836.1 - (AB023209) KIAA0992 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	60424179, 284768, 264687, 264769, 264689, 65274572, 21906767, 56182575, 21906768, 21908769, 55811957, 22278994, 22278995, 35696286, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 27486282, 264508, 264509, 264905, 264907, 18108370, 66712502, 60431528, 264828, 264909, 18108372, 18108374, 56182435, 18108376, 55810764, 55811576, 35696423, 35695855, 265006, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52646317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22279000, 265018, 265019, 264564, 18108351, 264448, 264566, 264288, 264486, 264567, 264766
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gjl2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264585, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gjl2085786 (AC002086) - similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22279002
2529	86670926 (5057, 5058)	Novel Protein sim. GBank gjl3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW.Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	29331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21906768, 33657023, 87168518, 22279000
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gjl2864625jemb CAA16972 - (AL021811) putative protein [Arabidopsis thaliana]			264593
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gjl437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5067, 5068)	Novel Protein sim. GBank gi 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]		UNCLASSIFIED	264259, 35696052, 264905, 265017, 21906769, 265020, 265022, 33657109, 22279000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gi 4468311[emb CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			65274572, 35696286, 60432289, 29331828, 66712502, 265006, 60432229, 265017, 265018, 265019, 264288, 264369, 264689, 21906768, 265020, 265021, 264636, 60170394, 22279002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gi 728836[sp P39193]ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	kinase		18108398, 56182575, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331826, 29331827, 29331828, 264905, 264511, 265009, 264910, 264596, 52646317, 18108351, 264681, 264683, 18108354, 264288, 264687, 264769, 264689, 21906765, 21906766, 21906767, 265021, 52645129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87168518, 60432113, 22279000, 22279002, 264567, 18108391, 65274572, 35696286, 29331822, 29331825, 29331827, 29331828, 35696052, 264906, 66712502, 264909, 265008, 265011, 264760, 264288, 264685, 35695917, 60170615, 264691, 33657023, 65274620, 33657109, 18108374, 35696423, 35695855, 264636, 264558, 60170394, 56182323, 83373044
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gi 4557026[ref NP_003913.1]pHERC - guanine nucleotide exchange factor p532	ubiquitin		22278996, 22278999, 29331822, 29331825, 29331828, 29146499, 264908, 264112, 60170831, 87168559, 264604, 265019, 264685, 264766, 87168518, 22279000, 264565, 264566
2538	36853454 (5075, 5076)			UNCLASSIFIED	
2539	94144916 (5077, 5078)			UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gi 1362647[pir S53876] - sex-regulated protein janus A - fruit fly (Drosophila pseudobscura)		UNCLASSIFIED	22278997, 29331828, 265008, 265009, 264758, 265010, 18108351, 264683, 264288, 21906765, 35695917, 265020, 18108374, 264567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gi 1711658[sp P54797]T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264488, 264768, 264689, 264511, 20281171, 264634, 264635, 264691, 264639, 29331824, 264603, 264604, 264905, 264907, 264908, 264766

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AAD40850.1 AF08310 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N- terminal Domain	UNCLASSIFIED	264488, 18108394, 52646365, 52648942, 65274572, 22278994, 35696286, 22278996, 264259, 52645080, 29331822, 29331824, 29331827, 35696052, 33656970, 264907, 264909, 52644045, 264510, 265006, 264512, 265007, 265008, 265009, 264910, 60431735, 52646317, 52644296, 265010, 265011, 265018, 265019, 18108351, 264683, 264288, 264685, 264687, 52644229, 264769, 21906768, 21906767, 21906769, 52644150, 33657023, 33657109, 52645129, 33657182, 27486261, 27486264, 33657349, 35695763, 18108374, 35696423, 35695855, 264631, 264634, 264635, 264558, 83373044, 18108385, 18108387, 87168518, 264563, 264564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1 - (AL096723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)		65274572, 56182575, 22278999, 264259, 29331826, 264907, 264510, 264511, 264592, 264595, 264764, 264369, 264288, 264684, 264766, 264689, 21906765, 21906767, 21906769, 80170615, 264692, 264693, 55811576, 65274791, 264636, 264556, 18108381, 60170394, 264639, 18108385, 60432113, 22279000
2544	94218548 (5087, 5088)	Novel Protein sim. GBank gi 2498110 sp Q63191 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52646365, 22278997, 264259, 60432049, 29331822, 29331825, 29331826, 29331827, 29331828, 264905, 264908, 265006, 265007, 265008, 87168559, 265017, 265018, 265019, 18108351, 264448, 264686, 264687, 264689, 21906765, 265020, 265021, 18108370, 18108374, 18108376, 18108381, 18108385, 18108387, 56526486, 22279000, 264482, 264563, 264567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gi 3327046 gb BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			29331825, 264906, 265009, 60170831, 265017, 264369, 21906767, 60170615, 264692, 33657109
2546	88033861 (5091, 5092)	Novel Protein sim. GBank gi 2996032 (AF054586) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	29331824, 265007, 22279002

2547	94143869 (5093, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34064.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56994075, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 60431735, 264594, 60433438, 21906754, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906765, 21906766, 21906767, 21906768, 29148627, 21906769, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27486261, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264558, 264559, 83373044, 18108385, 87168518, 22279002, 264564, 264566, 264486
2548	88179079 (5095, 5096)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696286, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 33657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432113, 22279000, 22279002, 264563, 264557
2549	94196893 (5097, 5098)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265018, 264688, 21906764, 21906765, 21906766, 21906767, 21906769, 265020, 265021, 52644150, 264691, 18108368, 60431602, 18108376, 35696423, 56182323, 18108387, 264567
2550	87778584 (5099, 5100)	Novel Protein sim. GBank gi 2143886 pir I52523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 264905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 264605, 265019, 264288, 21906766, 21906768, 21906769, 265020, 60170615, 264693, 33657109, 35696423, 264638, 56182323, 83373044, 22279000
2552	95332620 (5103, 5104)			UNCLASSIFIED	56182575, 35696286, 29331824, 29331826, 35696052, 29331828, 264508, 264907, 56182435, 265008, 264591, 33109954, 264760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811576, 35696423, 35695855, 56182323, 264558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gi 171658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION		UNCLASSIFIED	264686, 264488, 263976, 264766, 29331826, 35696052, 35696423, 264601, 264511, 264602, 264910, 264634, 264760, 264555, 264762, 264906, 264592, 264691, 264566, 264908, 264684, 264567, 264909, 264766
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gi 728835 sp P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 264508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gi 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 264509, 33657402, 264683, 264684, 264766, 264689, 33657023, 33657109, 35695855, 264558, 264567
2557	79437803 (5113, 5114)				264595
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gi 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 264906, 264511, 265018, 264448
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gi 4538998 emb CAB39619.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 264288, 264765, 264766, 264769, 21906765, 21906766, 60432113, 264482
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gi 5051399 emb CAB44995.1 - (AL078630) 573K1.3 (mm17M1-4 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gi 5326825 gb AAD42056.1 AF044953 (NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens])		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 265007, 60432229, 87168559, 265017, 265018, 265019, 264689, 21906766, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 264634, 264559, 18108385, 87168518, 22279002

2562	87645539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21908765, 55811957, 60170615, 33657023, 264693, 35695855, 87168518, 264486, 35696286, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264907, 264908, 264909, 52644045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	88095497 (5125, 5126)	Novel Protein sim. GBank gi 4886447 emb CAB43371.1 - (AL050270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352944 sp P47179 YJ9P_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR		sulfoltransferase	
2565	85530906 (5129, 5130)			UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi 628012 pir A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	18108370, 35695855, 264556, 264558, 18108383
2567	86143590 (5133, 5134)				265020, 60170615
2568	91233099 (5135, 5136)	Novel Protein sim. GBank gi 466009 sp P34548 YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810764, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313764 (5137, 5138)	Novel Protein sim: GBank gi 2599560 gb AAB84166.1 - (AF029674) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	18108394, 56182575, 56181686, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264906, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21906754, 87168559, 265017, 265018, 265019, 264682, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 29148827, 21906769, 35695917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35695763, 20281069, 263974, 18108374, 55810764, 35696423, 35695855, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264556
2570	94136754 (5139, 5140)	Novel Protein sim: GBank gi 4758954 ref NP_004567.1 pPP2 - protein phosphatase 2 (formerly 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278996, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35696052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35695855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim: GBank gi 732218 sp P34609 YO60_CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		situcl	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim: GBank gi 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 29331827, 35696052, 264100, 264104, 264110, 264592, 21906754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35695855, 60170394, 264559, 18108385

2573	95313929 (5145, 5146)	Novel Protein sim. GBank gi 399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 60424179, 65274572, 56182575, 56181686, 22278995, 56994075, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264104, 264107, 264508, 264906, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170615, 264690, 52644150, 284691, 264692, 33657023, 85274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 58182323, 60170394, 83373044, 18108384, 87168518, 60432113, 264482, 264564, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264764, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170615, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 48108385, 264482
2574	94746814 (5147, 5148)	Novel Protein sim. GBank gi 3334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED	
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED	264910, 264601, 264683, 264689, 264080
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264259, 35696052, 264906, 60433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi 4337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]		UNCLASSIFIED	29331825, 265018, 265019, 264685
2578	87786941 (5155, 5156)			UNCLASSIFIED	264488, 264906, 264908, 264910, 264596, 264603, 264604, 264605, 264766, 21906769, 264628, 264630, 264634, 264639, 264563
2579	87292879 (5157, 5158)			UNCLASSIFIED	29331822, 29331824, 264767

2580	88168788 (5159, 5160)	Novel Protein sim. GBank gi 2588628 (AC003080) - Similar to KIAA0299; 60% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87899048 (5161, 5162)	Novel Protein sim. GBank gi 4406642 gb AAD20049 - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	collagen	55994075, 29331824, 29331826, 29331828, 264905, 60433358, 60433438, 264758, 87168559, 21906769, 265022, 35695855, 263981
2582	87786789 (5163, 5164)	Novel Protein sim. GBank gi 2739367 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]		eph	264488, 264907, 264908, 264910, 264764, 264684, 264766, 264638, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112 emb CAA16521.1 - (AL021578) dJ453C12.2 (similar to transcription factor RBP. L) [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	transcript factor	55181686, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430941 (5167, 5168)			UNCLASSIFIED	264908, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi 2736151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]		kinase	264768
2586	91226136 (5171, 5172)				22278988, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433356, 33657402, 265018, 264762, 264288, 21906766, 21906767, 21906769, 265022, 264691, 83373044, 56526486, 22279002
2587	80430943 (5173, 5174)				264908, 265019, 264768, 264693, 55811576, 56182323
2588	80074385 (5175, 5176)			UNCLASSIFIED	264584
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 3021598 emb CAA71415 - (Y10389) nuclear protein [Xenopus laevis]		UNCLASSIFIED	35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264769, 35696423, 264636
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi 2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]	Contains protein domain (PF01055) - Glycosyl hydrolases family 31	glucoamylase	22278995, 29331830, 265008, 265010, 265017, 264639
2591	94192167 (5181, 5182)	Novel Protein sim. GBank gi 5702202 gb AAD47199.1 (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]		eph	264259, 29331822, 264105, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332648 (5183, 5184)	Novel Protein sim. GBank gi 3024998 sp G60936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 264906, 264909, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 55812038, 18108348, 21906754, 265011, 87168559, 265017, 265019, 264764, 264369, 264288, 264766, 265021, 60170615, 33657023, 33657109, 264629, 35696423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264565
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF151888) CGI-130 protein [Homo sapiens]		Im7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264369, 21906768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF151817) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108388, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21906768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264584, 264586, 264567
2595	79561676 (5189, 5190)			UNCLASSIFIED	264692
2596	87538637 (5191, 5192)	Novel Protein sim. GBank gi 4309681 gb AAD15478 - (AC006930) R33423_1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 60431528
2597	94784089 (5193, 5194)			UNCLASSIFIED	264905, 264509, 264908, 264762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264486
2598	88094948 (5195, 5196)	Novel Protein sim. GBank gi 1001351 dbj BAA10838 - (D64006) hypothetical protein [Synechocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264688, 21906766, 35695917, 264691, 33657023, 33657109, 18108370, 18108374, 264564, 264585
2599	87642888 (5197, 5198)	Novel Protein sim. GBank gi 3941737 (AF109719) - BAT2 [Mus musculus]		MHC	264766, 264769, 21906768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22278900, 264566
2600	87787846 (5199, 5200)	Novel Protein sim. GBank gi 4263521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	35696286, 264093, 264288, 21906769, 35696423, 35695855

2601	91243070 (5201, 5202)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	36182575, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 264906, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33657109, 18108370, 18108376, 58182323, 18108381, 18108385, 22279002, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank gi 4406632 gb AAD20047 - (AF131801) Unknown [Homo sapiens]			
2603	94325821 (5205, 5206)	Novel Protein sim. GBank gi 3122387 sp O61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 5994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 58182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 264759, 33657084, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264683, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 5811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264693, 33657109, 27486262, 18108374, 35696423, 65274791, 35695855, 264555, 264636, 264637, 58182323, 83373044, 56526486, 87168518, 60432113, 22279000
2604	94676601 (5207, 5208)	Novel Protein sim. GBank gi 5454030 ref NP_006468.1 pRRP2 - RAS-related on chromosome 22		oncogene	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2605	94316756 (5209, 5210)	Novel Protein sim. GBank gi 3628745 dbj BAA33366 - (AB013721) mltugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	22278998, 264480, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264758, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906766, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2606	87746406 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gi 4826626 gb AAD30202.1 - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 66712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21906765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264639, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gi 2226005 (U49973) - ORF2: function unknown [Homo sapiens]			
2609	94843791 (5217, 5218)	Novel Protein sim. GBank gi 3024889 sp P56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)	Contains protein domain (PF00850) - Histone deacetylase family	histone	264488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21906765, 21906767, 21906769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2610	88177654 (5218, 5220)	Novel Protein sim. GBank gi 4336855 gb AAD17989 - (AF106473) leucine-rich-domain inter-acting protein 1: LeR inter-acting protein 1; LEAP1 [Mus musculus]		transcription factor	18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gi 3876761 emb CAA92994 - (Z68760) predicted using GeneFinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278999, 265017, 264684, 21906768, 22279000
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2613	79481496 (5225, 5226)			UNCLASSIFIED	264685
2614	87643948 (5227, 5228)	Novel Protein sim. GBank gi 5533081 gb AAD45009.1 AF16118 - (AF161181) P55T protein [Mus musculus]	Contains protein domain (PF00625) - Guanylate kinase		22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52644229, 21906765, 33657109, 27486264, 18108370, 263972, 264555, 60432113
2615	87381996 (5229, 5230)			UNCLASSIFIED	264768, 18108394, 264692, 264693, 264508, 264509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264685, 264766

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gij3876761[emb(CAA92994)] - (Z88760) predicted using GeneFinder; Similarity to Mouse FKBP-type peptidyl-prolyl cis-trans isomerases	Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	isomerase	22278995, 22278997, 22278998, 60432049, 60432289, 264628, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21906765, 21906767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264587
2617	86976888 (5233, 5234)	Novel Protein sim. GBank gij728831[spP39188]ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gij3319282 (AF049103) - Huntingtin interacting protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	UNCLASSIFIED	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264906, 264907, 66712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21906754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264689, 21906765, 21906766, 21906767, 35695917, 265020, 265022, 33657023, 264692, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108385, 18108388, 56526486, 264563
2619	87694000 (5237, 5238)	Novel Protein sim. GBank gij2431772 (U66411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00465) - Iron-containing alcohol dehydrogenases	dehydrogenase	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gij4322567[gb AAD1609] - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger	UNCLASSIFIED	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35696286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35696052, 264907, 66712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21906765, 21906768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002
2621	80253495 (5241, 5242)				264594, 264636
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gij4557341[refNP_001174.1]pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit			264488, 264906, 264907, 264908, 264512, 265007, 264758, 35695917, 264634, 264636, 264563, 264482
2623	91638306 (5245, 5246)	Novel Protein sim. GBank gij3880355[emb(CAB05299)] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148629

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gi 3880355 emb CAB05299 - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35696052, 29146499, 66712502, 52644045, 265007, 265008, 60433356, 33109954, 21906754, 265010, 265011, 265019, 264448, 264288, 21906765, 21906766, 21906767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 56182323, 18108385, 87168518, 22279002, 18108391, 264091, 264511, 263981
2625	86452068 (5249, 5250)	Novel Protein sim. GBank gi 2887429 db BAA24857 - (AB007887) KIAA0427 [Homo sapiens]	UNCLASSIFIED	265008
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gi 487416 L20302 - actin filament protein [Gallus gallus]	struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gi 88462 pir A27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human	UNCLASSIFIED	22278996, 265007, 265009, 264448, 21906767, 265021, 264558, 87168518
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gi 3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]	UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21906765, 21906768, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2629	81376490 (5257, 5258)	Novel Protein sim. GBank gi 4929595 gb AAD34058.1 AF15182 - (AF151821) CGI-63 protein [Homo sapiens]	synhase	29331825, 29331826, 264102, 265006, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2630	79188364 (5259, 5260)	Novel Protein sim. GBank gi 321605 pir JQ1161 - Gag protein - Visna virus (strain EV1)	UNCLASSIFIED	264636, 18108385
2631	94845909 (5261, 5262)	Contains protein domain (PF00098) - dna_rna_bind Zinc finger, CCHC class	dna_rna_bind	52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264766, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 65274791, 35695855, 264634, 264637, 52644332, 56182323, 60432113, 264566, 264486, 264685
2632	36730414 (5263, 5264)			

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gij1139548[dbj]BAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)		22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265006, 265007, 265008, 265009, 55812038, 33657084, 55811386, 265010, 265011, 87168559, 265018, 265019, 264683, 264288, 264686, 29148629, 33657023, 264693, 33657182, 35695763, 55811578, 264638, 56182323, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264585
2634	87330821 (5267, 5268)	Novel Protein sim. GBank gij5441611[emb]CAB46854.1] - (AJ388555) hypothetical protein [Canis familiaris]		UNCLASSIFIED	29331826, 263972, 264089
2635	86623144 (5269, 5270)	Novel Protein sim. GBank gij4680663[gb]AAD27721.1[AF132946] CGI-12 protein [Homo sapiens]			22278997, 264259, 29331824, 66714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148629, 18108376, 55811578, 35695855, 87168518, 22279000
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3879146[emb]CAB07646] - (Z93386) Similarity to Yeast hypothetical 52.9 KD protein (SW:P43616); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D69025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40		264569, 29331822, 29331828, 265008, 60170831, 264681, 264765, 264685, 29148627, 21906769, 29148784, 265022, 60170615, 264635, 18108385, 56526486, 22279002, 264567
2637	95011298 (5273, 5274)	Novel Protein sim. GBank gij4758208[ref]NP_004081.1[IpDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)]	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264687, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 35695917, 265021, 60170615, 264691, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264554, 264555, 264556, 264486, 264567

2638	94326733 (5275, 5276)	Novel Protein sim. GBank gij4929689 gb AAD34105.1 AF15186 - (AF151866) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	50424179, 52644507, 52646842, 18108398, 56182575, 22278995, 22278996, 35696286, 22278997, 22278999, 264259, 60432049, 29331822, 60424269, 29331826, 35696052, 29146498, 264905, 52644045, 56182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264768, 52644229, 56181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33657109, 35695763, 18108374, 55810764, 35696423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank gj 2190007 dbj BAA20355 - (AB004109) phosphatidylserine synthase II [Cricetus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 264909, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33657109, 264628, 35696423, 264555, 264639, 264563, 264564, 264565, 264566, 264486
2640	87781330 (5279, 5280)	Novel Protein sim. GBank gj 3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm. score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm. score: 67.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11668834 (5281, 5282)			UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank gj 2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526486, 22279002
2643	87643961 (5285, 5286)	Novel Protein sim. GBank gj 4490304 emb CAB38795.1 - (AL035678) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264690, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	88177671 (5287, 5288)	Novel Protein sim. GBank gj 3789797 gb AAC67502.1 - (AF059568) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl_recp	264107, 264687
2645	17277228 (5289, 5290)			UNCLASSIFIED	265007
2646	84148542 (5291, 5292)	Novel Protein sim. GBank gij1706722 sp P49749 EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2)		UNCLASSIFIED	264909, 264687, 264632, 83373044

2647	91212978 (5283, 5284)			UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 264259, 29331822, 56182181, 29331825, 60424269, 60432289, 35696052, 66712502, 264908, 265007, 55812038, 33109954, 21906754, 33657084, 265018, 264448, 264288, 56181562, 21906765, 21906766, 21906768, 21906769, 35695917, 265020, 265021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810764, 35696423, 56182323, 60432113, 22279002, 264564
2648	87600587 (5295, 5296)				29146498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263976, 18108377, 35696423, 60432113
2649	94128783 (5297, 5298)	Novel Protein sim. GBank gj 3041852 (AC004539) - unknown function; similar to Y09105 (P1D:g1666171) [Homo sapiens]		UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432289, 66712502, 56182435, 60170831, 60432229, 33657402, 33109954, 21906754, 265017, 264886, 264688, 21906765, 21906768, 60170615, 264693, 263967, 18108370, 263976, 60170394, 60432113, 22279002, 264563, 264685
2650	87297533 (5298, 5300)	Novel Protein sim. GBank gj 5360271 [dbj BAA81908.1] - (AB029335) HrPET-3 [Haloecynthia roretzi]			
2651	88068745 (5301, 5302)	Novel Protein sim. GBank gj 4240225 [dbj BAA74891.1] - (AB020675) KIAA0868 protein [Homo sapiens]	Contains protein domain (PF00054) - Laminin G domain		29331824, 29331826, 29331827, 265007, 55812038, 21906754, 18108366, 18108384, 22279002, 264567
2652	10343125 (5303, 5304)			UNCLASSIFIED	264692
2653	87798735 (5305, 5306)	Novel Protein sim. GBank gj 4493956 [emb CAB11123.2] - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c), Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR:....		UNCLASSIFIED	265018, 18108370, 18108387, 264566
2654	95103240 (5307, 5308)				60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 265021, 263976, 55810764, 65274791, 56182323, 83373044, 65274727
2655	91228018 (5309, 5310)	Novel Protein sim. GBank gj 3875272 [emb CAB02861] - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transcript factor	56182575, 56181686, 264092, 264259, 56182181, 60432289, 264907, 33657402, 55812038, 21906754, 87168559, 265017, 264448, 264369, 264288, 21906765, 21906766, 21906767, 21906768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2656	84562601 (5311, 5312)	Novel Protein sim. GBank gj 3043718 [dbj BAA25523] - (AB011169) KIAA0597 protein [Homo sapiens]			264693

2657	52561728 (5313, 5314)	Novel Protein sim. GBank gi 569509 dbj BAA83038.1 - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	264693
2658	88062454 (5315, 5316)	Novel Protein sim. GBank gi 3668089 (AC005757) - R32611_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21906768, 35695917, 264693, 35695855, 264637, 87168518, 264486, 264567
2659	87600755 (5317, 5318)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	264909, 264910, 265018, 264369, 264769, 21906769, 264693, 263972, 18108388, 264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433358, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 28148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2660	91718472 (5319, 5320)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - !!!!! ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00036) - EF hand	kinase	264488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433358, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21906765, 28148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22279000, 22279002
2661	95342817 (5321, 5322)	Novel Protein sim. GBank gi 4758048 ref NP_004739.1 pCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 264760, 264448, 264369, 264288, 21906765, 21906768, 265022, 264691, 33657023, 27486262, 60431528, 18108374, 35695855, 18108388, 264482, 264555, 264556, 264558, 264486
2662	80228739 (5323, 5324)	Novel Protein sim. GBank gi 3874714 emb CAA91263 - (Z66494) similar to choline dehydrogenase; cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264906, 264909, 264757, 264758, 264767, 264691, 33657023, 264638
2663	87780623 (5325, 5326)	Novel Protein sim. GBank gi 1389670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2664	85518329 (5327, 5328)	Novel Protein sim. GBank gi 4884409 emb CAB43311.1 - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35696286, 22278999, 29331822, 35696052, 264906, 264907, 264909, 264510, 264511, 264512, 264593, 60433438, 265019, 264681, 21906765, 21906766, 21906767, 21906768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2665	87770662 (5329, 5330)	Novel Protein sim. GBank gi 5106956 gb AAD39906.1 AF113615) FHL/FH2 domain-containing protein FHOS [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2666	87826472 (5331, 5332)	Novel Protein sim. GBank gi 2500570 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	264907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567
2667	87422720 (5333, 5334)	Novel Protein sim. GBank gi 2500570 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0564.1			

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi 5454186 ref NP_006327.1 p2YG - ZYG homolog	UNCLASSIFIED	56181688, 35696286, 22278998, 22278999, 56182181, 29331824, 60424269, 29331825, 35696052, 29331828, 66712502, 56182435, 60433356, 264758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 264448, 264369, 264288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 264692, 33657109, 35695763, 60431528, 18108374, 35698423, 55811576, 264634, 60431850, 83373044, 18108385, 87168518, 22279000, 264563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi 2147012 pir JC4899 - proline rich protein - rat		264489, 264689, 21906767, 65274572, 56182575, 21906768, 29148627, 21906769, 29148629, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170615, 52644150, 60432049, 264259, 264691, 33657023, 264692, 29331822, 29331824, 29331825, 60432289, 33657109, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264905, 264908, 52644045, 264909, 56182435, 35696423, 65274791, 35695855, 265008, 264910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi 1723523 sp Q10362 YDBB_SCHPO - HYPOTHETICAL 94.9 KD PROTEIN C22E12.11C IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	18108370, 263974
2671	91214836 (5341, 5342)	Novel Protein sim. GBank gi 4768277 gb AAD29444.1 AF06425 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 264288, 265021, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 18108376, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi 4966346 gb AAD34677.1 AC00634 - (AC006341) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	UNCLASSIFIED	264767

2673	87430749 (5345, 5346)	Novel Protein sim. GBank gij5457337[embjCAB41505.2] - (AJ236676) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - Poly(ADP-ribose) polymerase catalytic region.	polymerase	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21906768, 21906769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2674	94847721 (5347, 5348)	Novel Protein sim. GBank gij4758824[ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264488, 22278996, 35696286, 264091, 264259, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2675	79563835 (5349, 5350)			UNCLASSIFIED	264691
2676	79628393 (5351, 5352)			UNCLASSIFIED	264906, 265008
2677	94329600 (5353, 5354)	Novel Protein sim. GBank gij1079042[pir IS52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264490, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52644045, 265006, 285007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 83373044, 18108387, 22279000, 22279002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gjl86760 pir A0465 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52646842, 35696286, 22278999, 264259, 29331825, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265008, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264682, 264683, 264764, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108384, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gjl1709233 sp P07514 INC5R_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase		264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264566, 264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gjl4589604 dbj BAA76824.1 - (AB023197) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2681	90933844 (5361, 5362)	Novel Protein sim. GBank gjl728837 sp P39194 ALU7 - HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 55528486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gjl423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265006, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264764, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gjl511435 gb AAD40286.1 - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264489, 264769, 264635, 264636

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gi 4886469 emb CAB43385.1 - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	88054289 (5369, 5370)	Novel Protein sim. GBank gi 3342729 (AC005331) - R31341_2 [Homo sapiens]	UNCLASSIFIED		
2686	87628690 (5371, 5372)	Novel Protein sim. GBank gi 4508044 db BAA77027.1 - (AB026190) Kelch motif containing protein [Homo sapiens]	struct	Contains protein domain (PF01344) - Kelch motif	264259, 29331822, 60432289, 29331827, 29331830, 264909, 264512, 264596, 264769, 264534, 264555, 264556, 264557, 264558, 60170394, 264559, 264486
2687	87898183 (5373, 5374)	Novel Protein sim. GBank gi 5281314 gb AAD41475.1 AF13312 - (AF133123) transcription factor IIC102 [Homo sapiens]	transcriptfactor	Contains protein domain (PF00515) - TPR Domain	18108394, 18108396, 22278996, 35699286, 22278997, 29331826, 29331828, 66712502, 21906754, 265011, 264760, 264761, 264763, 264689, 21908765, 35696423, 264559, 18108385, 264563
2688	79959584 (5375, 5376)				264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gi 3880023 emb CAA97339 - (Z73098) Similarity to yeast hypothetical protein (Swiss Prot accession number Q09695); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]		Contains protein domain (PF00560) - Leucine Rich Repeat	22278997, 22278998, 22278999, 29331824, 35696052, 264908, 264908, 56182435, 264512, 264910, 265009, 60433438, 21906754, 18108351, 264682, 264683, 264767, 21906765, 21906766, 21906768, 33657023, 33657182, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]	struct	Contains protein domain (PF00620) - RhoGAP domain	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gi 4107276 emb CAA67130 - (X98506) acetyl-CoA synthetase [Solanum tuberosum]	synthase		65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264564, 264566
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gi 3513303 (AC005594) - R26984_1 [Homo sapiens]	peptidase	Contains protein domain (PF00326) - Prolyl oligopeptidase family	
2693	20438807 (5385, 5386)				264592
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gi 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN	UNCLASSIFIED		264559
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gi 4972740 gb AAD34765.1 - (AF132177) unknown [Drosophila melanogaster]	collagen		35696286, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264566
2696	87874040 (5391, 5392)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	synthase		264594, 21906768, 18108370, 18108372

2697	91638472 (5393, 5394)	Novel Protein sim. GBank gi 5689473 dbj BAA83020.1 - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87168474, 265010, 265011, 87168559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21906768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87168518, 22279002, 264563, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank gi 841318 (U22818) - mutant sterol regulatory element binding protein-2 [Cricetus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 265019, 264288, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87780650 (5397, 5398)			UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	Novel Protein sim. GBank gi 5174395 ref NP_006006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181562, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank gi 1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264595, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108384, 18108388, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank gi 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264556, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank gi 5689399 dbj BAA82983.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar)		60432289, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335694[gbjAAB63294] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264905, 264906, 264907, 52644045, 264511, 33857402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264887, 264769, 265021, 264691, 264692, 18108362, 264693, 18108370, 18108374, 264634, 264635
2705	87771745 (5409, 5410)				264489, 264509, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264586, 264486
2706	94326789 (5411, 5412)	Novel Protein sim. GBank gij3255952[embjCAA16821.1] - (AL021728) /prediction=(method:: /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 56994075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264909, 52644045, 56182435, 265006, 265007, 60433438, 55812038, 21908754, 52644296, 265010, 264601, 265017, 265019, 264681, 264448, 264682, 264288, 264686, 264687, 264688, 21906766, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33657023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000, 22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129, 65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565, 29331822, 18108370, 18108374, 83373044
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417294 (AC004381) - Unknown gene product [Homo sapiens]			22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52645129, 65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565, 29331822, 18108370, 18108374, 83373044
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bbj147178 - DARPP-32-dopamine and cAMP-regulated phosphoprotein (human, brain, Peptide, 204 aa)]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264369, 264288, 264765, 264693, 264565, 29331822, 18108370, 18108374, 83373044
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127.1 [Homo sapiens]	UNCLASSIFIED		29331824, 264759, 264693, 18108382, 18108388
2710	87627879 (5419, 5420)	Novel Protein sim. GBank gij4468311[embjCAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			

2711	94111820 (5421, 5422)	Novel Protein sim. GBank gi 3122400 sp O35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21908764, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 264508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87188518, 87188474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264764, 264568, 264288, 264766
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gi 5081315 gb AAD39343.1 AF07660 - (AF076607) prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	264488, 35696288, 22278998, 264259, 29331824, 60432229, 35696052, 264508, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433356, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906768, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 264691, 264692, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87168518, 60432113 66714117, 264906, 264563
2713	88003064 (5425, 5426)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5428)			UNCLASSIFIED	264636
2715	94122454 (5429, 5430)	Novel Protein sim. GBank gi 4321968 gb AAD15897 - (AF067430) Smarce1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264636
2716	88003068 (5431, 5432)	Novel Protein sim. GBank gi 2477513 (AC002398) - F25965_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117, 264908, 264369, 264693, 264556, 264563
2717	80077461 (5433, 5434)	Novel Protein sim. GBank gi 3327046 dbj BAA31591 - (AB014516) KIAA0616 protein [Homo sapiens]			264593, 264558
2718	79604062 (5435, 5436)				264693
2719	88180423 (5437, 5438)	Novel Protein sim. GBank gi 746495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87168559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gi 1335873 (U46690) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	18108374, 60424179, 264489, 56182435, 21906765, 21906766, 35696423, 22278997, 265020, 265022, 265008, 265008, 264092, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108386, 60424269, 29331826, 18108385, 52645129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22279002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 66712502, 52644045, 264909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gi 4929663 gb AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023	22278995, 35696286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21906766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 56182323, 22279000
2722	91638807 (5443, 5444)	Novel Protein sim. GBank gi 3212997 gb AAC23434.1 - (AC004997) match to ESTs AA667999 (NID:g2626700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g172314); similar to various tre-like proteins including: AF040654 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - TSC domain	35696286, 22278999, 21906754, 265017, 264762, 264288, 21906765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)		UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264766, 264687, 264629, 264636, 264486
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gi 4680681 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]	ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21906767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gi 3169705 (AC004760) - F17127_1 [Homo sapiens]	UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21906754, 265011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35696423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gi 3342738 (AC005328) - R26660_1, partial CDS [Homo sapiens]	MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gij731267ispj39219RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - RNA pseudouridylate synthase	- synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 284509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21905754, 33657084, 55811388, 265018, 265019, 284767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264636, 56182323, 87168518, 60432113, 22279000, 264584, 264585
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	18108394, 56182435, 21906767, 55811957, 35695855, 265021, 264690, 264556, 264259, 284557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gij2408095jemb[CAB16300] - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	284887, 29331824, 29331826, 35696052, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108368, 18108374, 264557, 264558, 264559, 18108387, 55528486, 264566, 264486
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gij1723239ispjQ10166jAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase		264259, 35696052, 265006, 264758, 264762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gij3880433jemb[CAA91399] - (Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	UNCLASSIFIED	284687, 264489, 18108358, 56182435, 284689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 284555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 284389, 264567
2733	87363060 (5465, 5466)			UNCLASSIFIED	29331825, 264509, 264909
2734	94140286 (5467, 5468)	Novel Protein sim. GBank gij451962[jdbj BAAT5670.1] - (AB017614) OASIS protein [Mus musculus]	Contains protein domain (PF00170) - bZIP transcription factor	transcription factor	60424179, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5468, 5470)	Novel Protein sim. GBank gi 3850569 (AC005278) - ESTs gb T21276, gb T45403, and gb AA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278996, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank gi 2558501 dbj BA22896 - (D63850) hepatoma-derived growth factor [Mus musculus]			264488, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proleophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank gi 3417386 emb CAA75495 - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 60432229, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52844229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 60431850, 264639, 56182323, 18108382, 18108385, 65274727, 22279002, 264564
2741	88047518 (5481, 5482)	Novel Protein sim. GBank gi 3242764 (AC005154) - similar to protein U28928 (PID:g861306) [Homo sapiens]		UNCLASSIFIED	22278996, 52644045, 52644229, 21906768, 21908769, 265020, 60170615, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank gi 4758412 ref NP_004472.1 pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 2 (GalNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264905, 264758, 55812038, 264369, 29146627
2743	87627891 (5485, 5486)	Novel Protein sim. GBank gi 446831 emb CAB37992 - (AL031432) dJ46SN24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264905, 264908, 265006, 60433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 60432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331826, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 264482, 264448, 264486, 264369, 264288

2745	87740125 (5488, 5490)	Novel Protein sim. GBank gij4405795[gbjAAD19826] - (AF038963) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	35696286, 264509, 264905, 264907, 264908, 264909, 264510, 264512, 265008, 264758, 264601, 265017, 264604, 264763, 264288, 264686, 264769, 264693, 35696423, 35695855, 264634, 264636, 264563, 264564, 264565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gij4758738[reflNP_004680.1]pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	UNCLASSIFIED	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 264906, 264907, 264908, 264909, 52644045, 285006, 60170831, 264596, 55812038, 265018, 264683, 264288, 21906765, 21906767, 21906768, 21906769, 265020, 264690, 33657023, 264693, 33657109, 18108368, 18108374, 264558, 18108385, 22279000, 264563
2747	94112677 (5493, 5494)	Novel Protein sim. GBank gij4557803[reflNP_000262.1]pNPC1 - Niemann-Pick disease, type C1		glycoprotein	264569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 264908, 264909, 265009, 33109954, 55811386, 87188474, 285010, 87168559, 264603, 265019, 264760, 264686, 264768, 21906769, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35696423, 35695855, 264556, 56182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gij4191272[emb CAA09984] - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00846) - F-box domain.		65274572, 29331828, 264112, 264511, 265019, 264760, 264767, 264768, 264769, 21906768, 21906769, 265020, 27486262, 56526486, 87168518, 22279000
2749	87346307 (5497, 5498)				264259, 264908, 264510, 265008, 265009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gij1872498 (U74297) - PiUS [Oryctolagus cuniculus]		UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 264595, 33657084, 265011, 265019, 18108351, 264288, 264686, 264769, 264689, 55811957, 264693, 27486264, 18108370, 18108374, 264558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)			UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88082675 (5503, 5504)	Novel Protein sim. GBank gij3041859 (AC004534) - OG-2 homeodomain protein-like; similar to U65067 (PID:g1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2753	94138972 (5505, 5506)	Novel Protein sim. GBank gi 3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	56182575, 56994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 284288, 56181562, 21906767, 21906768, 265021, 264693, 18108374, 65274791, 264632, 56182323, 22279002, 264563, 264567
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin-like protein [Pisum sativum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35696052, 29331828, 264906, 264908, 264909, 265011, 265017, 265018, 265019, 264288, 21908765, 21906767, 265022, 33657023, 264693, 56182323, 18108382, 22279000
2755	88001472 (5509, 5510)	Novel Protein sim. GBank gi 2996653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465908 (5511, 5512)			UNCLASSIFIED	264594
2757	95361590 (5513, 5514)	Novel Protein sim. GBank gi 1173539 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - eph Src homology domain 2		85585842, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gi 3608372 (AF053768) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	91005312 (5517, 5518)	Novel Protein sim. GBank gi 2072200 (U94863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 264508, 56182435, 21906754, 55811957, 264629, 264636, 56182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gi 4914573 (emb) [CAB43685.1] - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - nuclease Ank repeat		22278998, 29331822, 29331830, 265010, 265019, 264288, 21906765, 21908768, 21906769, 265020, 56182323, 22279002, 264563
2762	87592699 (5523, 5524)	Novel Protein sim. GBank gi 3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264906, 264909, 265006, 265007, 264757, 265010, 265011, 265017, 265019, 18108351, 264448, 264683, 264686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108365, 33657109, 18108368, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518
2763	87539968 (5525, 5526)	Novel Protein sim. GBank gi 3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264369, 35696423
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gi 2905643 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases		52646842, 264259, 29331822, 29331825, 29331826, 29331828, 33656970, 264905, 264907, 29331830, 265006, 265009, 21906754, 265019, 264448, 21908769, 27486282, 56182323, 56526486, 87168518, 264487

2765	94315105 (5528, 5530)	Novel Protein sim. GBank gi 4688672 emb CAA17688.2 - (AL022018) /prediction=(method:: /prediction=(method:: /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264758, 55612038, 33109954, 265010, 87168559, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264768, 264767, 264768, 56181562, 21906764, 21906765, 21906768, 35695917, 265021, 264691, 264692, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35696423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264639, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gi 5441611 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264685, 264689, 35695917, 265022, 264693, 264628, 65274791, 264635, 264555, 264558, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gi 1079451 pir A55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5536)	Novel Protein sim. GBank gi 5441322 emb CAB46721.1 - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35696286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35696052, 264508, 264509, 264905, 264908, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265019, 264760, 264681, 18108351, 264764, 264288, 264766, 264686, 264768, 18108357, 264769, 264689, 21906766, 21906768, 21906769, 35695917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264486, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gi 5419859 emb CAB6375.1 - (AL096725) hypothetical protein [Homo sapiens]		tubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264691, 33657023, 264692, 33657109, 18108374, 55811576, 264634, 264636, 56182323, 83373044, 60432113
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gi 5701965 emb CAB52157.1 - (AL109736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21906765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2771	86084071 (5541, 5542)	Novel Protein sim. GBank gi 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 264389
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gi 488553 ref NP_005465.1 pNY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264766, 21906769, 33657109, 263978, 264555, 264636, 264557, 83373044, 264563, 264564, 264486
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gi 3288888 (AC005253) - R26445_1 [Homo sapiens]		UNCLASSIFIED	18108374, 264686, 264687, 263976, 56182435, 264689, 55810764, 21906766, 35696423, 55811576, 65274791, 56181686, 55811957, 35695855, 264110, 265021, 264112, 265022, 265006, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27486261, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264906, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264784, 264288, 264684, 264766, 263974
2774	87818908 (5547, 5548)	Novel Protein sim. GBank gi 465852 sp P34388 YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21906754, 87168559, 265017, 265018, 264288, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22279000, 264482

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4688132 gb AAD27775.1 AF07704 - (AF077042) 30S ribosomal protein S7 homolog (Homo sapiens)	Contains protein domain (PF00177) - Ribosomal protein S7p/S5e	- ribosomal prot	264488, 22278995, 56994075, 22278996, 35696288, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 265007, 21906754, 265017, 265019, 264448, 264682, 264369, 264288, 18108354, 52644229, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264488, 264567
2776	87791557 (5551, 5552)				56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21906754, 5581386, 265017, 265019, 264448, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 60170615, 55810764, 55811576, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)			UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)			UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF132970) CGI-36 protein (Homo sapiens)		UNCLASSIFIED	22278997, 264259, 29331824, 66714117, 35696052, 265006, 264512, 264448, 264288, 29148627, 18108364, 20281149, 18108370, 264629
2780	94679397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pHKG - HPK/GCK-like kinase	Contains protein domain (PF00780) - CNH domain	kinase	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF069502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	60424179, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 56181582, 21906765, 21906766, 21906768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	65274572, 22278996, 22278998, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264760, 264683, 264288, 264766, 264685, 264688, 264768, 52644229, 264689, 21906768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5566)	Novel Protein sim. GBank gi 728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		tm7	264909, 264628, 263978, 263981
2784	87614360 (5567, 5568)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gi 2134933 pir S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 265020, 264584
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gi 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901266 (5573, 5574)	Novel Protein sim. GBank gi 5174507 ref NP_006020.1 pMA11 - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170615, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	58080644 (5575, 5576)	Novel Protein sim. GBank gi 3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	55491275 (5577, 5578)	Novel Protein sim. GBank gi 2495729 sp Q92556 Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gi 5101772 emb CAB45135.1 - (AJ242978) p621 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264259, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264764, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gi 2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	95083783 (5583, 5584)	Novel Protein sim. GBank gi 2854163 gb AAC02581.1 - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264906, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264766, 52644229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274791, 35695855, 264636, 264556, 264558, 56182323, 83373044, 18108385, 56526486, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264689, 265022, 264691, 18108388, 264567

2795	95334888 (5589, 5590)	Novel Protein sim. GBank gij5454146[ref]NP_006348.1[puBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35696286, 22278988, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331826, 29331827, 35698052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264686, 21906764, 21906765, 21906768, 21906769, 21906769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2786	94848857 (5591, 5592)	Novel Protein sim. GBank gij4680651[gb AAD27715.1 AF13294 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433356, 264594, 264595, 55812038, 264596, 21906754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264762, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274791, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2787	95110790 (5593, 5594)	Novel Protein sim. GBank gij4838557[gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 29146499, 264509, 264906, 56182435, 264757, 21906754, 265010, 265017, 265019, 264681, 264682, 264683, 264686, 21906765, 21906767, 21906768, 21906769, 29148629, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2788	86198005 (5595, 5596)	Novel Protein sim. GBank gij2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264488, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264486, 264567

2799	88090651 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331826, 35696052, 29331828, 264909, 60433356, 33657402, 33109954, 87168474, 264448, 52844229, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 264634, 60432113, 22279000, 264488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168559, 265017, 265019, 264448, 264288, 264766, 264686, 60170815, 264691, 264692, 27486265, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264564, 264566, 264567, 265007, 264687
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74929.1 - (AB020713) KIAA0906 protein [Homo sapiens]		glycoprotein	
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - Sugar (and other) transporter	transport	264448, 35695855
2803	79577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC00658 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	264639
2804	57111131 (5607, 5608)			peptidase	264566
2805	87398486 (5609, 5610)				264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482
2806	87898951 (5611, 5612)	Novel Protein sim. GBank gi 168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5613, 5614)	Novel Protein sim. GBank gij4468310[embjCAB37991] - (AL031432) dJ465N24.1 (PUTATIVE novel protein similar to predicted yeast and worm proteins) [Homo sapiens]		UNCLASSIFIED	52644507, 52645156, 52646842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 35696052, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433358, 264594, 60433438, 52646317, 21906754, 33109954, 33657084, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265021, 265022, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486264, 27486265, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87168518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gij5541863[embjCAB51071.1] - (AL096857) hypothetical protein [Homo sapiens]	MHC		60432289, 264510, 265010, 265017, 265018, 264681, 264686, 265021, 264690, 22279000, 264566
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gij2772561 (AC004002) - similar to ciliary dynein beta heavy chain. 78% Similarity to P23098 (PID:g118965) [Homo sapiens]	ATPase-associated		18108351
2810	87259032 (5619, 5620)			UNCLASSIFIED	264569, 22278996, 264091, 264259, 29331828, 29146499, 29148629, 29148784, 264693
2811	91235845 (5621, 5622)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g118643) and AA085546 (NID:g1628773) [Homo sapiens]	UNCLASSIFIED		22278999, 264259, 66712502, 264693
2812	88093334 (5623, 5624)			UNCLASSIFIED	264106
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gij4240273[dbjBAA74915.1] - (AB020699) KIAA0892 protein [Homo sapiens]	UNCLASSIFIED		56182575, 29331828, 264906, 66712502, 55811388, 265017, 265018, 265019, 264683, 265020, 87168518, 60432113
2814	90980906 (5627, 5628)	Novel Protein sim. GBank gij3548791 (AC005620) - (R33590_1) [Homo sapiens]	transcription factor		65274572
2815	79774521 (5629, 5630)			UNCLASSIFIED	264907, 264909
2816	95358229 (5631, 5632)	Novel Protein sim. GBank gij5420389[embjCAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21906765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gi 1293846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 33695917, 33657109, 263978, 264634, 264636, 264639, 264584, 264565, 264566, 264488, 264567
2818	86073579 (5635, 5636)	Novel Protein sim. GBank gi 549986 (U13149) - possible apoptosis-associated protein [Pennisetum ciliare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87793527 (5637, 5638)			UNCLASSIFIED	264909, 264511
2820	87765744 (5639, 5640)	Novel Protein sim. GBank gi 4929773 [gb AAD34147.1] (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	18108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108365
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gi 399144 [sp P02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264636
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gi 2224671 [dbj BAA20820] - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21906765, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gi 399144 [sp P02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gi 399144 [sp P02747] C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)				264760
2826	94311905 (5651, 5652)	Novel Protein sim. GBank gi 3859683 [emb CAA22020] - (AL033503) conserved hypothetical protein [Candida albicans]			52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35696423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320519 (5653, 5654)	Novel Protein sim. GBank gi 399144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264488, 263994, 264489, 65274572, 29331822, 66714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21906754, 265011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811857, 264534, 264690, 264691, 264692, 264693, 263972, 264629, 35695855, 264631, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264563, 264564, 264565, 264566, 264567, 264486, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi 3598974 AF077000 - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35696052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264766, 264686, 55811957, 18108370, 18108374, 55810764, 35696423, 55811576, 56182323, 83373044, 87168518
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi 4680889 gb AAD27734.1 AF13295 - (AF132959) CG1-25 protein [Homo sapiens]			22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 66712502, 264510, 264511, 264593, 60433438, 21906754, 265011, 264603, 18108351, 264288, 21906765, 21906768, 21906769, 29148629, 52644150, 264693, 35657109, 18108374, 264634, 18108385, 60432113, 22279000, 264565, 264486
2830	88087109 (5659, 5660)	Novel Protein sim. GBank gi 2498867 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			265008, 265019, 264639, 22279002
2831	87614717 (5651, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21906767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi 2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi 4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi 2351568 U76618 - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	264259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 264907, 264909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906767, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775392 (5675, 5676)	Novel Protein sim. GBank gi 973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)			UNCLASSIFIED	264555
2840	87774685 (5679, 5680)	Novel Protein sim. GBank gi 1575515 (U64899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			264509, 264511, 265011, 264288, 264769, 265020, 264634, 264636, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gi 2224605 dbj BAA20790 - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF000076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_na_bind	56182575, 35696052, 264907, 264908, 264909, 264910, 264593, 264595, 264766, 265022, 264691, 33657182, 35695763, 18108370, 35695855, 264631, 264559, 264563, 264567
2842	80080086 (5683, 5684)				264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gi 5578957 emb CAB51350.1 - (AL050306) dJ47587.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 264764, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gi 585123 sp Q08878 FBLC_MOUSE - FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT-MEMBRANE PROTEIN 90) (BM-90)	Contains protein domain (PF00008) - EGF-like domain		264685
2845	94321719 (5689, 5690)	Novel Protein sim. GBank gi 5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	29146498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gi 5306263 gb AAD41995.1 AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gi 3399676 (AC005390) - R31180.1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264566
2848	87612943 (5695, 5696)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264490, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264763, 264764, 264765, 264766, 264686, 264628, 264629, 264555, 264636, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	88084283 (5697, 5698)	Novel Protein sim. GBank gi 3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390, 35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000
2850	87623636 (5699, 5700)			UNCLASSIFIED	

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321619gb AAD15788.1 - (AF051098) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35895855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g129645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - WW domain	kinase	56182575, 55811150, 264690, 27486262, 27486265, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - leich protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079096) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	dna_ma_bind	35896286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723856 (5709, 5710)	Novel Protein sim. GBank gij1504040 dbj BAA13219 - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	22278994, 29331822, 29331824, 29331825, 264906, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88093359 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085546 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486262, 265007, 265009, 285017, 264482, 264583, 18108351
2857	95348286 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - PHD-finger	struct	22278995, 35896286, 29331824, 29331825, 35896052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35895763, 22279002, 264563
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585 sp P35227 ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	dna_ma_bind	264559, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264906, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769, 21906766, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264629, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264584, 264566, 264486, 264567
2859	80937675 (5717, 5718)	Novel Protein sim. GBank gij4325320 gb AAD17331.1 - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2860	87532589 (5719, 5720)	Novel Protein sim. GBank gi 469186 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylylate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264510, 264511, 33109954, 18108351, 264683, 264765, 264369, 264686, 21906765, 264691, 264692, 264693, 18108388, 22279002, 264482
2861	86698507 (5721, 5722)	Novel Protein sim. GBank gi 3941730 (AF108083) - BS4 [Homo sapiens]			264369, 264692
2862	87569585 (5723, 5724)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein		UNCLASSIFIED	264691, 264638
2863	91220421 (5725, 5726)	Novel Protein sim. GBank gi 3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF000096) - struct Zinc finger, C2H2 type		56394075, 35696286, 22278998, 29331822, 29331824, 35696052, 29331828, 264106, 264511, 55812038, 33657084, 55811386, 265018, 265019, 21906765, 21906766, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657349, 264629, 18108376, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2864	87420030 (5727, 5728)	Novel Protein sim. GBank gi 1079451 pir JA55463 - Tropomodulin, skeletal muscle - chicken	struct		264259, 264910
2865	95312191 (5729, 5730)	Novel Protein sim. GBank gi 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 264482
2866	95105480 (5731, 5732)	Novel Protein sim. GBank gi 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		65274572, 22278996, 22278998, 22278999, 264259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 264448, 264764, 52644150, 83373044
2867	86908001 (5733, 5734)	Novel Protein sim. GBank gi 4580997 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		264488, 264768, 21906768, 22278998, 265022, 264259, 264508, 264905, 264907, 264511, 264910, 264635, 264636, 264637, 265011, 265017, 265018, 265019, 264563, 264088, 264566, 264764, 264369, 264567, 264486, 264288, 264766

2868	95303283 (5735, 5736)	Novel Protein sim. GBank gij1282868[embj]CAA63923] - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35896052, 29331828, 264508, 52844045, 264828, 285006, 265007, 285008, 265009, 264591, 60432229, 264593, 60433358, 264595, 21906754, 265017, 265019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35896423, 35895855, 264632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gij5306263[gblAAD41995.1]AC00623] - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567
2872	95312197 (5743, 5744)	Novel Protein sim. GBank gij112205[pirj]B39066 - proline-rich protein 15 - rat	kinase	263981
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35896423, 35898286, 35895917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35896052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264906, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gjl3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645156, 52646365, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 29331825, 66714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 265007, 265009, 60433356, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 265018, 265019, 264682, 264369, 264288, 264688, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22279000, 22279002, 264563, 264565
2875	88083726 (5749, 5750)	Novel Protein sim. GBank gjl2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	glycoprotein	22278996, 22278997, 22278999, 29331826, 29331828, 29146499, 66712502, 265008, 265017, 18108351, 264683, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 264487
2876	88090854 (5751, 5752)	Novel Protein sim. GBank gjl2979530 (AC004449) - R33683_2 [Homo sapiens]	IgI	
2877	94747028 (5753, 5754)	Novel Protein sim. GBank gjl4704208 [emb] (CAB41646.1) - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]		52646365, 65274572, 56182575, 22278997, 22278998, 22278999, 60432049, 52645080, 60424269, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33657084, 265019, 55811150, 264448, 264369, 21906766, 21906768, 21906769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264558, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88095309 (5755, 5756)	Novel Protein sim. GBank gjl3876775 [emb] (CAB03067) - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264905, 264509, 264907, 264909, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2879	8769122 (5757, 5768)	Novel Protein sim. GBank gi 4895145 gb AAD32752.1 - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - Uracil-DNA glycosylase	UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 265017, 264564, 264565, 264567, 264684, 264369
2880	94851439 (5759, 5760)	Novel Protein sim. GBank gi 4680703 gb AAD27741.1 AF13296 - (AF132966) CGI-32 protein [Homo sapiens]			264488, 52646365, 52646842, 22278994, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644296, 87168559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906769, 35695917, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35695855, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264567, 264486
2881	87650539 (5761, 5762)	Novel Protein sim. GBank gi 733571 (U23452) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gi 118112 (U41559) - No definition line found [Caenorhabditis elegans]			264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264681, 264682, 264686, 264687, 264688, 21906768, 21906769, 264693, 263967, 18108374, 55811576, 56182323, 22279002, 264566
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gi 4868008 gb AAD31087.1 AF10693 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264112, 264682
2884	87784643 (5767, 5768)				265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gi 2224697 dbj BAA20832 - (AB002376) KIAA0378 [Homo sapiens]		UNCLASSIFIED	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gi 1255889 (U53344) - T07H6.5 gene product [Caenorhabditis elegans]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	60432049, 264259, 29331828, 264908, 264511, 264595, 60433438, 264598, 265017, 264605, 263969, 263972, 264555, 83373044, 87168518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gi 3882323 dbj BAA34521.1 - (AB018344) KIAA0801 protein [Homo sapiens]		UNCLASSIFIED	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gi 4508015 ref NP_003447.1 pZNF2 - zinc finger protein 205	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87606562 (5777, 5778)				UNCLASSIFIED	56994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264766
2891	88094428 (5781, 5782)	Novel Protein sim. GBank gi 3877750 emb CAB01508 - (Z78064) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65865 comes from this gene; cDNA EST EMBL:D69451 comes from this gene; cDNA EST EMBL:D66026 comes from this gene; cDNA EST EMBL:D69658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95419745 (5783, 5784)	Novel Protein sim. GBank gi 4929759 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	65274572, 35696286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263987, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755985 (5787, 5788)	Novel Protein sim. GBank gi 5689015 gb AAD46135.1 - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type	transcriptfactor		264259, 265006, 60433438, 52644296, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gi 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	8752122 (5791, 5792)	Novel Protein sim. GBank gi 4885549 ref NP_005456.1 pPK8G - protein kinase B gamma	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase		18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29146499, 264906, 264908, 265007, 265009, 265018, 265019, 264369, 264685, 264689, 21906766, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gi 4502877 ref NP_001296.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278996, 35696286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35696052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433356, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 60431528, 18108374, 55810764, 55811576, 35696423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5797, 5798)				UNCLASSIFIED	264764, 21906764, 264692
2900	94233538 (5798, 5800)	Novel Protein sim. GBank gi 4581470 emb CAB40137.1 - (Y18483) SLC7A8 protein [Homo sapiens]			glycoprotein	65274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gi 4759272 ref NP_004614.1 pTTC4 - tetrairicopeptide repeat domain 4			phosphatase	22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906766, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 263981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gi 2414615 emb CAB16364 - (Z99259) hypothetical protein [Schizosaccharomyces pombe]				264683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gi 1079318 pir S52241 - XLCL2 protein - African clawed frog				264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264683, 264769, 264689, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gi 5639823 gb AAD45885.1 AF14367 - (AF143676) multispinning nuclear envelope membrane protein nurim [Homo sapiens]			UNCLASSIFIED	52646365, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 265020, 263967, 18108374, 35695855, 264637, 264952, 18108385, 18108387
2905	84449926 (5809, 5810)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII			oncogene	265009, 264681, 264692
2906	95341051 (5811, 5812)	Novel Protein sim. GBank gi 4689256 gb AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]		Contains protein domain (PF00787) - PX domain	UNCLASSIFIED	22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695917, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264566

2807	91211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNA-J-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - eph DnaJ domain	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264369, 55811562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2908	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2909	87420225 (5817, 5818)		eph	264259, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi 4539335 emb CAB37483.1 - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi 469187 emb CAB38415.1 - (AL031588) dJ1163.J1.3 (novel protein similar to mouse B99) [Homo sapiens]	glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265006, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637 gb AAD34079.1 AF15184 - (AF151842) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264760, 264683, 264288, 264686, 265021, 264693, 18108368, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED Zinc finger, C2H2 type	52644507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)			264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gij5174485[re]NP_006030.1[pKIAA - endocytic receptor (macrophage mannose receptor family)]	Contains protein domain (PF000059) - eph Lectin C-type domain	264569, 264488, 264687, 264768, 21906766, 52648842, 21906767, 21906768, 58182575, 29148629, 35695917, 22278996, 22278997, 22278998, 265021, 22278999, 52644150, 264691, 264259, 60432049, 264692, 52645129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486262, 27486264, 27486265, 33657349, 29146498, 29146499, 264906, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433356, 56182323, 18108382, 55812038, 18108385, 33109954, 21906754, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 265019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264369, 264288, 264766 18108354, 264369, 264288, 264766
2916	95337780 (5831, 5832)	Novel Protein sim. GBank gij5104851[dbj]BAA80165.1[- (AP000061) 305aa long hypothetical dTDP-4- dehydrohamose reductase (Aeropyrum pernix)]	dehydrogenase	52645156, 65274572, 22278994, 22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264906, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433356, 52646317, 21906754, 33109954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486264, 35695763, 18108376, 55811576, 35696423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gij3169065[emb]CAA19260.1[- (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690529 (5835, 5836)	Novel Protein sim. GBank gij539218[pir]S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gij2564955 (AF030001) - unknown [Mus musculus]		66714117, 66712502, 263981

2920	87769523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 265011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486264, 27488265, 35696423, 35695855, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gij4580013 gb AAD24202.1 U83194 - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 59526486, 87168518, 22279000, 22279002
2922	87749762 (5843, 5844)	Novel Protein sim. GBank gij4589514 gb BAA76779.1 (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	264906, 264909, 264511, 265006, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29148627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gij4835268 emb CAB42898.2 (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	stuct	264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22279000, 264563, 264566
2924	87791967 (5847, 5848)	Novel Protein sim. GBank gij2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast [Saccharomyces cerevisiae]	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomalprot	265017, 264628, 20281152, 264556
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gij2388986 emb CAB11718 (Z88980) actin associated protein [Schizosaccharomyces pombe]	UNCLASSIFIED		56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 265022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2926	95343003 (5851, 5852)				29331828, 265011, 264768, 264689
2927	80408018 (5853, 5854)	Novel Protein sim. GBank gj 283032 pir S22456 - hydroxyproline-rich glycoprotein - perennial teosinte			264764, 264288, 264630, 264637
2928	20452179 (5855, 5856)			UNCLASSIFIED	264559
2929	91622920 (5857, 5858)	Novel Protein sim. GBank gj 3413320 emb CAA06915 - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264559, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52644045, 265009, 33109954, 52644296, 87168559, 264760, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52644045, 56182435, 265009, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 265018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170615, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264567
2931	94312693 (5861, 5862)	Novel Protein sim. GBank gj 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52645156, 22278997, 22278998, 29331822, 52645080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906766, 21906767, 21906768, 265020, 52644150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264556, 87168518, 60432113, 264566, 264906, 264907
2932	79632623 (5863, 5864)			helicase	264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52644045, 56182435, 265007, 265009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52644229, 21906765, 21906766, 21906768, 21906769, 265022, 52644150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567
2933	91720776 (5865, 5866)	Novel Protein sim. GBank gj 3378056 (AF017777) - helicase [Drosophila melanogaster]			

2934	86576025 (5867, 5868)				22278997, 22278998, 29331824, 33657402, 264691, 27486262, 264628, 87168518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 264448, 264769, 21906764, 21908765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gi 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:942735) [Homo sapiens]	Contains protein domain (PF00056) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811576, 18108387, 60432113, 264563
2937	94853096 (5873, 5874)	Novel Protein sim. GBank gi 5174409 ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264906, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264766, 52644229, 21908765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264565, 264486, 264567
2938	95419773 (5875, 5876)	Novel Protein sim. GBank gi 3319990 emb CAA76720 - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432229, 33657402, 60433438, 55812038, 21806754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21906765, 21908767, 21908768, 55811957, 35695917, 265020, 60170815, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263976, 35696423, 35695855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56526486, 60432113, 22279002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gi 3979900 emb CAA99909 - (Z75547) similar to WD domain, G-beta repeat: cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292i8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686

2940	95011103 (5879, 5880)			UNCLASSIFIED	22278996, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264764, 264369, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264566
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gij3413872jdbj[BAA32300] - (AB007824) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264557
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gij1172845jpp46629jRB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	264910, 265010, 264768
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gij4929653jgbjAAD34087.1 AF15185 - (AF151850) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 264593, 60433356, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264567
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gij4678282jembj[CAB41190.1] - (AL049660) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	- ATPase_associated	56994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424269, 60432289, 29331826, 29331828, 264905, 264907, 52644045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 60170615, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35698423, 35698855, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 56526486, 87168518, 60432113, 22279002, 264482, 264563, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gij728831jpp39188jALU1_HUMAN - !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424269, 60432289, 35696052, 264908, 265006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264369, 264288, 264687, 56181562, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264693, 60431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264566, 264567

2846	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286. (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264906, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264585, 264566, 264486, 264567
2847	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF056116) Alt-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2848	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52646842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2849	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir S67133 - probable membrane protein YOR24Dw - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278996, 22278997, 60432228, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52644229, 56181562, 21906767, 21906768, 21906769, 265022, 60170615, 33657023, 35696423, 263981, 264558, 60432113, 22279002
2850	95086870 (5899, 5900)	Novel Protein sim. GBank gi 466102 sp P34629 YOJ6_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695855, 264556, 56526486, 264486
2851	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264693

2952	95329952 (5903, 5904)	Novel Protein sim. GBank gij5596693jemb[CAB51405.1] - (AL096881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - CRALTRIO domain.	transcriptfactor	264687, 52645156, 21906766, 21906769, 22278996, 265020, 264690, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264906, 264907, 29331830, 264908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433356, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gij119522 sp P10658 SERC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00266) - Aminotransferases class-V	UNCLASSIFIED	18108396, 56994075, 22278996, 29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264906, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52846317, 21906754, 33657084, 52644296, 87168559, 264600, 264760, 264681, 18108351, 264764, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52645129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565
2954	88086288 (5907, 5908)	Novel Protein sim. GBank gij4885261 ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Transforming growth factor beta like domain	tgf	29331822
2955	87698426 (5909, 5910)	Novel Protein sim. GBank gij3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 264908, 52644045, 264512, 60432229, 265018, 265019, 55811150, 264769, 21906767, 21906768, 21906769, 265021, 60170615, 55810764, 264567
2956	85789745 (5911, 5912)	Novel Protein sim. GBank gij4689254 gb AAD27830.1 AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		22278996, 264259, 29331827, 264908, 21906768
2957	90933301 (5913, 5914)	Novel Protein sim. GBank gij4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor		cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 264448, 264763, 264683, 264288, 264685, 18108357, 29148829, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 56182323, 18108382, 18108385, 18108388, 56526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gij4240257 dbj BAA74907.1 - (AB020691) KIAA0884 protein [Homo sapiens]			264595, 264596, 264681, 264369, 264629, 264631, 264567

2959	95109420 (5917, 5918)	Novel Protein sim. GBank gi 988221 (U33005) - Tbc1 [Mus musculus]	Contains protein domain (PF00566) - TBC domain	oncogene	263994, 22278997, 264259, 60432049, 29331826, 29331828, 35696052, 29331830, 66712502, 56182435, 265006, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906767, 21906769, 265020, 60170615, 264692, 27486265, 18108374, 65274791, 35695855, 83373044, 56526486, 60432113
2960	87420091 (5918, 5920)			UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2961	95413416 (5921, 5922)	Novel Protein sim. GBank gi 596646 emb CAB05177.2 (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	22278997, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265006, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906769, 265020, 60170615, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2962	87912700 (5923, 5924)			UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264565, 264566, 284567, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gi 4240223 dbj BAA74890.1 (AB020674) KIAA0867 protein [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 29148627, 29148784, 265020, 33657023, 264693, 65274620, 33657182, 27486281, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)			UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2965	80384762 (5929, 5930)	Novel Protein sim. GBank gi4885447 ref NP_005452.1 pKRM1 - Kreisler (mouse) mal- related leucine zipper homolog			transcript factor	264259, 29331826, 264508, 264509, 264905, 264907, 264908, 264909, 264511, 265008, 264910, 264591, 264593, 264594, 33657402, 265011, 264760, 264762, 264764, 264288, 264685, 264766, 264692, 33657109, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264567, 18108391 60432289, 264682, 264448
2966	91725248 (5931, 5932)	Novel Protein sim. GBank gi5262751 emb CAB43690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]				
2967	94658303 (5933, 5934)	Novel Protein sim. GBank gi624225 (U19181) - Rabin3 [Rattus norvegicus]			UNCLASSIFIED	264488, 264508, 264509, 264908, 264909, 264511, 264910, 264594, 264758, 85658542, 264762, 264764, 265021, 264556, 18108381, 264584, 264486
2968	95302776 (5935, 5936)	Novel Protein sim. GBank gi4929715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)			264687, 52645156, 21906765, 52646365, 21906767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 264093, 264638, 264690, 52644150, 264259, 33657023, 52645080, 264693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486262, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 264563, 18108351, 264906, 264907, 264448, 66712502, 264566, 264369, 264288 52646842, 22278996, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331828, 264509, 264909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 265018, 265019, 264448, 264288, 264369, 52644229, 21906768, 21906769, 21906769, 29148784, 265020, 265021, 52644150, 264691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22279000
2969	95310957 (5937, 5938)	Novel Protein sim. GBank gi3024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)			eph	
2970	88088071 (5939, 5940)	Novel Protein sim. GBank gi3165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox		

2971	94196930 (5941, 5942)	Novel Protein sim. GBank gi 728637 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Im7	264488, 56182575, 35696286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21906754, 87168559, 265018, 265019, 18108351, 264689, 21906765, 21906767, 21906768, 265020, 265021, 60170615, 18108364, 264628, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87168518, 264564, 264567 265017, 35695917, 265021, 33657109, 22279002, 264563
2972	86625943 (5943, 5944)	Novel Protein sim. GBank gi 728636 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	
2973	91215301 (5945, 5946)	Novel Protein sim. GBank gi 2746789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2974	91673002 (5947, 5948)	Novel Protein sim. GBank gi 786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21906754, 55811386, 52644286, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264448, 264369, 264288, 52644229, 18108359, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810764, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87168518, 60432113, 22279000, 264482, 264487
2975	95325213 (5949, 5950)	Novel Protein sim. GBank gi 3880812 emb CAA19508 - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00632) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85658542, 265011, 265018, 264448, 264288, 264769, 21906767, 265020, 264691, 264559, 83373044
2976	67771202 (5951, 5952)	Novel Protein sim. GBank gi 5679136 gb AAD46874.1 AF16093 - (AF160934) BCDNA LD14189 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2977	91725254 (5953, 5954)	Novel Protein sim. GBank gi 5262751 emb CAB45690.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5956)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21906754, 265010, 265011, 265017, 265018, 265019, 264288, 264685, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2879	91725256 (5957, 5958)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56994075, 22278999, 264093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482
2880	86296600 (5959, 5960)			UNCLASSIFIED	265009, 21906767, 263981, 22279000
2881	87376330 (5961, 5962)				264629, 264564
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gij4929767 [gb]AAD34144.1 [AF15190] CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 18108365, 33657182, 33657349, 35696423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424179, 52646842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52644045, 265006, 60431735, 87168474, 265018, 265019, 18108351, 264448, 21906765, 21906768, 35695917, 33657023, 52645129, 18108370, 35696423, 83373044, 56526486, 60432113, 264404, 22279002
2884	94136467 (5967, 5968)	Novel Protein sim. GBank gij2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	ATPase associated		
2885	87099072 (5969, 5970)	Novel Protein sim. GBank gij103160 [pir]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810764, 264632, 264635, 60432113
2886	86284861 (5971, 5972)				55811957, 264566
2887	86455934 (5973, 5974)		UNCLASSIFIED		264369

2988	95357753 (5875, 5976)	Novel Protein sim. GBank gi 4678028 gb AAD27002.1 - (AF077207) HSPC021 [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331826, 60432289, 35696052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264369, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695855, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113671 sp P23964 ALUF_HUMAN - !!!!! ALU CLASS F WARNING ENTRY !!!!!	kinase	22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gi 2829836 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)			
2992	85425164 (5983, 5984)			
2993	94325363 (5985, 5986)			
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2496549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 29.7 KD PROTEIN CY339.02	transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265006, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695855, 83373044, 18108385, 22279000, 264565, 264566
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		264905, 264907, 265019, 18108351, 264683
2996	91013798 (5991, 5992)	Novel Protein sim. GBank gi 2829912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/IDEAH box helicase	65274572, 35696286, 264259, 29331824, 35696052, 29146499, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264689, 35695917, 60170615, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gj14589652[jb]BAA76848.1] - (AB023221) KIAA1004 protein [Homo sapiens]		homeobox	264488, 56182575, 264259, 66714117, 29331826, 35696052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27486261, 18108374, 35696423, 264634, 264635, 264636, 264557, 18108385, 87168518
2998	88095381 (5995, 5996)	Novel Protein sim. GBank gj13947589[emb]CAA22252] - (AL034364) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	52646365, 22278997, 264508, 264906, 18108351, 21906765, 21906767, 18108370, 18108374, 35696423, 264636, 264639
2998	94847055 (5997, 5998)	Novel Protein sim. GBank gj115408[sp]P18835[CC19_CAEEL - CUTICLE COLLAGEN 19		UNCLASSIFIED	56182575, 22278996, 29147620, 29331825, 29146498, 29146499, 264905, 66712502, 265006, 265009, 21906754, 85658542, 18108351, 29148627, 29148629, 60170615, 33657109, 27486262, 18108370, 18108374, 264556, 264557, 264558, 60170394, 18108385, 264563
3000	95099370 (5999, 6000)	Novel Protein sim. GBank gj1163174 (U32575) - similar to yeast Sec6p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]		UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35696052, 29146498, 264508, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 265008, 265009, 264910, 33657402, 264757, 264595, 264596, 264758, 21906754, 265011, 264600, 265017, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35695917, 265020, 264691, 264692, 33657023, 264693, 33657109, 33657182, 27486261, 264628, 264629, 18108374, 18108376, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20798451, 22279002, 264563, 264486, 264567
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gj12078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678048), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]		cathepsin	18108394, 52646842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52644296, 265017, 265019, 264288, 265020, 265021, 52644150, 264692, 35695763, 55810764, 35696423, 56182323, 18108387, 264563, 264564
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gj13599478 (AF085185) - Myosin-1A [Acanthamoeba castellanii]		UNCLASSIFIED	264498, 29331824, 29331825, 29331826, 29331827, 29331828, 264906, 264510, 265009, 21906754, 264682, 264688, 33657023, 264565

3003	86648078 (6005, 6006)	Novel Protein sim. GBank gij754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	264512, 264593, 264564, 264567, 264486
3004	88066876 (6007, 6008)	Novel Protein sim. GBank gij2224629(dj)[BAA20802] - (AB002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 264691, 33657109, 263972, 18108385
3005	87794843 (6009, 6010)	Novel Protein sim. GBank gij4680659(gb)AAD27719.1(AFI3294 - (AF132944) CGI-10 protein [Homo sapiens])	Contains protein domain (PF01360) - Monooxygenase	- oxygenase	29331822, 29331824, 29331827, 60433438, 265011, 265019, 21908766, 21908767, 21906768, 265020, 33657023, 33657349, 60170394, 22279002, 264567
3006	87422224 (6011, 6012)	Novel Protein sim. GBank gij3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	- MHC	264259, 29331822, 264512, 21906754, 265018, 264687, 21906765, 264691, 264555, 264556, 264558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gij2565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- transcription factor	52644507, 52645156, 65274572, 264909, 264512, 265018, 264760, 264448, 264765, 264689, 60170615, 18108374, 20281152, 264636, 52644332
3008	80416249 (6015, 6016)				264905, 264593, 264766, 264636
3009	91213387 (6017, 6018)	Novel Protein sim. GBank gij3127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	- synthase	52646842, 56182575, 22278995, 22278996, 264259, 29331825, 29331826, 29331827, 29331828, 35696052, 264508, 264509, 264907, 56182435, 264511, 265007, 264512, 265008, 264757, 264758, 55812038, 264759, 33109954, 21906754, 265010, 265011, 264600, 265017, 265018, 265019, 264760, 18108351, 264288, 264369, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 264691, 18108368, 27486262, 20281149, 18108370, 55811576, 264637, 264556, 264557, 18108381, 264558, 56182323, 264559, 18108385, 18108388, 22279002, 264486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gij4927370(gb)AAD33084.1(AF06797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens])	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	264686, 264687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 264692, 33657023, 29331822, 264693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 264909, 55811576, 35695955, 265008, 264556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 265019, 264564, 264682, 264764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gij5052319(gb)AAD38501.1(AFI1883 - (AF118838) citrin; adult-onset type II citrullinemia protein [Homo sapiens])	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	35696052, 56182435, 264758, 21906754, 265018, 264760, 264762, 18108351, 264682, 264448, 21906766, 65274620, 18108374, 264482, 264564
3012	87753087 (6023, 6024)			UNCLASSIFIED	263972

3013	91238799 (6025, 6026)	Novel Protein sim. GBank gij3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat		264488, 263394, 35696286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 264905, 264906, 264907, 264908, 264909, 56182435, 264511, 264512, 264910, 264591, 264592, 264593, 264594, 33657402, 60433438, 264595, 264596, 55812038, 264758, 33109954, 21906754, 265010, 265018, 264604, 264760, 264682, 264683, 264764, 264369, 264288, 264765, 264766, 264686, 264768, 264687, 21906767, 35695917, 265020, 33657023, 264692, 264693, 33657109, 264628, 264629, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 264563, 264565, 264566, 264567
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gij3878374[emb]CAA93081] - (Z69879) Similarity to Yeast Chi12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33316 comes from...		ATPase associated	264760
3015	86995466 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264906, 265007, 265008, 264910, 265011, 265017, 265019, 264691, 33657109, 18108370, 35695855, 264556, 264564
3016	87759945 (6031, 6032)	Novel Protein sim. GBank gij1168819[sp]P41733[CC81_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gij4589658[dbj]BAA76851.1] - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265006, 265007, 265008, 265009, 264591, 60433356, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 265020, 265022, 65274620, 52645129, 33657109, 33657182, 18108370, 263972, 18108374, 264631, 52644332, 83373044, 18108385, 18108388, 56526486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)				264558	
3019	94148231 (6037, 6038)	Novel Protein sim. GBank gi 3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264569, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432228, 29331827, 264908, 56182435, 265007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274791, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563	
3020	94318251 (6039, 6040)	Novel Protein sim. GBank gi 3414809 (AF061529) - rjs [Mus musculus]	Contains protein domain (PF00415) - ATPase associated Regulator of chromosome condensation (RCC1)		264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264765, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264556, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264488	
3021	80478512 (6041, 6042)	Novel Protein sim. GBank gi 3880889[embjCAB09005] - (Z95559) cDNA EST yk236d4.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk329g6.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482	
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264566	
3023	95305484 (6045, 6046)	Novel Protein sim. GBank gi 416592[spIP32323JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108376, 263978, 264635, 264558, 22279000	
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906769, 55811957, 35695917, 264690, 264555, 264559	
3025	65706629 (6049, 6050)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			264593, 55811576	

3026	87643662 (6051, 6052)	Novel Protein sim. GBank gj3024052[sp]P97924[KARI_RAT] - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263967, 20281149, 20281069, 263975, 263977, 20281071, 56526486, 22279000
3027	94844563 (6053, 6054)	Novel Protein sim. GBank gj4929647[gb]AAD34084.1[AF15184 - (AF151847) CGJ-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21908768, 21908769, 29148629, 35695917, 265020, 265021, 265022, 52644150, 264692, 33657023, 264693, 52645129, 33657109, 27486261, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56526486, 22279000, 22279002
3028	94231997 (6055, 6056)	Novel Protein sim. GBank gj3080521[emb]CAA186501 - (AL022599) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264683, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486265, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264564
3029	87619284 (6057, 6058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 264534, 264690, 264693, 263969, 18108370, 264558, 22279000, 22279002, 264482
3030	87544928 (6059, 6060)	Novel Protein sim. GBank gj3757726[emb]CAA187821 - (AL022727) dJ80119.1 (olfactory receptor-like protein [Hs6M1-1]) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	
3031	91677953 (6061, 6062)	Novel Protein sim. GBank gj4530587[gb]AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gj1019951 (U37429) - similar to M. musculus MER5 and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 29331828, 264907, 29331830, 264758, 33109954, 87188474, 87168559, 265019, 264288, 21906769, 265021, 264693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gj5031573 [ref] NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 265008, 264591, 21906754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695855, 264632, 264635, 264639, 264482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	264906, 264907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gj13738207 [emb] CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	264636
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gj1728837 [sp] P39194 [ALU7_HUMAN - III] ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	264907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gj4406590 [gb] AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gj5360093 [gb] AAD2865.1 [AF155099] NY-REN18 antigen [Homo sapiens]	Contains protein domain (PF00627) - UNCLASSIFIED UBA domain	22278996, 22278997, 264259, 264905, 265007, 265009, 60433356, 21906754, 265018, 265019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486262, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gj4757128 [emb] CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 29331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 264691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264564, 18108391
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gj4884278 [emb] CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]		264692, 264558, 18108382, 18108385, 264587
3041	88312357 (6081, 6082)	Novel Protein sim. GBank gj3876073 [emb] CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109954, 21906754, 87168559, 264600, 264663, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gj790236 (U21156) - sarcolemmal associated protein-2 [Oryctolagus cuniculus]	glycoprotein	264636

3043	87773026 (6085, 6086)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35696286, 60424269, 35696052, 264508, 264905, 66712502, 56182435, 55811386, 52644296, 55811150, 35695917, 60170615, 33657109, 18108374, 264634, 60431850
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gi 4104922 (AF042276) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiE/COQ5 methyltransferase family	glycoprotein	22278996, 22278998, 22278999, 29331824, 55182435, 264511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108368, 18108370, 60170394
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gi 4589680 dbj BAA76859.1 - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35696052, 264508, 264905, 264509, 264906, 264907, 264909, 264511, 265006, 264591, 264593, 33109954, 264604, 264764, 264683, 264288, 264766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264564, 264566
3046	88098247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52646317, 55811957, 60432113, 22279000, 22279002, 264482, 264564
3047	95089924 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52644150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629419 (6095, 6096)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264102, 29148784
3049	88229955 (6097, 6098)	Novel Protein sim. GBank gi 5454158 ref NP_006286.1 pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 264907, 264758, 87168559, 265018, 264448, 21906766, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643679 (6099, 6100)	Novel Protein sim. GBank gi 4589642 dbj BAA76843.1 - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 264288, 21906766, 265020, 264893, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 264693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gi 117528 sp P14755 CRYL_RABIT - LAMBDA-CRYSTALLIN		dehydrogenase	264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 (AL023828) cDNA EST EMBL:M89008 comes from this gene: cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	65274572, 56181606, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86943510 (6107, 6108)	Novel Protein sim. GBank gi 1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii	UNCLASSIFIED	35696286, 35696052, 29331830, 264908, 264909, 264512, 284910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264636, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]	transport	60424178, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424289, 60432289, 35696052, 56182435, 265006, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264689, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7 - HUMAN - !!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331826, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264691, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567

3057	95412746 (6113, 6114)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353...		struct	264508, 264905, 264907, 264908, 264909, 264510, 264512, 264910, 264592, 264594, 264767, 18108374, 264635, 264555, 264637, 264639, 264583, 264564, 264565, 264486
3058	78646226 (6115, 6116)			UNCLASSIFIED	264693
3059	87629425 (6117, 6118)	Novel Protein sim. GBank gi 4588034 gb AAD25962.1 AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264490, 264259, 29331824, 29331825, 29331827, 35696052, 29331828, 265007, 60433438, 265017, 265018, 265019, 264681, 264448, 264288, 264768, 21906765, 21906766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 264636, 18108385, 264563, 264567
3060	79346691 (6119, 6120)			UNCLASSIFIED	264567
3061	87740964 (6121, 6122)			UNCLASSIFIED	264112, 52644296, 21906768, 33657023, 263974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gi 4454690 gb AAD20863 - (AF070857) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	264908, 265008, 18108351, 264566
3063	80078023 (6125, 6126)	Novel Protein sim. GBank gi 2246532 (U03872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 264558
3064	91241526 (6127, 6128)	Novel Protein sim. GBank gi 4240315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52646365, 52646842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 66714117, 264508, 264907, 264908, 56182435, 265009, 60432229, 60433438, 55812038, 52644296, 265018, 264682, 264288, 264686, 264768, 264687, 52644229, 264689, 21906768, 264691, 264692, 264693, 18108370, 18108377, 55811576, 264636, 56182323, 264558, 264639, 18108385, 22279000, 22279002
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gi 5656743 gb AAD45960.1 AC00506 - (AC005067) Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencode [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 264093, 264094, 264095, 29331824, 60424269, 66714117, 264100, 264907, 265007, 264591, 60432229, 264593, 265011, 265019, 18108351, 264766, 264767, 21906765, 21906768, 264693, 20281069, 22279000, 22279002, 264482, 264566, 264567

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gij4884268[emb]CAB43245.1] - (AL050028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278996, 264905, 66712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264567
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gij4689258[gb]AAD27832.1[AF12185] sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264602, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264689, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264567, 264486
3068	85360651 (6135, 6136)	Novel Protein sim. GBank gij387819[emb]CAA88860] - (Z49068) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01926) - struct GTPase of unknown function		264112, 22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170615, 33657023, 18108370, 18108376, 264634, 264557, 60170394, 56182323, 18108385, 87168518, 22279000, 264482
3069	95412753 (6137, 6138)	EMBL:M89111 comes from this gene: cDNA EST EMBL:D27709 comes from this gene: cDNA EST EMBL:D27708 comes from this gene: cDNA EST EMBL:D73788 comes from this gene: cDNA EST yk353....			

3070	94319173 (6139, 6140)	Novel Protein sim. GBank gll3877788[embjCAB05527] - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk468c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...		synthase	264488, 22278994, 22278995, 22278996, 56994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21906754, 87168474, 265019, 18108351, 264448, 264683, 264288, 52644229, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 264634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	94325573 (6141, 6142)	Novel Protein sim. GBank gll4502425[re NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF000085) - Igf Thiodoxin		264488, 55274572, 18108398, 22278996, 35695826, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35696052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433356, 33657402, 60433438, 33109954, 52644296, 87168474, 265010, 265017, 264681, 264288, 264685, 264766, 264687, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35696423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gll1263289 (U47856) - fibroin-4 [Araneus diadematus]		transcript factor	

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gij134840[sp]P22528[CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)]		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gij3419847 (AC004982) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g588461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264567
3075	88095752 (6149, 6150)	Novel Protein sim. GBank gij4557349[ref]NP_000456.1[pBARD - BRCA1 associated RING domain 1]	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87819219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264691, 264693
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gij3023956[sp]Q00808[HET1_PODAN - VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gij3900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gij3875410[emb]CAB02876] - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21906768, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gij5257221[g]bAAD41265.1] - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264682, 264448, 264763, 264683, 264764, 264288, 264685, 264769, 264688, 264689, 21906765, 21906767, 21906769, 55811957, 35695917, 265020, 60170615, 52644150, 264692, 33657023, 264693, 65274620, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264555, 264484
3081	88094864 (6161, 6162)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_HUMAN - !!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!]		UNCLASSIFIED	18108398, 264509, 284905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264566
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	88095756 (6165, 6166)	Novel Protein sim. GBank gij869241 (U29488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22279000
3084	87448568 (6167, 6168)	Novel Protein sim. GBank gij476774(pir)A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264766, 35695917, 265020, 18108374, 35696423, 264631, 264556, 264565, 264566, 264567, 264486
3085	87795781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	265011, 264681
3086	87769942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263987, 263974, 55810764, 263981, 18108385, 264487
3087	87462988 (6173, 6174)				52646365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21906767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264591
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4689146(jgb)AAD27782.1(AF07704) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35696286, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170815, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank gi 1354050 (U47024) - MEM3 [Mus musculus]	UNCLASSIFIED	60424179, 52645156, 65274572, 56182575, 56181686, 22278995, 35696286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264906, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21906754, 33109954, 52646317, 55811386, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265022, 60170615, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486261, 27486265, 35695763, 18108374, 18108376, 55810764, 35696423, 55811576, 65274791, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22279000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank gi 3873932[emb CAB01859] - (Z79596) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...	UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264683, 264685, 264766, 264768, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264563, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gi 1710756 sp P15880 RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - ribosomal prot Ribosomal protein S5	264488, 60424179, 18108396, 22278995, 56994075, 22278996, 3569286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 29331828, 29146498, 29146499, 264508, 264509, 264905, 264906, 264907, 29331830, 264908, 264909, 264113, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264591, 264592, 60431735, 264593, 264594, 60433438, 264595, 264758, 21906754, 265010, 265011, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 265019, 264760, 264762, 264681, 18108351, 264763, 264682, 264448, 264764, 264683, 264288, 264369, 264765, 264766, 264686, 264767, 264687, 264768, 264769, 264688, 21906764, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 29148784, 35695917, 265020, 265021, 264534, 60170615, 264690, 264691, 264692, 65274620, 33657109, 27486262, 264628, 264629, 18108374, 263978, 18108377, 35696423, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264556, 264638, 264557, 264558, 264639, 60170394, 18108385, 264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gi 5002587 emb CAB44347.1 - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED	264259, 29331824, 35696052, 264905, 265006, 60432229, 60431735, 264684, 264369, 264288, 264766, 21906767, 35696423, 83373044, 18108385
3094	94316675 (6187, 6188)	Novel Protein sim. GBank gi 400734 sp P31044 P8P_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	18108398, 264259, 60432289, 29331827, 264511, 264763, 264288, 264767, 265022, 264691, 264693, 65274791, 56182323, 264594, 264565

3095	94848162 (6189, 6190)	Novel Protein sim. GBank gi 4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 33656970, 29146499, 264508, 264905, 264509, 29331830, 264909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 264288, 264886, 264768, 264769, 264689, 21906765, 21906766, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 264952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264566, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gi 3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein [Homo sapiens]	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	
3097	88264895 (6183, 6194)	Novel Protein sim. GBank gi 4468288 emb CAB37981 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) [Homo sapiens]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gi 303603 dbj BAA02145.1 - (D12621) cytochrome P-450 TBV [Homo sapiens]		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gi 1083764 pir B48013 - proline- rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	79602134 (6201, 6202)			UNCLASSIFIED	264908, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gi 5305706 gb AAD41781.1 AF12853 - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	- struct	35696286, 22278996, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21906767, 60170615, 264692, 33657023, 264638, 22279000, 264482, 264564
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gi 464584 sp P35292 RB17_MOUSE - RAS-RELATED PROTEIN RAB-17		UNCLASSIFIED	35695917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gi 50322207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94146603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264764, 264288, 264766, 264768, 264687, 264769, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95361416 (6211, 6212)	Novel Protein sim. GBank gi 1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264905, 264907, 264908, 52644045, 56182435, 264112, 265008, 265009, 55812038, 265017, 265018, 264683, 264686, 264687, 264768, 52644229, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52644150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gi 3341441 emb CAA76851 - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265008, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906766, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 56526486, 264482, 264487
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gi 50322207 ref NP_005696.1 pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	56182435, 264288, 264690, 264564

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[embjCAB44347.1] - (Y17454) LSR1 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	struct	264490, 264908, 265007, 264910, 264593, 264883, 264684, 264887, 21906767, 21906768, 264693, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95090716 (6218, 6220)	Novel Protein sim. GBank gij1076211[prjS50755] - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264488, 65274572, 22278995, 22278997, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264908, 264510, 265006, 265007, 265008, 265009, 60432229, 33657402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906766, 21906767, 21906768, 265020, 60170615, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264563, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	264488, 18108388, 66712502, 265017, 265018, 265019, 264448, 21906767, 265020, 33657023, 18108365, 18108388, 35696423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3900848 (AC005023) - match to EST AA361117 (NID:2013436) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	
3113	88207098 (6225, 6226)	Novel Protein sim. GBank gij2459910 (AF005856) - anon2A5 [Drosophila yakuba]		tm7	18108397, 22278999, 264259, 29331824, 35896052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906767, 21906769, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22279000, 22279002
3114	79843167 (6227, 6228)	Novel Protein sim. GBank gij4966270[gbjAAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase), Score=57.4, E-value=1e-13, N=1 [C...	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	hydrolase	
3115	94117996 (6229, 6230)	Novel Protein sim. GBank gij5032225[refjNP_005676.1]pWBSC - Williams-Beuren syndrome chromosome region 11		transcriptfactor	60424179, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812038, 55811386, 265018, 264288, 264689, 21906769, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	79642855 (6231, 6232)			UNCLASSIFIED	264905, 264758, 21906764, 264690
3117	87771288 (6233, 6234)			UNCLASSIFIED	264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264564

3118	94665848 (6235, 6236)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1 - (Z78018) predicted using Genefinder; similar to serine/threonine kinase; cDNA EST yk353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00008) - EGF-like domain	igf	52645156, 52646942, 65274572, 56182575, 22278995, 56994075, 22278996, 35690286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 29331830, 52644045, 56182435, 264510, 284511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264682, 264684, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264486, 265006, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF00328) - Histidine acid phosphatase		
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	94110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR - acrosin			52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)			UNCLASSIFIED	264638
3123	88083003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g1345860) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	Kinase	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766899 (6247, 6248)			UNCLASSIFIED	264905
3125	91216607 (6249, 6250)	Novel Protein sim. GBank gi 4980826 gb AAD35412.1 AE001714 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	- dehydrogenase	56181686, 264259, 66714117, 60432289, 29331828, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 29148627, 29148629, 33657023, 33657109, 18108382, 56526486

3126	95337205 (6251, 6252)			UNCLASSIFIED	22278999, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264763, 264683, 264389, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35696286, 22278996, 22278999, 29331826, 264908, 60433438, 87168559, 264604, 21906765, 21906769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gjl2828280lenb CAA16694.1 - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gjl3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21906754, 265017, 265018, 21906768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gjl3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331828, 52644045, 56182435, 60433356, 264600, 264882, 264763, 264764, 264389, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566, 264636
3130	14993960 (6259, 6260)	Novel Protein sim. GBank gjl3329465 (AF064553) - NSD1 protein [Mus musculus]			
3131	95351469 (6261, 6262)	Novel Protein sim. GBank gjl1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21906754, 33657084, 87168474, 264448, 264766, 21906769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 65274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gij4680647[gb]AAD27713.1[AF132933] (AF132933) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52644507, 52646842, 52646365, 65274572, 56182575, 22278994, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52644045, 56182435, 264910, 60170831, 60432229, 60433356, 33657402, 55812038, 52646317, 21906754, 52644296, 85658542, 87168559, 265017, 265018, 265019, 264448, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526486, 87168518, 60432113, 22279002
3133	87379414 (6265, 6266)	Novel Protein sim. GBank gij4507613[re]NP_003738.1[p]TNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265006, 265007, 87168559, 264760, 21906767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264685, 264628, 264566
3134	94649816 (6267, 6268)	Novel Protein sim. GBank gij1729827[sp]P54633[TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	86389356 (6269, 6270)	Novel Protein sim. GBank gij3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278996, 264095, 29331826, 33657402, 18108348, 263974
3136	94845839 (6271, 6272)	Novel Protein sim. GBank gij627101[p]ijS44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257947 (6273, 6274)	Novel Protein sim. GBank gij3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 18108351, 264682, 264769, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	94130186 (6275, 6276)	Novel Protein sim. GBank gjl4406759jgb AAD20070 - (AC006836) hypothetical protein [Arabidopsis thaliana]			264569, 264488, 264907, 264511, 264593, 33109954, 87168559, 264681, 264684, 264685, 264686, 264687, 264768, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (6277, 6278)	Novel Protein sim. GBank gjl228938jprf 1814452C - Hyp-rich glycoprotein [Zea diploperennis]	UNCLASSIFIED		22278997, 22278998, 22278999, 264905, 265018, 265019, 21906765, 265020, 264636, 264557
3140	91222682 (6278, 6280)	Novel Protein sim. GBank gjl932jemb CAA37773 - (X53744) 68kDa subunit of signal recognition particle [Canis familiaris]	struct		22278995, 56994075, 35696286, 264908, 264909, 60433356, 21906754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35895855, 264630, 264555, 264566
3141	87323564 (6281, 6282)	Novel Protein sim. GBank gjl3213227 (AF035209) - putative v-SNARE Vti1a [Mus musculus]	UNCLASSIFIED		56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264369, 21906766, 29148627, 265020, 264628, 264629, 264631, 18108385
3142	95419028 (6283, 6284)	Novel Protein sim. GBank gjl2498197 sp Q95245 C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)	cytochrome		52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29146499, 56182435, 265007, 60170831, 60432229, 33657402, 264595, 60433438, 264758, 21906754, 264288, 264766, 264687, 52644229, 21906765, 21906767, 21906768, 60170615, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	85351475 (6285, 6286)	Novel Protein sim. GBank gjl5420387 emb CAB46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 60433356, 60433438, 55812038, 265011, 265019, 264760, 264763, 264448, 264764, 264884, 264288, 264685, 264686, 264768, 264689, 21906765, 21906766, 21906767, 21906769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263976, 55811576, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87168518, 60432113, 22279000, 22279002, 264563, 264566, 264486

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gij488446[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278999, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21906765, 21906766, 21906767, 265020, 265021, 52644150, 27486261, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 284587
3145	86611657 (6288, 6290)	Novel Protein sim. GBank gij3879709[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from this gene	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21906766, 29148627, 21906769, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gij2135746[pir]S69890 - milogen Inducible gene mig-2 - human	Contains protein domain (PF00169) - struct PH domain		264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21906766, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264584
3147	94848512 (6283, 6294)	Novel Protein sim. GBank gij387427[emb]CAB07315.1] - (Z92825) predicted using Genefinder: cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	56181886, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433356, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22279002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gij5225322[gb]AAD40851.1[AF08310] - (AF083108) siruin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56526486, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gij4200446 (AF102777) - FYVE finger-containing phosphoinositide kinase [Mus musculus]	Contains protein domain (PF01363) - eph FYVE zinc finger		29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gij3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - transferase Glutathione S-transferases.		264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264686, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gij172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - oncogene Zinc finger, C2-H2 type		29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21906754, 87168559, 264605, 21906768, 52644150, 27486264, 35696423, 22279000

3153	95317298 (6305, 6306)	Novel Protein sim. GBank gil4895041gb AAD32705.1 AF14395 - (AF143957) coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat	264488, 5264365, 35698286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87168474, 87168559, 264601, 265019, 264448, 264682, 264764, 264288, 264369, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264691, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87168518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264691, 33657023, 264693, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gil4880661gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]	ATPase associated	264510, 264512, 33657402, 264681, 264683, 33657023, 18108370, 264634, 264639, 18108385, 264563, 264488
3155	87762394 (6308, 6310)	Novel Protein sim. GBank gil728837isp P39194 ALU7_HUMAN - !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!	UNCLASSIFIED	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21906769, 35695917, 265020, 265022, 264692, 18108370, 35696423, 56182323, 22279002
3156	88259577 (6313, 6314)	Novel Protein sim. GBank gil530076gb AAD45821.1 AC006017 N-acetylglucosaminyltransferase; similar to Q10473 (PID:g1709559) [Homo sapiens]	transferase Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108366, 52645129, 35696423, 52644332, 264488, 263974
3156	80034118 (6315, 6316)	Novel Protein sim. GBank gil5306064gb AAD41895.1 AF15677 - (AF156778) ASB-3 protein [Homo sapiens]	kinase Contains protein domain (PF00023) - Ank repeat	
3159	84124114 (6317, 6318)	Novel Protein sim. GBank gil5531272[emb] CAB50897.1 - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED	56182575, 22278999, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21906768, 265020, 264691, 264692, 33657109, 18108374, 35696423, 264555, 60170394, 22279000
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gil3930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	struct Contains protein domain (PF00023) - Ank repeat	18108351, 264555, 264556, 264557, 264558, 264559

3161	88074111 (6321, 6322)			264488, 22278995, 22278997, 22278998, 264259, 29331822, 60432289, 29331828, 52644045, 265017, 265018, 264448, 264288, 21906764, 21906767, 265020, 18108374, 264636, 264566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (U2SMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis,Hypertension, Congenital heart defects, Aortic stenosis ,Atrial septal defect (ASD),Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases,Tuberous sclerosis, Scleroderma, Obesity,Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation,Idiopathic thrombocytopenic purpura , Immunodeficiencies,Graft vesus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalceimia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy,Lesch-Nyhan syndrome, Multiple sclerosis,Ataxia-telangiectasia,Leukodystrophies,Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation,Idiopathic thrombocytopenic purpura, autoimmune disease,allergies, immunodeficiencies,transplantation, Graft vesus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH.56.3(UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27(thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema , Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PREC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (U1MVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHMC-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleen/TP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA_B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5.1:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen I		

Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences

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 <213> Homo sapiens

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 Pro Pro Pro Ile Ser Ala Ala Arg Leu Ser Arg Met Ser Leu Val Glu
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 Arg Cys Ser Ala Ser Ala Ser Cys Ser Ala Val Leu Arg Asp Trp Ala
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Thr Val His Lys Val Met Val Ala Glu Gly Ala Asp Ile Ala Glu Glu
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 Tyr Tyr Phe Ser Ile Leu Leu Asp Arg Gly Glu Arg Arg Tyr Leu Ala
 65 70 75 80
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 Asp Asp Ala Lys Ala Arg Glu Ile Leu Ser Glu Ala Gly Phe Pro Asp
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 Tyr Arg Asp Glu Asp Ala Thr Leu Val Glu Val Asn Pro Met Ile Lys
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 Tyr Val Lys Leu Asp Gly Asn Val Gly Val Ile Gly Asn Gly Ala Gly
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 Leu Val Met Ser Thr Leu Asp Cys Val Ala Tyr Ala Gly Glu Asn Phe
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 Ser Ala Glu Ile Met Ala Asn Gly Leu Asp Leu Ile Met Ser Asp Glu
 260 265 270
 Gln Val Arg Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys
 275 280 285
 Asp Gln Val Ala Leu Gly Ile Lys Gly Ala Leu Glu Lys Leu Gly Asp
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 Ser His Leu Ala Thr Thr Leu Gly Pro Val Lys Val Gly Ala Arg Arg
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 Val Val Leu Pro Asp Leu Ser Ser Glu Gly Phe Ala Cys Pro Ala Arg
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Asn Ser Trp Leu Pro Gly Met Leu Asp Asp Leu Phe Gln Ser Met Phe
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<212> PRT

<213> Homo sapiens

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<210> 13

<211> 2034

<212> DNA

<213> Homo sapiens

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<211> 222

<212> PRT

<213> Homo sapiens

<400> 14

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			20					25					30		
Val	Arg	Thr	Leu	Tyr	Leu	Val	Ser	Thr	Thr	Val	Asp	Arg	Met	Ser	His
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Val	Leu	Trp	Pro	Tyr	Leu	Leu	Gln	Phe	Leu	Thr	Pro	Val	Arg	Phe	Thr
	50					55					60				
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      100              105              110
Ser Ser Ser Pro Tyr Leu Gly Asp Gly Arg Gly Ala Ala Ala Leu Arg
      115              120              125
Leu Leu Ser Val Leu His Pro Asn Ile His Pro Leu Leu Gly Gln His
      130              135              140
Trp Glu Thr Thr Val Pro Leu Leu Leu Gly Tyr Leu Asp Glu His Thr
      145              150              155
Glu Glu Thr Leu Pro Gln Glu Glu Trp Glu Glu Lys Leu Leu Met Val
      165              170              175
Arg Ala Gly Val Arg Pro Ile Leu Gly Leu Lys Val Leu Ser Gly Leu
      180              185              190
Gly Gly Ala Gly Val Ala Glu Ala Gly Pro Pro Ala Ser Thr Ser Pro
      195              200              205
Arg Gly Leu Ala Gly Glu Pro Arg Ile Arg Gln His Gln Gly
      210              215              220

```

<210> 15
 <211> 363
 <212> DNA
 <213> Homo sapiens

```

<400> 15
naccggttgc tggctcgcca cggcaagggc catgtcggct gcgatatctg caagccggcg
60
gtgggttcga tccttgctc gtgctggaac cagccgatca tggacccggc gttggtgccg
120
ttgcaggaca ccaatgacac cttcatggcc aacatgcaga agaacgggtac ctattcgatc
180
atccccgcta tcgccggcgg cgagatcacc ccggacaaac tgatcgccct cggcgcggtg
240
gcgaagaaat acgatctgta caccaagatc accggcggcc agcggatcga cctgttcggc
300
gccagtttgc acgaattgcc gcagatctgg ggcgagctgg tggatgccgg attcgagacc
360
ggt
363

```

<210> 16
 <211> 121
 <212> PRT
 <213> Homo sapiens

```

<400> 16
Xaa Ala Leu Leu Ala Arg His Gly Lys Gly His Val Gly Cys Asp Ile
1      5      10      15
Cys Lys Pro Ala Val Gly Ser Ile Leu Ala Ser Cys Trp Asn Gln Pro
20     25     30
Ile Met Asp Pro Ala Leu Val Pro Leu Gln Asp Thr Asn Asp Thr Phe
35     40     45
Met Ala Asn Met Gln Lys Asn Gly Thr Tyr Ser Ile Ile Pro Arg Ile
50     55     60
Ala Gly Gly Glu Ile Thr Pro Asp Lys Leu Ile Ala Leu Gly Ala Val

```

```

65              70              75              80
Ala Lys Lys Tyr Asp Leu Tyr Thr Lys Ile Thr Gly Gly Gln Arg Ile
      85              90              95
Asp Leu Phe Gly Ala Gln Leu His Glu Leu Pro Gln Ile Trp Gly Glu
      100              105              110
Leu Val Asp Ala Gly Phe Glu Thr Gly
      115              120

```

<210> 17
 <211> 682
 <212> DNA
 <213> Homo sapiens

```

<400> 17
gaattccatt ttgtggagta agaggtgact ggggtatagg gtacaacca tagccatcca
60
tggttcattt tgttttgaat ataattggct agaagatata catatatcta tgtaacttcc
120
tctagcatcc tccagtatgg aggctgcatt aagactgcat gaaggagagg gagagaaggg
180
agaaacagag cagctggaca agaggacagg tataggggaat aaggggagaag ccagtaaggc
240
aggaaagacc ctccgtgaca aagggggcagg gaacagaact caaacattta atggcaggta
300
acccagggtta gaatggtaaa ttgaaaggtg aatataaagg gagaatggtg aaatgaattt
360
tctgaaatta attgctgtgt ttatagtttt tagccatgca tcggaatcac ctcaggactc
420
cactcccaat caattatata tctggggggag gaccaaggcg ttggtatttt tcagaagctc
480
cactgggtgat tctgacagca cagctaggat taagaaactg atcaatggga acagcatgcc
540
tggtgcagag gagcttcctt gggaaatgtc acacacagaa catcaatctt ccttccccac
600
tcctgagatc cctcattctt tggcaccagg aacagttgca attagtaaac cctggttccc
660
tgctgtctca caaatcgcaa ga
682

```

<210> 18
 <211> 110
 <212> PRT
 <213> Homo sapiens

```

<400> 18
Met Asn Phe Leu Lys Leu Ile Ala Val Phe Ile Val Phe Ser His Ala
1      5      10      15
Ser Glu Ser Pro Gln Asp Ser Thr Pro Asn Gln Leu Tyr Ile Trp Gly
      20      25      30
Arg Thr Lys Ala Leu Val Phe Phe Arg Ser Ser Thr Gly Asp Ser Asp
      35      40      45
Ser Thr Ala Arg Ile Lys Lys Leu Ile Asn Gly Asn Ser Met Pro Val
      50      55      60
Ala Glu Glu Leu Pro Trp Glu Met Ser His Thr Glu His Gln Ser Ser

```

```

65          70          75          80
Phe Pro Thr Pro Glu Ile Pro His Ser Leu Ala Pro Gly Thr Val Ala
          85          90          95
Ile Ser Lys Pro Trp Phe Pro Ala Val Ser Gln Ile Ala Arg
          100          105          110

```

<210> 19
 <211> 515
 <212> DNA
 <213> Homo sapiens

```

<400> 19
cttggctggc agacatggga cctgcttccc tcttacaccc cagtcttggc aaggatcatg
60
ccccatctc aactatgtta gccagtctgg ctgttcactt agtcactaca gtttgcttct
120
cgtctgcagt gcagtcttgg gctataagaa acactggggc actcaatacc tcccccttt
180
tggcccttct cctcctctgg tccatgggtg gggttggggg gagcccagtt tcagcaccag
240
cagctggagc ccataccaca ctcatttttc agttctggct gtgggagccc ctcccacagg
300
tttcagttcc ccaagcccca ggctgagtt ttttttattg caaaagctgg ttgttgttgt
360
ggctagctcc caggcgtgtg aggtgcagct tgctaagtaa gagctaggaa agagaatagg
420
gtcctgctgt aggtgtccag tctgaaggaa tgctgggat acttcctcaa gcagttcctt
480
ctcacagtct cctggctgct ccgcatgtca gatct
515

```

<210> 20
 <211> 130
 <212> PRT
 <213> Homo sapiens

```

<400> 20
Met Gly Pro Ala Ser Leu Leu His Pro Ser Leu Gly Lys Asp His Ala
1          5          10          15
Pro Ile Ser Thr Met Leu Ala Ser Leu Ala Val His Leu Val Thr Thr
20          25          30
Val Cys Phe Ser Ser Ala Val Gln Ser Trp Ala Ile Arg Asn Thr Gly
35          40          45
Pro Leu Asn Thr Ser Pro Leu Leu Ala Leu Leu Leu Leu Trp Ser Met
50          55          60
Gly Gly Val Gly Gly Ser Pro Val Ser Ala Pro Ala Ala Gly Ala His
65          70          75          80
Thr Thr Leu Ile Phe Gln Phe Trp Leu Trp Glu Pro Leu Pro Gln Val
85          90          95
Ser Val Pro Gln Ala Pro Gly Leu Ser Phe Phe Tyr Cys Lys Ser Trp
100          105          110
Leu Leu Leu Trp Leu Ala Pro Arg Val Arg Cys Ser Leu Leu Ser
115          120          125
Lys Ser

```

130

<210> 21
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 21
 gtgcgcacaa aagagcacgt tcgcaagggg aggaagagcg tgccaccggt tctgccgagc
 60
 tagacgcggg gcctatgggt gcggaggacc atggagtga gcgagtaaga ctagatgatg
 120
 caacaaatgt gcctgagggt gaaatggcac gagccagtgc caatgagggc atgacacctg
 180
 ttaaccacga caaataccct tctgtccttt taaatgaagc ggcccaggct tcattactgg
 240
 atacaatgac tgcttgcaact gatgggttca caattgagca attggagctt acacgatctc
 300
 tatgttatga aagagtatta gcacatcgat cctcatggga tcgttcagcc ctggctcaag
 360
 aattaaagca agttgtccaa ggcatccatn
 390

<210> 22
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Val Ala Glu Asp His Gly Val Lys Arg Val Arg Leu Asp Asp Ala
 1 5 10 15
 Thr Asn Val Pro Glu Gly Glu Met Ala Arg Ala Ser Ala Asn Glu Gly
 20 25 30
 Met Thr Pro Val Asn His Asp Lys Tyr Pro Ser Val Leu Leu Asn Glu
 35 40 45
 Ala Ala Gln Ala Ser Leu Leu Asp Thr Met Thr Ala Cys Thr Asp Gly
 50 55 60
 Phe Thr Ile Glu Gln Leu Glu Leu Thr Arg Ser Leu Cys Tyr Glu Arg
 65 70 75 80
 Val Leu Ala His Arg Ser Ser Trp Asp Arg Ser Ala Leu Ala Gln Glu
 85 90 95
 Leu Lys Gln Val Val Gln Gly Ile His
 100 105

<210> 23
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 23
 ntctcggagg ccgacagcct ggcgggctgg aagccctcgg tgtaccacgt gctgctcatc
 60
 ctgggcctgt tcgccgtgct gctgtcctgc tgcgcctcgg ccatgtacac cagcgtggag
 120

ggctgggact acgtggactc gctctacttc tgcttcgtca ccttcagcac catcggtctc
 180
 ggggacctgg tgagcagcca gcacgccgcc taccggaacc aggggctcta ccgcctgggc
 240
 aacttcctct tcatactgct cggcgtgtgc tgcatttact cgctcttcaa cgcatctcc
 300
 atcctcatca agcaggtgct caactggatg ctgcgcaagc tgagctgccg ctgctgcgcg
 360
 cgctgctgcc cggctcctgg cgcgc
 385

<210> 24
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 24
 Xaa Ser Glu Ala Asp Ser Leu Ala Gly Trp Lys Pro Ser Val Tyr His
 1 5 10 15
 Val Leu Leu Ile Leu Gly Leu Phe Ala Val Leu Leu Ser Cys Cys Ala
 20 25 30
 Ser Ala Met Tyr Thr Ser Val Glu Gly Trp Asp Tyr Val Asp Ser Leu
 35 40 45
 Tyr Phe Cys Phe Val Thr Phe Ser Thr Ile Gly Phe Gly Asp Leu Val
 50 55 60
 Ser Ser Gln His Ala Ala Tyr Arg Asn Gln Gly Leu Tyr Arg Leu Gly
 65 70 75 80
 Asn Phe Leu Phe Ile Leu Leu Gly Val Cys Cys Ile Tyr Ser Leu Phe
 85 90 95
 Asn Val Ile Ser Ile Leu Ile Lys Gln Val Leu Asn Trp Met Leu Arg
 100 105 110
 Lys Leu Ser Cys Arg Cys Cys Ala Arg Cys Cys Pro Ala Pro Gly Ala
 115 120 125

<210> 25
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 25
 ccatgggaga gaccgtgcat tttcttctag gtctgcgtgg gaagtcactg cagagtttctg
 60
 aggaggggag ttcccagctc tgtatttttg aagggtcagt cttgttgctt ggaccagtga
 120
 ggagccccgt gggatccaga ctcgagtggg tggagccggg gcaggtggga gcagagacac
 180
 tggaggaaag ctggtcgaat gcaactgtgta tttggaggca gaaccagcag agggtcctct
 240
 gggttgagtg tagggcaaaa gagaaagaag gcaccaagcc tggggctctgg gttttctctc
 300
 ttacacttgc tgggtggacg gtggtgccac tgaatga
 337

<210> 26

<211> 111
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Gly Glu Thr Val His Phe Leu Leu Gly Leu Arg Gly Lys Ser Leu
 1 5 10 15
 Gln Ser Phe Glu Glu Gly Ser Ser Gln Leu Cys Ile Phe Glu Gly Ser
 20 25 30
 Val Leu Leu Leu Gly Pro Val Arg Ser Pro Val Gly Ser Arg Leu Glu
 35 40 45
 Trp Val Glu Pro Gly Gln Val Gly Ala Glu Thr Leu Glu Glu Ser Trp
 50 55 60
 Ser Asn Ala Leu Cys Ile Trp Arg Gln Asn Gln Gln Arg Val Leu Trp
 65 70 75 80
 Val Glu Cys Arg Ala Lys Glu Lys Glu Gly Thr Lys Pro Gly Val Trp
 85 90 95
 Val Phe Ser Leu Thr Leu Ala Gly Trp Thr Val Val Pro Leu Asn
 100 105 110

<210> 27
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 27
 ccgacgtcga atatccatgc agccgcgccg aggatggaga gagcgatgga gcaactcaac
 60
 cgcctgacgc gctcgtctgcg ccgcgcgcgc accgtggagt tgccccgagga taatgaaact
 120
 gctgtttata cattaatgcc aatgggttatg gctgatcaac acaggtctgt ttctgaacta
 180
 ctatcaaatt caaaatttga tgtcaattat gcattcggac gtgtgaaaag aagcttgctt
 240
 cacattgcag caaattgtgg atcgggtggaa tgcttggttt tgctgttaaa gaaaggagca
 300
 aatcctaact atcaagatat ttcaggctgt aca
 333

<210> 28
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 28
 Pro Thr Ser Asn Ile His Ala Ala Ala Pro Arg Met Glu Arg Ala Met
 1 5 10 15
 Glu Gln Leu Asn Arg Leu Thr Arg Ser Leu Arg Arg Ala Arg Thr Val
 20 25 30
 Glu Leu Pro Glu Asp Asn Glu Thr Ala Val Tyr Thr Leu Met Pro Met
 35 40 45
 Val Met Ala Asp Gln His Arg Ser Val Ser Glu Leu Leu Ser Asn Ser
 50 55 60
 Lys Phe Asp Val Asn Tyr Ala Phe Gly Arg Val Lys Arg Ser Leu Leu

65		70		75		80									
His	Ile	Ala	Ala	Asn	Cys	Gly	Ser	Val	Glu	Cys	Leu	Val	Leu	Leu	Leu
				85					90					95	
Lys	Lys	Gly	Ala	Asn	Pro	Asn	Tyr	Gln	Asp	Ile	Ser	Gly	Cys	Thr	
			100					105					110		

<210> 29
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 29
 ncgccgtccg tgctggctat tatgacggcg ggtagcgacc agggcgagga ggtcaactcg
 60
 gagagctatt tgagcgccgt gacgccgctg agtcccaaag agattcgtca gctgccccgc
 120
 tacaatatca cgatcaagcg cgtcgtgaac atgacgggca agggccgcac gccgagctgg
 180
 tactcgctcg tcgtggctgg caatggctcg ggctcgtgg gctatggcga aggcaaagat
 240
 actaacatca gccgcgcgaa caaaaaggcg ttccacgcgc cggtgaaaaa catggacttg
 300
 gtatcgggcc accggtcgaa gaggggcgcc aacacgctcg agccccccgt cgagggccgc
 360
 tggggcgcta cgcgt
 375

<210> 30
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 30															
Xaa	Pro	Ser	Val	Leu	Ala	Ile	Met	Thr	Ala	Gly	Ser	Asp	Gln	Gly	Glu
1				5				10					15		
Glu	Val	Asn	Ser	Glu	Ser	Tyr	Leu	Ser	Ala	Val	Thr	Pro	Leu	Ser	Pro
			20					25					30		
Lys	Glu	Ile	Arg	Gln	Leu	Pro	Arg	Tyr	Asn	Ile	Thr	Ile	Lys	Arg	Val
			35				40					45			
Val	Asn	Met	Thr	Gly	Lys	Gly	Arg	Thr	Pro	Ser	Trp	Tyr	Ser	Leu	Val
		50				55					60				
Val	Ala	Gly	Asn	Gly	Arg	Gly	Leu	Val	Gly	Tyr	Gly	Glu	Gly	Lys	Asp
65					70					75				80	
Thr	Asn	Ile	Ser	Arg	Ala	Asn	Lys	Lys	Ala	Phe	His	Ala	Ala	Val	Lys
				85					90					95	
Asn	Met	Asp	Leu	Val	Ser	Val	His	Arg	Ser	Lys	Ser	Gly	Ala	Asn	Thr
			100					105					110		
Leu	Glu	Pro	Pro	Val	Glu	Gly	Arg	Trp	Gly	Ala	Thr	Arg			
			115				120					125			

<210> 31
 <211> 375
 <212> DNA
 <213> Homo sapiens

<400> 31

accggtcttg gcctcagctt tgctctgaaa ttgaagtcgg tgccaaaagt ggggaagagc
60
gggagcaggc acttacgagc ctgcgcgtca gggatgcttc ctgggcccct gagagtgcag
120
agattcctgg atccagagct gcggctgggc ggctgcagct gcgcctggga gtgcagggct
180
cccgccctgc cagctcaaaa ggaaatgggg gctcctgcct gttcctggct cctgttggcc
240
ctgcagagtg cacaaacctt gccgcgcttc ctccactgca gcttacgtct ttgcagcagc
300
cactccccgat gggctgccac tgccatctgt gagaccataa tgtgtgcaat ttgagactca
360
tggcctgcat tgttt
375

<210> 32

<211> 118

<212> PRT

<213> Homo sapiens

<400> 32

Met	Gln	Ala	Met	Ser	Leu	Lys	Leu	His	Thr	Leu	Trp	Ser	His	Arg	Trp
1				5					10					15	
Gln	Trp	Gln	Pro	Ile	Gly	Ser	Gly	Cys	Cys	Lys	Asp	Val	Ser	Cys	Ser
			20					25					30		
Gly	Gly	Ser	Ala	Ala	Arg	Phe	Val	His	Ser	Ala	Gly	Pro	Thr	Gly	Ala
			35				40					45			
Arg	Asn	Arg	Gln	Glu	Pro	Pro	Phe	Pro	Phe	Glu	Leu	Ala	Gly	Arg	Glu
	50					55				60					
Pro	Cys	Thr	Pro	Arg	Arg	Ser	Cys	Ser	Arg	Pro	Ala	Ala	Ala	Leu	Asp
65					70				75					80	
Pro	Gly	Ile	Ser	Ala	Leu	Ser	Gly	Ala	Gln	Glu	Ala	Ser	Leu	Thr	Arg
				85				90					95		
Arg	Leu	Val	Ser	Ala	Cys	Ser	Arg	Ser	Ser	Pro	Leu	Leu	Ala	Pro	Thr
			100				105						110		
Ser	Ile	Ser	Glu	Gln	Ser										
			115												

<210> 33

<211> 351

<212> DNA

<213> Homo sapiens

<400> 33

ccatgcagcc caaccgttgg cgataaagtc cgttttaggcg ataccaattht atgggcaacc
60
attgaacaag atttattaac caaaggatgat gagggtgaaat ttgggtggcgg taaaagtgtg
120
cgtgatggta tggcgcaaag cggcaccgca actcgcgaca atccaaatgt attggatttt
180
gtgattacca atgtgatgat cattgatgcc aaattaggca ttatcaaagc cgatattggg
240

attcgcgatg gtcgtattgt cgggtatcgga caagcaggta accctgacac catggatgac
 300
 gtcacgccaa acatgattat cgggtgctagc acagaagtac ataacggtgc a
 351

<210> 34
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 34
 Pro Cys Ser Pro Thr Val Gly Asp Lys Val Arg Leu Gly Asp Thr Asn
 1 5 10 15
 Leu Trp Ala Thr Ile Glu Gln Asp Leu Leu Thr Lys Gly Asp Glu Cys
 20 25 30
 Lys Phe Gly Gly Lys Ser Val Arg Asp Gly Met Ala Gln Ser Gly
 35 40 45
 Thr Ala Thr Arg Asp Asn Pro Asn Val Leu Asp Phe Val Ile Thr Asn
 50 55 60
 Val Met Ile Ile Asp Ala Lys Leu Gly Ile Ile Lys Ala Asp Ile Gly
 65 70 75 80
 Ile Arg Asp Gly Arg Ile Val Gly Ile Gly Gln Ala Gly Asn Pro Asp
 85 90 95
 Thr Met Asp Asp Val Thr Pro Asn Met Ile Ile Gly Ala Ser Thr Glu
 100 105 110
 Val His Asn Gly Ala
 115

<210> 35
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 35
 nngctagctg caccaccacc tgttcatgca ggcagagcgg ccacccctca tggaagaaga
 60
 ggaatccact gtattgggca caggcttctt gctggacctt ggcaagcagg tgcttggctg
 120
 gtaccaggaa gtccagcgtg tacctcagtg cgtcctcccg ataagtcctc tccaccacct
 180
 ggaacacctg gcccaacagg gtgggggctg ttgcctcaaa ggggtggatac agggcggcga
 240
 gagtgtcttg cacacagtec tccactggct caggctccat ggctcggcgc cgggccgcgt
 300
 ccgacgcttg gtcggggcggg cggggccggg cgcgccaccg cctcccttca cgcgt
 355

<210> 36
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 36
 Xaa Leu Ala Ala Pro Pro Pro Val His Ala Gly Arg Ala Ala Thr Pro

```

      1             5             10             15
His Gly Arg Arg Gly Ile His Cys Ile Gly His Arg Leu Pro Ala Gly
      20             25             30
Pro Trp Gln Ala Gly Ala Trp Leu Val Pro Gly Ser Pro Ala Cys Thr
      35             40             45
Ser Val Arg Pro Pro Asp Lys Ser Ser Pro Pro Pro Gly Thr Pro Gly
      50             55             60
Pro Thr Gly Trp Gly Leu Leu Pro Gln Arg Val Asp Thr Gly Arg Arg
      65             70             75             80
Glu Cys Ser Ala His Ser Pro Pro Leu Ala Gln Ala Pro Trp Leu Gly
      85             90             95
Ala Gly Pro Arg Pro Thr Leu Gly Arg Ala Gly Gly Ala Gly Arg Ala
      100             105             110
Thr Ala Ser Leu His Ala
      115

```

<210> 37
 <211> 492
 <212> DNA
 <213> Homo sapiens

```

<400> 37
acgcgtggcc ttcgtctgcc accaggaccg actcagcccc accgggtttc cggacccgcc
60
gcaaccatga caagggcgat gttgtgatct gggtggattc cttctccgac atgctcgagg
120
gatcggatct ctccggcgta gtcacggtgc ttgccgaggc cggctatcgc ccacgggtcc
180
tcgccgacga cgtctgctgc gggttgacgt ggatcactac cggtcagctc gacgggtgctc
240
ggcgtcggct gcgcgctggt ctcgacgtgc tggcaccctc gtcagacgcc agcgtcccag
300
tcgttgggct agagccgtcc tgcactaccg tctggcggtga tgacgcactc cgcctcctgc
360
cagatgatcc gcgcgtccac cgggtagcca gaaacatgca taccgtcgcc gagatgcttg
420
aggcagcaca gtggacccca ccctcgctag caggccacac cctcgtegct cagccccatt
480
gtcatcccgc gg
492

```

<210> 38
 <211> 127
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Met Leu Glu Gly Ser Asp Leu Ser Ala Val Val Thr Val Leu Ala Glu
1             5             10             15
Ala Gly Tyr Arg Pro Arg Val Leu Ala Asp Asp Val Cys Cys Gly Leu
      20             25             30
Thr Trp Ile Thr Thr Gly Gln Leu Asp Gly Ala Arg Arg Arg Leu Arg
      35             40             45
Ala Gly Leu Asp Val Leu Ala Pro Leu Ser Asp Ala Ser Val Pro Val

```

50		55		60
Val Gly Leu Glu Pro Ser Cys Thr Thr Val Trp Arg Asp Asp Ala Leu				
65		70		75
Arg Leu Leu Pro Asp Asp Pro Arg Val His Arg Val Ala Arg Asn Met				80
	85		90	
His Thr Val Ala Glu Met Leu Glu Ala Ala Gln Trp Thr Pro Pro Ser				95
	100		105	110
Leu Ala Gly His Thr Leu Val Ala Gln Pro His Cys His Pro Ala				
	115		120	125

<210> 39
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 39
 aacgaaggtn ccgtacgcgc tctgaaagcc ctgcgtaaag agcggtccga tcgccgggaa
 60
 gtgatgngca ccgccaaaat gcagggtggc gaagccgcga gttcaggcaa gattgtcttt
 120
 gaaatggaag acgtttatta cagcattgcc ggaaaacaac tgggtgagcaa cttctctgcg
 180
 caagtcatgc gtgggtgataa aattgcgctg attggcccga acggttgtgg taaaacgacg
 240
 ttgctgaaac tgatgttaag taagattcag gcagacagcg gccgtgttca ctgcggtact
 300
 aaactggaag ttgcgtactt cgaccagcac cgtgctgagc tggatcctga gcgtacggtg
 360
 atggataacc tggccgaagg taagcaggaa gtgatggtaa atggcgtgt an
 412

<210> 40
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 40
Asn Glu Gly Xaa Val Arg Ala Leu Lys Ala Leu Arg Lys Glu Arg Ser
1 5 10 15
Asp Arg Arg Glu Val Met Xaa Thr Ala Lys Met Gln Val Val Glu Ala
20 25 30
Ala Ser Ser Gly Lys Ile Val Phe Glu Met Glu Asp Val Tyr Tyr Ser
35 40 45
Ile Ala Gly Lys Gln Leu Val Ser Asn Phe Ser Ala Gln Val Met Arg
50 55 60
Gly Asp Lys Ile Ala Leu Ile Gly Pro Asn Gly Cys Gly Lys Thr Thr
65 70 75 80
Leu Leu Lys Leu Met Leu Ser Lys Ile Gln Ala Asp Ser Gly Arg Val
85 90 95
His Cys Gly Thr Lys Leu Glu Val Ala Tyr Phe Asp Gln His Arg Ala
100 105 110
Glu Leu Asp Pro Glu Arg Thr Val Met Asp Asn Leu Ala Glu Gly Lys
115 120 125
Gln Glu Val Met Val Asn Gly Arg Val

130

135

<210> 41
 <211> 1080
 <212> DNA
 <213> Homo sapiens

<400> 41
 gaattcaagt ggacacaggc tccacgcccc cgtctcaccg ataagagcta caagcacaac
 60
 tactatgacg agcgggtttc gctcgaagag cgtcttgagc gcactgtggc taaggatttc
 120
 gtcacgacgg aggtcgagcc catgtgggat gcggctgatg tcatgcggat gggtaaggat
 180
 ctcttcatcc agcacggtct gacgacaaat cggaagtcaa tggagtgggt taagcgttac
 240
 taccgccgatt tccgcgttca cgcggtgaat ttccctgggg atccgtaccc gatccatata
 300
 gacgcgacct ttgtgccgct tcgtccgggg ctcatacatca acaaccgaa tcgtccactg
 360
 ccgcaggagc agaggaagat ctcgaggcc aatgactggc agatcggtga tgctgctcag
 420
 ccggcgcacg acacgcctcc agaattgtgc tactcgtctg tgtggctatc aatgaactgc
 480
 ttggtacttg atccgaagac ggtcatctgc gaggcctcgg aagttcatca gatggagcag
 540
 atggacaagc tgggtatgaa cgtcatcccc gtcgccttcc gtgacgcgta cccattcggc
 600
 ggaggtctcc actgcgccac agctgatgta tatcgagaag gtacctgtga ggactacttc
 660
 ccgaatcagg tcgacgaccc gaccttgggt tgagaaaacc ccgtgggtcat gtcatactg
 720
 acggatctcg gtggctcggc acggaactta cgttgctcgt taccgggccg ccgggtctga
 780
 tatggcagta tcacgcctag caaaaaggag catgtcatgg acatggagcc gggcatcatc
 840
 aacgtcaaac aggaagttcc aggcgtcggc acgatgaacc agaaagtggg attcgtgtcc
 900
 atgcttcttt ctgcaacggg tatgggggtg gtgggtactt tcgggcgtct cagcactcct
 960
 gtggatccca cgacgggcag taagtacatc atcgggtgatt ttttggccac tggtaggatg
 1020
 atagtcgggg tcctgggatt tctgcttatt atcgtcatac ttggaaaatg gtctgagctc
 1080

<210> 42
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 42
 Glu Phe Lys Trp Thr Gln Ala Pro Arg Pro Arg Leu Thr Asp Lys Ser
 1 5 10 15
 Tyr Lys His Asn Tyr Tyr Asp Glu Arg Val Ser Leu Glu Glu Arg Leu


```

      20      25      30
Glu Arg Thr Val Ala Lys Asp Phe Val Thr Thr Glu Val Glu Pro Met
      35      40      45
Trp Asp Ala Ala Asp Val Met Arg Met Gly Lys Asp Leu Phe Ile Gln
      50      55      60
His Gly Leu Thr Thr Asn Arg Lys Ser Met Glu Trp Phe Lys Arg Tyr
      65      70      75      80
Tyr Pro Asp Phe Arg Val His Ala Val Asn Phe Pro Gly Asp Pro Tyr
      85      90      95
Pro Ile His Ile Asp Ala Thr Phe Val Pro Leu Arg Pro Gly Leu Ile
      100      105      110
Ile Asn Asn Pro Asn Arg Pro Leu Pro Gln Glu Gln Arg Lys Ile Phe
      115      120      125
Glu Ala Asn Asp Trp Gln Ile Val Asp Ala Ala Gln Pro Ala His Asp
      130      135      140
Thr Pro Pro Glu Leu Cys Tyr Ser Ser Val Trp Leu Ser Met Asn Cys
      145      150      155      160
Leu Val Leu Asp Pro Lys Thr Val Ile Cys Glu Ala Ser Glu Val His
      165      170      175
Gln Met Glu Gln Met Asp Lys Leu Gly Met Asn Val Ile Pro Val Ala
      180      185      190
Phe Arg Asp Ala Tyr Pro Phe Gly Gly Gly Leu His Cys Ala Thr Ala
      195      200      205
Asp Val Tyr Arg Glu Gly Thr Cys Glu Asp Tyr Phe Pro Asn Gln Val
      210      215      220
Asp Asp Pro Thr Leu Val
      225      230

```

<210> 43
 <211> 358
 <212> DNA
 <213> Homo sapiens

```

<400> 43
gggcccccca catagtggac acaggtttct gggatgtcag catggagtgc caagaggtgg
60
gtgaccacct ggtggggaat aaggcgcttc tgggacatag aggctgcctt ccagctgcgc
120
ctggcagagc tgttgacaca acagcatggt ctgcagtgcc gggccactgc cacgcacacc
180
gatgtccttt aaggatggat ttgggttttc ggattcgcgt ggcctatcag cgggagtgccc
240
agatcctgaa ggaagtgcag agcccagagg ggatgatctc gctgagggac acagctgcct
300
ccctccgcct tgagagagac acaaggcagt tgccactgct caccagtgcc ctgcacgn
358

```

<210> 44
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 44
Met Glu Cys Gln Glu Val Gly Asp His Leu Val Gly Asn Lys Ala Leu

```

1				5					10					15				
Leu	Gly	His	Arg	Gly	Cys	Leu	Pro	Ala	Ala	Pro	Gly	Arg	Ala	Val	Asp			
			20						25					30				
Thr	Thr	Ala	Trp	Ser	Ala	Val	Pro	Gly	His	Cys	His	Ala	His	Arg	Cys			
		35						40					45					
Pro	Leu	Arg	Met	Asp	Leu	Gly	Phe	Arg	Ile	Arg	Val	Ala	Tyr	Gln	Arg			
	50					55					60							
Glu	Ser	Gln	Ile	Leu	Lys	Glu	Val	Gln	Ser	Pro	Glu	Gly	Met	Ile	Ser			
65					70					75				80				
Leu	Arg	Asp	Thr	Ala	Ala	Ser	Leu	Arg	Leu	Glu	Arg	Asp	Thr	Arg	Gln			
			85						90					95				
Leu	Pro	Leu	Leu	Thr	Ser	Ala	Leu	His										
			100					105										

<210> 45

<211> 905

<212> DNA

<213> Homo sapiens

<400> 45

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gtcgcagcata aaggagtatt tgcgcagcag cagtatgatg ctctcgttga ggcggggttc
60
gcggctcctg gaatcccaga gcagtatggt ggcgcagggt cggtatgcgat tgcgtccgca
120
ataatcatgg aagaggtcgc tcgagtctgt gcgtcgtcgt ccaccgtcat atcgtccaat
180
gagcttggtgta ccgtccctct cctcaaatac ggtagcgagg agcagaggaa acgttatctt
240
tctgaagttg cttcgggtaa ggcacttttc ggatatgcgc tctccgaggc tgatgctgga
300
tcagatccag ctgcacttaa gtgtcgagcc gacgaagatg gggacagttt cgtcctgaat
360
ggcggttaagg cttgggtcac ggaggctggc gaggccaagt acctggtgat atttgcggtt
420
actgaccag acgatccgcg ccacagaatc agcgcggtga tgggtccatgc agatgacccg
480
ggcattagct acgggggtcc ggagcacaaa atgggggatac gcgggtcagt taccagggaa
540
gtgggttttca agaatacgcg tatccccaag gaacgagtaa ttggccgctc agggcacggt
600
ctgagtgttg ctctaggtac gcttgataac tctcgtgtct cgattgctgc tcaagcagtg
660
ggaattgccc aaggagcttt agacattgcc acggattacg tccagaagcg caagcagttt
720
ggccagccac tgtccaatth tgagggaatc cagttcatgc tcgcagacat ggcaatgcgt
780
ttggaggcgg cgcgagcgct gacatactct gcagctgac gtagtgggcg ccagactgac
840
gatgtgagtt acttcggcgc ggcggccaaa tgtttcgctt ccgacacagc gatggcagtg
900
tgcac
905

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<210> 46

<211> 301
 <212> PRT
 <213> Homo sapiens

<400> 46

Val	Asp	Asp	Lys	Gly	Val	Phe	Ala	Gln	Gln	Gln	Tyr	Asp	Ala	Leu	Val
1				5				10						15	
Glu	Ala	Gly	Phe	Ala	Ala	Pro	Gly	Ile	Pro	Glu	Gln	Tyr	Gly	Gly	Asp
			20					25					30		
Gly	Ala	Asp	Ala	Ile	Ala	Ser	Ala	Ile	Ile	Met	Glu	Glu	Val	Ala	Arg
			35				40					45			
Val	Cys	Ala	Ser	Ser	Ser	Thr	Val	Ile	Ser	Ser	Asn	Glu	Leu	Gly	Thr
	50					55					60				
Val	Pro	Leu	Leu	Lys	Tyr	Gly	Ser	Glu	Glu	Gln	Arg	Lys	Arg	Tyr	Leu
65				70						75				80	
Ser	Glu	Val	Ala	Ser	Gly	Lys	Ala	Leu	Phe	Gly	Tyr	Ala	Leu	Ser	Glu
			85					90					95		
Ala	Asp	Ala	Gly	Ser	Asp	Pro	Ala	Ala	Leu	Lys	Cys	Arg	Ala	Asp	Glu
			100				105						110		
Asp	Gly	Asp	Ser	Phe	Val	Leu	Asn	Gly	Val	Lys	Ala	Trp	Val	Thr	Glu
	115						120					125			
Ala	Gly	Glu	Ala	Lys	Tyr	Leu	Val	Ile	Phe	Ala	Val	Thr	Asp	Pro	Asp
	130					135					140				
Asp	Pro	Arg	His	Arg	Ile	Ser	Ala	Leu	Met	Val	His	Ala	Asp	Asp	Pro
145				150					155					160	
Gly	Ile	Ser	Tyr	Gly	Ala	Pro	Glu	His	Lys	Met	Gly	Ile	Arg	Gly	Ser
			165					170					175		
Val	Thr	Arg	Glu	Val	Val	Phe	Lys	Asn	Thr	Arg	Ile	Pro	Lys	Glu	Arg
			180					185					190		
Val	Ile	Gly	Arg	Arg	Gly	His	Gly	Leu	Ser	Val	Ala	Leu	Gly	Thr	Leu
	195					200						205			
Asp	Asn	Ser	Arg	Val	Ser	Ile	Ala	Ala	Gln	Ala	Val	Gly	Ile	Ala	Gln
	210				215						220				
Gly	Ala	Leu	Asp	Ile	Ala	Thr	Asp	Tyr	Val	Gln	Lys	Arg	Lys	Gln	Phe
225				230					235					240	
Gly	Gln	Pro	Leu	Ser	Asn	Phe	Glu	Gly	Ile	Gln	Phe	Met	Leu	Ala	Asp
			245					250					255		
Met	Ala	Met	Arg	Leu	Glu	Ala	Ala	Arg	Ala	Leu	Thr	Tyr	Ser	Ala	Ala
		260						265				270			
Asp	Arg	Ser	Gly	Arg	Gln	Thr	Asp	Asp	Val	Ser	Tyr	Phe	Gly	Ala	Ala
	275					280						285			
Ala	Lys	Cys	Phe	Ala	Ser	Asp	Thr	Ala	Met	Ala	Val	Cys			
	290					295					300				

<210> 47
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 47

aagcttgtag agctagtcg aagcggactg tcggtacgcc aagctgctaa aagatgtggg
 60
 atgcatttta ccgctgcgta tgccgtagct acggaagctg ggtgccatat ccggttaagt
 120

cagtatgctc ggaaagtccg ccagacgcag ttaagagtgg aatacctgcg ccttcggctg
 180
 gcgagcctgc ctggtggtga tgctggcgcg gcagtaggaa ttgatcgtcg actgcgttta
 240
 gatttcgaaa aaggactcac caaatcccag ggctgcagag aagagttcat acccgtcggc
 300
 gaagacgcca gcacgtataa cagacttatg aaagcgctgc gccaacgcca tgatgtcatc
 360
 aaatccggaa agcttgccc
 379

<210> 48
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met His Leu Thr Ala Ala Tyr Ala Val Ala Thr Glu Ala Gly Cys His
 1 5 10 15
 Ile Arg Leu Ser Gln Tyr Ala Arg Lys Val Arg Gln Thr Gln Leu Arg
 20 25 30
 Val Glu Tyr Leu Arg Leu Arg Leu Ala Ser Leu Pro Gly Gly Asp Ala
 35 40 45
 Gly Ala Ala Val Gly Ile Asp Arg Arg Leu Arg Leu Asp Phe Glu Lys
 50 55 60
 Gly Leu Thr Lys Ser Gln Gly Arg Arg Glu Glu Phe Ile Pro Val Gly
 65 70 75 80
 Glu Asp Ala Ser Thr Tyr Asn Arg Leu Met Lys Ala Leu Arg Gln Arg
 85 90 95
 His Asp Val Ile Lys Ser Gly Lys Leu Ala
 100 105

<210> 49
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 49
 tgatcatgat gctggcatgg actattctgg tccctgttcc tctctcacct gctgaaggac
 60
 atccctctaa tttttgtgtc tccttctgta tcatcaaatt ttccctctct actgagtctc
 120
 ttgcatctcc ttggaagcat gctgtactat gtcccatcct taaagaactc ccttctgtctg
 180
 cacattaccc totgccagct ggctcatttt tctgctcccc ttacagggga aactcttcaa
 240
 aaagttatct ccacctcctt ccattctcatg ttctcttgaa cctgcagtac tgggtgctcc
 300
 ctccttttg
 309

<210> 50
 <211> 101
 <212> PRT

<213> Homo sapiens

<400> 50

```

Met Met Leu Ala Trp Thr Ile Leu Val Pro Val Pro Leu Ser Pro Ala
 1              5              10              15
Glu Gly His Pro Ser Asn Phe Cys Val Ser Phe Cys Ile Ile Lys Phe
      20              25              30
Ser Leu Ser Thr Glu Ser Leu Ala Ser Pro Trp Lys His Ala Val Leu
      35              40              45
Cys Pro Ile Leu Lys Glu Leu Pro Leu Ser Ala His Tyr Pro Leu Pro
      50              55              60
Ala Gly Ser Phe Phe Cys Ser Pro Leu Gln Gly Asn Ser Ser Lys Ser
65              70              75              80
Tyr Leu His Leu Leu Pro Ser His Val Leu Leu Asn Leu Gln Tyr Trp
      85              90              95
Val Leu Pro Pro Phe
      100

```

<210> 51

<211> 512

<212> DNA

<213> Homo sapiens

<400> 51

```

agaatctttga agaattgccca cactgtcttc ctccctgctt ataatttcct tattccctag
60
gatgtgatcc ttgttcttgg ggcctcacat ggcagctgga tctctggcga ttgcatctga
120
gttccagaca ccaggatgga aaagaaaaga aggaggggca agaggaaccc ccagatgctc
180
cttaagagct actgcgtggc attcccactt gcatctcatt tgctcgatcg ctgtcactgt
240
gccctaacga gctgcaagga cactggggaa atgagctctgt cttgtacttc atgtgccctt
300
caaaatcttc tgttgctgag ggagaagagg ccagccggta ttgaggaaca actagcactt
360
tctgcttccg cgtcccaggg ggacgtgggt gtgttgaatc cacaccgggg gtgcggacct
420
ctgaggctgg gctggatggg acatcaggtg ggcctctgt ttcatttatg tgacctccca
480
tcaggtcttc tggttggatc ctgctttcta ga
512

```

<210> 52

<211> 125

<212> PRT

<213> Homo sapiens

<400> 52

```

Met Glu Lys Lys Arg Arg Gly Lys Arg Asn Pro Gln Met Leu Leu
 1              5              10              15
Lys Ser Tyr Cys Val Ala Phe Pro Leu Ala Ser His Leu Leu Asp Arg
      20              25              30
Cys His Cys Ala Leu Thr Ser Cys Lys Asp Thr Gly Glu Met Ser Leu

```

```

      35          40          45
Ser Cys Thr Ser Cys Ala Pro Gln Asn Leu Leu Leu Leu Arg Glu Lys
  50          55          60
Arg Pro Ala Gly Ile Glu Glu Gln Leu Ala Leu Ser Ala Ser Ala Ser
  65          70          75          80
Gln Gly Asp Val Gly Val Leu Asn Pro His Arg Gly Cys Gly Pro Leu
      85          90          95
Arg Leu Gly Trp Met Gly His Gln Val Gly Pro Leu Phe His Leu Cys
      100          105          110
Asp Leu Pro Ser Gly Leu Leu Val Gly Ser Cys Phe Leu
      115          120          125

```

<210> 53
 <211> 474
 <212> DNA
 <213> Homo sapiens

```

<400> 53
accggtacac ctacgtcacc cgtaaaaacc gacgcaatac ccggatcgcc tcgtcctcaa
60
aaaattcgat cccgtcgtgc gtcgtcacat tgagttcaag gaggcccgct aatggccaaa
120
aagtccaaga ttgtcgccca gaagaaacgt gagaagctcg tagcccaata cgccgaaagg
180
cgcgccgaac tcaaggccat catgaagtgc ccaactgcct cattggacga acgcatggag
240
gcacgcgta agctgtctcg cctgccgcgc gattcatccc ccgtgcggtt acgtaaccgt
300
gaccaagtcg acggggcgcc ccgcggtctac gttggcaagg ccggtgtgtc ccgtatccgt
360
ttccgtgaga tggcccaccg cggcgaaactc cccggaatcg cgaagtcaag ctggtgaagc
420
catggcagta ccgaagcgaa agaagtcccg ttcgaccacg cgtcataggc gggc
474

```

<210> 54
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 54
Met Ala Lys Lys Ser Lys Ile Val Ala Gln Lys Lys Arg Glu Lys Leu
  1          5          10          15
Val Ala Gln Tyr Ala Glu Arg Arg Ala Glu Leu Lys Ala Ile Met Lys
      20          25          30
Cys Pro Thr Ala Ser Leu Asp Glu Arg Met Glu Ala Ser Arg Lys Leu
      35          40          45
Ser Arg Leu Pro Arg Asp Ser Ser Pro Val Arg Leu Arg Asn Arg Asp
      50          55          60
Gln Val Asp Gly Arg Pro Arg Gly Tyr Val Gly Lys Ala Gly Val Ser
  65          70          75          80
Arg Ile Arg Phe Arg Glu Met Ala His Arg Gly Glu Leu Pro Gly Ile
      85          90          95
Ala Lys Ser Ser Trp

```

100

<210> 55
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 55
 ccatggccca ggacagccgg catatcgggt acgactacgg tacaccggtg gcgccacagt
 60
 tcggcgcagc caagcccgca gcgtgctgcc aggcgcaagc gacaaacacc ggcccgtggg
 120
 tgggtgttcga ccatgtgcgt tgcacccacg acacctttct gatcgacgtc tttctcaacc
 180
 agcccgatgc caccgcgcag cagggtcaatg ccgacaaccc gcactacgtc gggcgtttca
 240
 gccgcacggg catggggcctg gtggatgaca agggccggtg cattacccag ggcgtatcgc
 300
 gcgcgttgaa tcgggcgcgc agcaccaagg cgctgaacct gggaccgagt gacgcggcgc
 360
 agttatcggg gaggcgta
 378

<210> 56
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 56
 Met Ala Gln Asp Ser Arg His Ile Gly Tyr Asp Tyr Gly Thr Pro Val
 1 5 10 15
 Ala Pro Gln Phe Gly Ala Ala Lys Pro Ala Ala Cys Cys Gln Ala Gln
 20 25 30
 Ala Thr Asn Thr Gly Pro Trp Val Val Phe Asp His Val Arg Cys Thr
 35 40 45
 His Asp Thr Phe Leu Ile Asp Val Phe Leu Asn Gln Pro Asp Ala Thr
 50 55 60
 Ala Gln Gln Val Asn Ala Asp Asn Pro His Tyr Val Gly Arg Phe Ser
 65 70 75 80
 Arg Ile Gly Met Gly Leu Val Asp Asp Lys Gly Arg Cys Ile Thr Gln
 85 90 95
 Gly Val Ser Arg Ala Leu Asn Ala Ala Arg Ser Thr Lys Ala Leu Asn
 100 105 110
 Leu Gly Pro Ser Asp Ala Ala Gln Leu Ser Val Arg Arg
 115 120 125

<210> 57
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 57
 agaccaccc gacacagatc aggagtcgtc atgtccagaa agaagaaggc cggcatcctc
 60

accgcaggcg gtgattgccc cgggctcaac gccgctatcc gcggatttgg caaggctgcc
 120
 atccgccagc acgacatgga gctcatcggt attcaggacg gctttcttgg attggcggga
 180
 aaccgcacca tctcccttgg cccgcgtgcc ctctcaggca tcttgacggt cggcgggacc
 240
 atcctgggaa ctagccgtga caaggatcaat cacatgatta tcgacggcga ggaacgggat
 300
 atggtcccca ccaccgtcga gaattacgag aagctggggc ttgacgcttt ggtgactttg
 360
 ggtggcggtg gcaccgcaa gaacgcgt
 388

<210> 58

<211> 129

<212> PRT

<213> Homo sapiens

<400> 58

Arg	Pro	Thr	Arg	His	Arg	Ser	Gly	Val	Val	Met	Ser	Arg	Lys	Lys	Lys
1				5				10					15		
Val	Gly	Ile	Leu	Thr	Ala	Gly	Gly	Asp	Cys	Pro	Gly	Leu	Asn	Ala	Ala
			20					25					30		
Ile	Arg	Gly	Phe	Gly	Lys	Ala	Ala	Ile	Arg	Gln	His	Asp	Met	Glu	Leu
		35					40					45			
Ile	Gly	Ile	Gln	Asp	Gly	Phe	Leu	Gly	Leu	Ala	Gly	Asn	Arg	Thr	Ile
	50					55				60					
Ser	Leu	Gly	Pro	Arg	Ala	Leu	Ser	Gly	Ile	Leu	Thr	Val	Gly	Gly	Thr
65					70					75				80	
Ile	Leu	Gly	Thr	Ser	Arg	Asp	Lys	Val	Asn	His	Met	Ile	Ile	Asp	Gly
			85					90					95		
Glu	Glu	Arg	Asp	Met	Val	Pro	Thr	Thr	Val	Glu	Asn	Tyr	Glu	Lys	Leu
			100					105					110		
Gly	Leu	Asp	Ala	Leu	Val	Thr	Leu	Gly	Gly	Gly	Gly	Thr	Ala	Lys	Asn
		115					120						125		

Ala

<210> 59

<211> 417

<212> DNA

<213> Homo sapiens

<400> 59

ggtaccatcg gagctcgaca agaaatgggt gggatgaagtc gtggcttctg ctccacccag
 60
 tgccctcatg ggtagcccca cctgaatatc ttcattgcctg tgcatttctc ctgatgttca
 120
 cgtgtgccct gtgtttttac gcatctgtga tcgtgcaccc acgcgtctca gagaggagcc
 180
 cgtttgggaa tccggagaat gtgcgctggc ggaagagcgt cacacactgg aagcaaaccct
 240
 cagaccgcgt ggacaagacc aaggatgaaa tggaacacga ggccttggtg gaaggggaacc
 300

tggcaaccga ggcaagccta gtggttctgg acacactgga gatcatcgtg cagacgggtga
360
tgctttcaga agcccgaggag agcgtcttgg gggcagtgct gaaggttgtg ctgtaca
417

<210> 60
<211> 101
<212> PRT
<213> Homo sapiens

<400> 60
Met Phe Thr Cys Ala Leu Cys Phe Tyr Ala Ser Val Ile Val His Pro
1 5 10 15
Arg Val Ser Glu Arg Ser Pro Phe Gly Asn Pro Glu Asn Val Arg Trp
20 25 30
Arg Lys Ser Val Thr His Trp Lys Gln Thr Ser Asp Arg Val Asp Lys
35 40 45
Thr Lys Asp Glu Met Glu His Glu Ala Leu Val Glu Gly Asn Leu Ala
50 55 60
Thr Glu Ala Ser Leu Val Val Leu Asp Thr Leu Glu Ile Ile Val Gln
65 70 75 80
Thr Val Met Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu
85 90 95
Lys Val Val Leu Tyr
100

<210> 61
<211> 304
<212> DNA
<213> Homo sapiens

<400> 61
agatcttcac agccttagac ttttttcatg ggtgccttac agttttggag gtccctatcc
60
gcacacatat ttgcaggctt ggagagagtg tgtgggggca tgtactttcg gtgggtcaag
120
tatgaagaag caggccttat aaacacatat tctgacctta acctgtactt cagaagagga
180
ccgctgactc accaaggagg cctgaaggac aaggcagcat ctctgtcttc acatgagtcc
240
tcccctagac cgggcccatg gccaggcctg accacagagc tcccattgcc tttcctgcac
300
gcgt
304

<210> 62
<211> 92
<212> PRT
<213> Homo sapiens

<400> 62
Met Gly Ala Leu Gln Phe Trp Arg Ser Leu Ser Ala His Ile Phe Ala
1 5 10 15

Gly Leu Glu Arg Val Cys Gly Gly Met Tyr Phe Arg Trp Val Lys Tyr
 20 25 30
 Glu Glu Ala Gly Leu Ile Asn Thr Tyr Ser Asp Leu Asn Leu Tyr Phe
 35 40 45
 Arg Arg Gly Pro Leu Thr His Gln Gly Gly Leu Lys Asp Lys Ala Ala
 50 55 60
 Ser Leu Ser Ser His Glu Ser Ser Pro Arg Pro Gly Pro Trp Pro Gly
 65 70 75 80
 Leu Thr Thr Glu Leu Pro Leu Pro Phe Leu His Ala
 85 90

<210> 63
 <211> 577
 <212> DNA
 <213> Homo sapiens

<400> 63
 cgcgtaagg ggggtctacac cgggacgatt aacgcctcgg tgggagtatt catcaccgcg
 60
 ctgacgggtgc tagctgggtg gctcacccta gccgggcgta tcagtgtcgg ggaactcgtc
 120
 accgtgggtcg ggctggccca aaccctcggc cctccgctgc gagcactggg cgtcgacacc
 180
 gcgacgatgt tggccaccgc ccacgcctcc ggggaccgat tctgtgagtt gcgtgatagc
 240
 ccggcagcct ggcagatcca ccccgacgac ggtgcccgc caacaccggg tgatggcccg
 300
 gtggagttgc acatcccggg cagggatttc cagcttgacg tcgccggcgg caccatgtg
 360
 ggtatcatgg cgcctcaatc ggtctgtgac gccttggccg aggcgataga ccacggctcc
 420
 gagaccgtct tgaatggggg tcccgccagt cgcctcaacc ctgcccacg gcgtcgtctg
 480
 gtgctgggtg ctccccgctc ccccgaaactg ttcgacgata ctgcccgtgc gaacatcgtg
 540
 cttgacagcc agacgactgt cgccaggctg aatgcat
 577

<210> 64
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 64
 Arg Val Lys Gly Val Tyr Thr Gly Thr Ile Asn Ala Ser Val Gly Val
 1 5 10 15
 Phe Ile Thr Ala Leu Thr Val Leu Ala Gly Trp Leu Thr Leu Ala Gly
 20 25 30
 Arg Ile Ser Val Gly Glu Leu Val Thr Val Val Gly Leu Ala Gln Thr
 35 40 45
 Leu Gly Pro Pro Leu Arg Ala Leu Gly Val Asp Thr Ala Thr Met Leu
 50 55 60
 Ala Thr Ala His Ala Ser Gly Asp Arg Phe Cys Glu Leu Arg Asp Ser
 65 70 75 80

```

Pro Ala Ala Trp Gln Ile His Pro Asp Asp Gly Ala Arg Thr Thr Pro
      85                      90                      95
Gly Asp Gly Pro Val Glu Leu His Ile Pro Val Arg Asp Phe Gln Leu
      100                    105                    110
Asp Val Ala Gly Gly Thr His Val Gly Ile Met Ala Pro Gln Ser Val
      115                    120                    125
Cys Asp Ala Leu Ala Glu Ala Ile Asp His Gly Ser Glu Thr Val Leu
      130                    135                    140
Asn Gly Val Pro Ala Ser Arg Leu Asn Pro Ala Gln Arg Arg Arg Leu
145                    150                    155                    160
Val Leu Val Ala Pro Arg Ser Pro Glu Leu Phe Asp Asp Thr Ala Arg
      165                    170                    175
Ala Asn Ile Val Leu Asp Ser Gln Thr Thr Val Ala Arg Leu Asn Ala
      180                    185                    190

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<210> 65
 <211> 339
 <212> DNA
 <213> Homo sapiens

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<400> 65
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120
cgccttggcg tacccttcgg catcatcgac ctttcgcttg cccctactgc cgaattggga
180
gattcggggg cccacatcct tgagcatatg ggattggacc aagtaggcac gcacggcaca
240
actgctgctt tggctctgct taacgacgcc gtaaagaaag gcggcatgat ggctgcccc
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339

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<210> 66
 <211> 113
 <212> PRT
 <213> Homo sapiens

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<400> 66
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Ala Glu Glu Val Lys Lys Ala Ala Phe Lys Ile Thr Arg Ala Gly Gln
      20      25      30
Leu Val Gly Thr Met Ala Ser Glu Arg Leu Gly Val Pro Phe Gly Ile
      35      40      45
Ile Asp Leu Ser Leu Ala Pro Thr Ala Glu Leu Gly Asp Ser Gly Ala
      50      55      60
His Ile Leu Glu His Met Gly Leu Asp Gln Val Gly Thr His Gly Thr
65      70      75      80
Thr Ala Ala Leu Ala Leu Asn Asp Ala Val Lys Lys Gly Gly Met
      85      90      95
Met Ala Cys Pro Arg Val Gly Gly Leu Ser Gly Ser Phe Ile Pro Gly
100      105      110

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Ser

<210> 67

<211> 446

<212> DNA

<213> Homo sapiens

<400> 67

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 120
 caaggggtcc ttcgacgcca acgagcttgc cgtaactcct gatactgaca ccgtcatcca
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 300
 taacccgaca gcccaggcat ggcgcgattt cgtatgcgtc gagaccgggg cctgcaagga
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<210> 68

<211> 133

<212> PRT

<213> Homo sapiens

<400> 68

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Arg	Gly	Val	Arg	Gly	Ala	Ser	Trp	His	Asn	Phe	Ala	Thr	Gly	Asp	Lys
		20						25					30		
Gly	Ser	Phe	Asp	Ala	Asn	Glu	Leu	Ala	Val	Thr	Pro	Asp	Thr	Asp	Thr
		35					40					45			
Val	Ile	Gln	Gly	Val	Gly	Pro	Ala	Leu	Ala	Leu	Leu	Asp	Ser	Ala	Trp
	50					55					60				
Gly	Arg	Gln	Ile	His	Val	Glu	Thr	Thr	Gly	Cys	Pro	Ser	Ala	Val	Val
65					70					75				80	
Trp	Asn	Pro	Arg	Ser	Ser	Ser	Thr	His	Ala	Asp	Asn	Pro	Thr	Ala	Gln
			85						90					95	
Ala	Trp	Arg	Asp	Phe	Val	Cys	Val	Glu	Thr	Gly	Ala	Cys	Lys	Asp	Asn
		100						105				110			
Ala	Val	Ile	Val	Ala	Pro	His	Ser	Asp	Leu	Thr	Met	Ser	Thr	Arg	Ile
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Ser	Val	Glu	Thr	Leu											
		130													

<210> 69

<211> 552

<212> DNA

<213> Homo sapiens

<400> 69

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120
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180
agcncatgg ccccttcctt cagtgggaata ccaaaaccag gaatgaaaag catgcccggg
240
aaatccccaa gtgccccagc gccttccaag gaaggggagc ggagccggag tgggaagctg
300
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360
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420
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540
ctttcctgta ca
552

<210> 70

<211> 184

<212> PRT

<213> Homo sapiens

<400> 70

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			20					25					30		
Gln	Leu	Cys	Pro	Arg	Cys	Gln	Lys	Ser	Pro	Pro	Arg	Leu	Pro	Ala	Ser
		35				40					45				
Ser	Pro	Lys	Gly	Gly	Ser	Ser	Thr	Val	Pro	Arg	Arg	Ser	Xaa	Met	Ala
	50				55					60					
Pro	Ser	Leu	Ser	Gly	Ile	Pro	Lys	Pro	Gly	Met	Lys	Ser	Met	Pro	Gly
65					70					75				80	
Lys	Ser	Pro	Ser	Ala	Pro	Ala	Pro	Ser	Lys	Glu	Gly	Glu	Arg	Ser	Arg
				85					90					95	
Ser	Gly	Lys	Leu	Ser	Ser	Gly	Leu	Pro	Gln	Gln	Lys	Pro	Gln	Leu	Asp
			100					105					110		
Gly	Arg	His	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Ala	Ser	Ser	Glu	Gly	Lys
		115					120					125			
Gly	Pro	Gly	Gly	Thr	Thr	Leu	Asn	His	Ser	Ile	Ser	Ser	Gln	Thr	Val
		130				135					140				
Ser	Gly	Ser	Val	Gly	Thr	Thr	Gln	Thr	Thr	Gly	Ser	Asn	Xaa	Pro	Ser
145					150					155				160	
Val	Phe	Ser	Tyr	Leu	Ser	Pro	Ser	Ser	Asn	Thr	Thr	Ile	Pro	Thr	Leu
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Pro	Arg	Leu	His	Leu	Ser	Cys	Thr								
				180											

<210> 71
 <211> 316
 <212> DNA
 <213> Homo sapiens

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 120
 ttacgtacct tcgcccgtatt ccggtttcatc ttgccaaacg cattgatacg aactgcaggt
 180
 ggccgcgaag taaatctacg agacttacaa gcttatgctc taaaagggtg cctaaacggt
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 300
 attcaagact tggagt
 316

<210> 72
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 72
 Arg Val Glu Met Ala Phe Glu Leu Lys Arg Leu His Ile Asp Ser Val
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 20 25 30
 Glu Ala Leu Arg Pro Leu Asn Ile Leu Arg Thr Phe Ala Val Phe Arg
 35 40 45
 Phe Ile Leu Pro Asn Ala Leu Ile Arg Thr Ala Gly Gly Arg Glu Val
 50 55 60
 Asn Leu Arg Asp Leu Gln Ala Tyr Ala Leu Lys Gly Gly Leu Asn Gly
 65 70 75 80
 Ile Met Val Gly Gly Tyr Leu Thr Thr Gly Gly Arg Ser Pro Gln Asp
 85 90 95
 Asp Leu Gln Met Ile Gln Asp Leu Glu
 100 105

<210> 73
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 73
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 120
 ccacgagtga ccgctgctac cccgccgtgg aacttcgccc tgtctattac cgccggatcc
 180

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 360
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<210> 74
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 74
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 20 25 30
 Val Asp Gly Ala Gln Phe Val Pro Pro Arg Val Thr Val Val Thr Pro
 35 40 45
 Pro Trp Asn Phe Ala Leu Ser Ile Thr Ala Gly Ser Thr Leu Ala Ala
 50 55 60
 Leu Ala Ala Gly Ser Ser Val Leu Leu Lys Pro Ala Pro Gln Ala Arg
 65 70 75 80
 His Cys Ala Ala Val Ile Ser Glu Cys Leu Trp Glu Ala Gly Ile Pro
 85 90 95
 Arg Asp Val Leu Gln Leu Val Asp Val Glu Glu Asn Glu Ala Gly Lys
 100 105 110
 His Leu Val Ser His Pro Glu Val Asp Arg Val Ile Leu Thr Gly Gly
 115 120 125

<210> 75
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 75
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 cgcattgagg cgctggccga gctctatgcc gatcccaaga ccagggtggt gagcttctgg
 120
 accatgggct tcaaccagca caccgcgggc gtctggtgca acaatctcgt ctacaacatc
 180
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 240
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 300
 atggtggtca ccagcaaggc gcaccgcgac atcgccgaga agatctggca gctgccggaa
 360
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 405

<210> 76

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 76
 Glu Phe Val Ser Glu Tyr Thr Leu Glu Asn Ser Ala Glu Met Ser Gly
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 20 25 30
 Lys Thr Arg Val Val Ser Phe Trp Thr Met Gly Phe Asn Gln His Thr
 35 40 45
 Arg Gly Val Trp Cys Asn Asn Leu Val Tyr Asn Ile His Leu Leu Thr
 50 55 60
 Gly Lys Ile Ser Thr Pro Gly Asn Ser Pro Phe Ser Leu Thr Gly Gln
 65 70 75 80
 Pro Ser Ala Cys Gly Thr Ala Arg Glu Val Gly Thr Phe Ser His Arg
 85 90 95
 Leu Pro Ala Asp Met Val Val Thr Ser Lys Ala His Arg Asp Ile Ala
 100 105 110
 Glu Lys Ile Trp Gln Leu Pro Glu Gly Pro Val Pro Asp Lys Pro Gly
 115 120 125
 Tyr His Ala Val Leu Gln Ser
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<210> 77
 <211> 5816
 <212> DNA
 <213> Homo sapiens

<400> 77
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 360
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<210> 78
 <211> 799
 <212> PRT
 <213> Homo sapiens

<400> 78
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 20 25 30
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 35 40 45
 Asn Asn Leu Leu Arg Leu Pro Phe Gly Cys Gly Glu Gln Asn Met Ile
 50 55 60
 His Phe Ala Pro Asn Val Phe Val Leu Lys Tyr Leu Gln Lys Thr Gln
 65 70 75 80
 Gln Leu Ser Pro Glu Val Glu Arg Glu Thr Asp Tyr Leu Val Gln
 85 90 95
 Gly Tyr Gln Arg Gln Leu Thr Tyr Lys Arg Gln Asp Gly Ser Tyr Ser
 100 105 110
 Ala Phe Gly Glu Arg Asp Ala Ser Gly Ser Met Trp Leu Thr Ala Phe
 115 120 125
 Val Leu Lys Ser Phe Ala Gln Ala Arg Ser Phe Ile Phe Val Asp Pro
 130 135 140
 Arg Glu Leu Ala Ala Ala Lys Ser Trp Ile Ile Gln Gln Gln Gln Ala
 145 150 155 160
 Asp Gly Ser Phe Leu Ala Val Gly Arg Val Leu Asn Lys Asp Ile Gln
 165 170 175
 Gly Gly Ile His Gly Ile Val Pro Leu Thr Ala Tyr Val Val Val Ala
 180 185 190
 Leu Leu Glu Thr Gly Thr Ala Ser Glu Glu Glu Arg Gly Ser Thr Asp
 195 200 205
 Lys Ala Arg His Phe Leu Glu Ser Ala Ala Pro Leu Ala Met Asp Pro
 210 215 220
 Tyr Ser Cys Ala Leu Thr Thr Tyr Ala Leu Thr Leu Leu Arg Ser Pro
 225 230 235 240
 Ala Ala Pro Glu Ala Leu Arg Lys Leu Arg Ser Leu Ala Ile Met Arg
 245 250 255
 Asp Gly Val Thr His Trp Ser Leu Ser Asn Ser Trp Asp Val Asp Lys
 260 265 270
 Gly Thr Phe Leu Ser Phe Ser Asp Arg Val Ser Gln Ser Val Val Ser
 275 280 285
 Ala Glu Val Glu Met Thr Ala Tyr Ala Leu Leu Thr Tyr Thr Leu Leu
 290 295 300
 Gly Asp Val Ala Ala Ala Leu Pro Val Val Lys Trp Leu Ser Gln Gln

305					310					315				320
Arg	Asn	Ala	Leu	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Cys	Val
				325					330					335
Leu	Gln	Ala	Leu	Ala	Glu	Tyr	Ala	Ile	Leu	Ser	Tyr	Ala	Gly	Gly
			340					345					350	
Asn	Leu	Thr	Val	Ser	Leu	Ala	Ser	Thr	Asn	Leu	Asp	Tyr	Gln	Glu
		355					360				365			
Phe	Glu	Leu	His	Arg	Thr	Asn	Gln	Lys	Val	Leu	Gln	Thr	Ala	Ala
	370				375						380			Ile
Pro	Ser	Leu	Pro	Thr	Gly	Leu	Phe	Val	Ser	Ala	Lys	Gly	Asp	Gly
385					390					395				400
Cys	Leu	Met	Gln	Ile	Asp	Val	Thr	Tyr	Asn	Val	Pro	Asp	Pro	Val
			405						410					415
Lys	Pro	Ala	Phe	Gln	Leu	Leu	Val	Ser	Leu	Gln	Glu	Pro	Glu	Ala
		420						425					430	Gln
Gly	Arg	Pro	Pro	Pro	Met	Pro	Ala	Ser	Ala	Ala	Glu	Gly	Ser	Arg
	435						440					445		Gly
Asp	Trp	Pro	Pro	Ala	Asp	Asp	Asp	Asp	Pro	Ala	Ala	Asp	Gln	His
	450				455					460				His
Gln	Glu	Tyr	Lys	Val	Met	Leu	Glu	Val	Cys	Thr	Arg	Trp	Leu	His
465				470						475				480
Gly	Ser	Ser	Asn	Met	Ala	Val	Leu	Glu	Val	Pro	Leu	Leu	Ser	Gly
			485					490						495
Arg	Ala	Asp	Ile	Glu	Ser	Leu	Glu	Gln	Leu	Leu	Leu	Asp	Lys	His
		500						505					510	Met
Gly	Met	Lys	Arg	Tyr	Glu	Val	Ala	Gly	Arg	Arg	Val	Leu	Phe	Tyr
	515						520					525		Phe
Asp	Glu	Ile	Pro	Ser	Arg	Cys	Leu	Thr	Cys	Val	Arg	Phe	Arg	Ala
	530					535				540				Leu
Arg	Glu	Cys	Val	Val	Gly	Arg	Thr	Ser	Ala	Leu	Pro	Val	Ser	Val
545				550						555				560
Asp	Tyr	Tyr	Glu	Pro	Ala	Phe	Glu	Ala	Thr	Arg	Phe	Tyr	Asn	Val
			565						570					575
Thr	His	Ser	Pro	Leu	Ala	Arg	Glu	Leu	Cys	Ala	Gly	Pro	Ala	Cys
		580					585						590	Asn
Glu	Val	Glu	Arg	Ala	Pro	Ala	Arg	Gly	Pro	Gly	Trp	Phe	Pro	Gly
	595						600					605		Glu
Ser	Gly	Pro	Ala	Val	Ala	Pro	Glu	Glu	Gly	Ala	Ala	Ile	Ala	Arg
	610					615				620				Cys
Gly	Cys	Asp	His	Asp	Cys	Gly	Ala	Gln	Gly	Asn	Pro	Val	Cys	Gly
625				630						635				640
Asp	Gly	Val	Val	Tyr	Ala	Ser	Ala	Cys	Arg	Leu	Arg	Glu	Ala	Ala
			645						650					655
Arg	Gln	Ala	Ala	Pro	Leu	Glu	Pro	Ala	Pro	Pro	Ser	Cys	Cys	Ala
		660						665						670
Glu	Gln	Arg	Leu	Pro	Ala	Ser	Ser	Ser	Ser	Thr	Tyr	Gly	Asp	Asp
	675						680					685		Leu
Ala	Ser	Val	Ala	Pro	Gly	Pro	Leu	Gln	Gln	Asp	Val	Lys	Leu	Asn
	690					695				700				Gly
Ala	Gly	Leu	Glu	Val	Glu	Asp	Ser	Asp	Pro	Glu	Pro	Glu	Gly	Glu
705				710						715				720
Glu	Asp	Arg	Val	Thr	Ala	Gly	Pro	Arg	Pro	Pro	Val	Ser	Ser	Gly
			725						730					735
Leu	Glu	Ser	Ser	Thr	Gln	Ser	Ala	Ser	Pro	Phe	His	Arg	Trp	Gly

<400> 81

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 tgacttaaat ttgataccag aaatgtcagt gtggctttgc ttgaacagcc gcgtgcgggg
 120
 cctctatgag tggaatccag tctcatggcc ccccccattg ctctgtttac cctggaggag
 180
 gctactccat gaggtgggt cgggtggcac tgccctgggg ctgcatgtac atgtgtgtgc
 240
 atgnntgtgt gcatgtgcgt gtgcacgtgt nngtgtgtgc ccgtgtgcat gtgcccgtgt
 300
 gcgtgtctgt gctgtgtgtg tgcggtgcat tgtgcgtgtc tgtgcgtgnc tgtgtgtgtg
 360
 cgtgcatgtg tgtgcacgtg tgtgcatgtg cacgtgtgcg caccctgtgt catgtccgtg
 420
 tgcacgcgt
 429

<210> 82

<211> 79

<212> PRT

<213> Homo sapiens

<400> 82

Gly	Trp	Leu	Arg	Trp	His	Cys	Leu	Gly	Ala	Ala	Cys	Thr	Cys	Val	Cys
1				5				10						15	
Met	Xaa	Val	Cys	Met	Cys	Val	Cys	Thr	Cys	Xaa	Cys	Val	Pro	Val	Cys
			20					25					30		
Met	Cys	Pro	Cys	Ala	Cys	Leu	Cys	Cys	Val	Cys	Ala	Cys	Met	Cys	Ala
		35					40				45				
Cys	Leu	Cys	Val	Xaa	Val	Cys	Val	Arg	Ala	Cys	Val	Cys	Thr	Cys	Val
	50					55					60				
His	Val	His	Val	Cys	Ala	Pro	Val	Cys	Met	Ser	Val	Cys	Thr	Arg	
65					70					75					

<210> 83

<211> 411

<212> DNA

<213> Homo sapiens

<400> 83

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 cgtgcgctct ttaaaaagcg caaaggcttt tataagtctg atgtgctttt tttcaggccc
 120
 ggaaagacgc gatccgtaga taaaataggg ccgctttatc gcaaattggc ttatggttac
 180
 cgtttccgca tcgatttgca gctgcggaaa aaaaggcctg tggtcgatgc cgttgtggat
 240
 gatttcgatt ttcgctttgt cgatgccaaag ccctatcaaa tcgtttcgca aaaactcgct
 300
 cgcggcgacg atcttttgca cctttgtaag cccccgcttt atctgcatgc gcatcatgcg
 360
 gtcgctcttt tctttgagca tgacggaaac gatggaattg acgacggcga c
 411

<210> 84
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Leu Lys Glu Lys Ser Asp Arg Met Met Arg Met Gln Ile Lys Arg
 1 5 10 15
 Gly Leu Thr Lys Val Gln Lys Ile Val Ala Ala Ser Glu Phe Leu Arg
 20 25 30
 Asn Asp Leu Ile Gly Leu Gly Ile Asp Lys Ala Lys Ile Glu Ile Ile
 35 40 45
 His Asn Gly Ile Asp His Arg Pro Phe Phe Pro Gln Leu Gln Ile Asp
 50 55 60
 Ala Glu Thr Val Thr Ile Lys Pro Phe Ala Ile Lys Arg Pro Tyr Phe
 65 70 75 80
 Ile Tyr Gly Ser Arg Leu Ser Gly Pro Glu Lys Lys His Ile Glu Leu
 85 90 95
 Ile Lys Ala Phe Ala Leu Phe Lys Glu Arg Thr Lys Ser Pro His Pro
 100 105 110
 Leu Val Ile Ala Gly Ala Glu Gly Pro Ser Ser Glu Glu Val His
 115 120 125

<210> 85
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 85
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 60
 atcctcgacg cggtgaaact gctgagttcg ctccggcttca aggtgatcgc cacctcgggc
 120
 acccagcggtt tcctggtgga gaacggagta ccggcggaaa agatcaacaa ggtgctggaa
 180
 ggccgcccgc acattgttga cgcaattacc aacggcgagg tgcaactcgt tttcaatacc
 240
 accgagggggc cacaggcgct ggctgacagc cgctcggttc gacgcgctgc cctcttgcat
 300
 aaagtgccat attacaccac tctttcaggt gca
 333

<210> 86
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 86
 Xaa Arg Val Pro Arg Lys Gly Thr Met Phe Val Ser Val Arg Glu Thr
 1 5 10 15
 Asp Lys Ala Arg Ile Leu Asp Ala Val Lys Leu Leu Ser Ser Leu Gly
 20 25 30
 Phe Lys Val Ile Ala Thr Ser Gly Thr Gln Arg Phe Leu Val Glu Asn

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35						40					45				
Gly	Val	Pro	Ala	Glu	Lys	Ile	Asn	Lys	Val	Leu	Glu	Gly	Arg	Pro	His
50						55					60				
Ile	Val	Asp	Ala	Ile	Thr	Asn	Gly	Glu	Val	Gln	Leu	Val	Phe	Asn	Thr
65						70					75				
Thr	Glu	Gly	Pro	Gln	Ala	Leu	Ala	Asp	Ser	Arg	Ser	Leu	Arg	Arg	Ala
85						90					95				
Ala	Leu	Leu	His	Lys	Val	Pro	Tyr	Tyr	Thr	Thr	Leu	Ser	Gly	Ala	
100						105					110				

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<210> 87
<211> 355
<212> DNA
<213> Homo sapiens
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<400> 87
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60
ctcctgagcg atgttcattc ggtaggggta cagggtgacg ggcgtactta tggttctccc
120
attgtgcttc gcccggtgac gagtgaggac gccatgactg cggactgggc acgtatccca
180
tatgacgtac tggaaaagat ctcgactcgc attacgaatg cgtgtccgca aatcaaccgg
240
gtgggtactcg atatcacatc taaaccgccg gccaccatcg agtgggaatg agccccgtct
300
caccgtgaac atgacatggc ccgcaccttt cttggggcgg gccatgccgt gttag
355
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<210> 88
<211> 96
<212> PRT
<213> Homo sapiens
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<400> 88															
Thr	Arg	Glu	Glu	Met	Gly	Ala	Ala	Gly	Leu	Asp	Arg	Lys	Val	Trp	Gln
1				5				10						15	
Cys	Pro	Val	Val	Leu	Leu	Ser	Asp	Val	His	Ser	Val	Gly	Val	Gln	Gly
			20					25					30		
Asp	Gly	Arg	Thr	Tyr	Gly	Ser	Pro	Ile	Val	Leu	Arg	Pro	Val	Thr	Ser
		35				40						45			
Glu	Asp	Ala	Met	Thr	Ala	Asp	Trp	Ala	Arg	Ile	Pro	Tyr	Asp	Val	Leu
	50				55						60				
Glu	Lys	Ile	Ser	Thr	Arg	Ile	Thr	Asn	Ala	Cys	Pro	Gln	Ile	Asn	Arg
65				70						75				80	
Val	Val	Leu	Asp	Ile	Thr	Ser	Lys	Pro	Pro	Ala	Thr	Ile	Glu	Trp	Glu
				85				90					95		

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<210> 89
<211> 351
<212> DNA
<213> Homo sapiens
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<400> 89

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nacgcgtcaa caccaggcta cgggtgggtat gatcatgata agggctggga cccgcaggag
 60
 agggcaagag ttatataata gacgggtgta tgggtttaag gtatacatgg tgatgagaca
 120
 ggtgattgga taaggccaga gggttgggcg gggttctgcc cctgctgaag cctggtgggg
 180
 cccaggtctg tgatctggga ccggaacaac acatctgctc tgggcctgct ggatgtggcg
 240
 caagccctgg aacagaacca cagcctcaag tccatgccgc tgccactgaa tgacgtaacc
 300
 caggctcatc gcagccggcc agaactcaca actcgagcgg tccatcagat c
 351

<210> 90

<211> 61

<212> PRT

<213> Homo sapiens

<400> 90

Ser	Leu	Val	Gly	Pro	Arg	Ser	Val	Ile	Trp	Asp	Arg	Asn	Asn	Thr	Ser
1				5				10						15	
Ala	Leu	Gly	Leu	Leu	Asp	Val	Ala	Gln	Ala	Leu	Glu	Gln	Asn	His	Ser
			20				25						30		
Leu	Lys	Ser	Met	Pro	Leu	Pro	Leu	Asn	Asp	Val	Thr	Gln	Ala	His	Arg
		35				40						45			
Ser	Arg	Pro	Glu	Leu	Thr	Thr	Arg	Ala	Val	His	Gln	Ile			
	50					55					60				

<210> 91

<211> 327

<212> DNA

<213> Homo sapiens

<400> 91

nggtgggtcc tctcgcagga caggtaatcc tgagacctac gcagctccct ggagctctgc
 60
 acgtcgaagc ccagcagggc ctcttcagag tccctggggc agccagcaca cacaaagtcc
 120
 cggaaggggc tgtagactcc ctgccagcgg ctttcccggg gaaggcacc acgcccagct
 180
 gcctcttgca ggtactgctc gggctctggtg ggagggcagc cgtgtccagc acaccctgtg
 240
 tgtgcagtcc tctccctgcc ccaactgccga acgagccctc cacggtgaag ccattggggg
 300
 acgtgacctt gcccttcccc atgaggt
 327

<210> 92

<211> 107

<212> PRT

<213> Homo sapiens

<400> 92

Met Gly Lys Gly Lys Val Thr Phe Pro Asn Gly Phe Thr Val Glu Gly

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```

      1           5           10           15
Ser Phe Gly Ser Gly Ala Gly Arg Gly Leu His Thr Gln Gly Val Leu
      20           25           30
Asp Thr Ala Ala Leu Pro Pro Asp Pro Ser Ser Thr Cys Lys Arg Gln
      35           40           45
Leu Gly Val Gly Ala Phe Pro Gly Lys Ala Ala Gly Arg Glu Ser Thr
      50           55           60
Ala Pro Ser Gly Thr Leu Cys Val Leu Ala Ala Pro Gly Thr Cys Arg
      65           70           75           80
Arg Pro Cys Trp Ala Ser Thr Cys Arg Ala Pro Gly Ser Cys Val Gly
      85           90           95
Leu Arg Ile Thr Cys Pro Ala Arg Gly Pro Thr
      100           105

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<210> 93
 <211> 394
 <212> DNA
 <213> Homo sapiens

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<400> 93
nccgcgtacg acaagcagta cctcgagggg cgttacggtg cggacccata cctgagcaac
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atgctcgaat gggacggcgg acatgagcaa taggccgcca aagcacagcg agaggaaggc
120
ggcgcgctct gcggcctcgc ggatgaagga ggggtggtcg cgcaagagac gccccgcgcc
180
ttttgtaccg ataaatcccg ggcgccacct gatcgtgacc gagggtagca aaacggaacc
240
gctctatttc gaggetatca ggttgctgt caacaaccgt tatcacggcc agtgggtgac
300
aatggaagtt gtcgttaccg gcaagcatac caggggactt ctcgatcgtg cagtcaactt
360
ggcggaagaa agtgccacag gattcactca cgta
394

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<210> 94
 <211> 109
 <212> PRT
 <213> Homo sapiens

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<400> 94
Met Leu Ala Gly Asn Asp Asn Phe His Cys His Pro Leu Ala Val Ile
      1           5           10           15
Thr Val Val Asp Thr Gln Pro Asp Ser Leu Glu Ile Glu Arg Phe Arg
      20           25           30
Phe Arg Thr Leu Gly His Asp Gln Val Ala Pro Gly Ile Tyr Arg Tyr
      35           40           45
Lys Arg Arg Gly Ala Ser Leu Ala Arg Pro Pro Leu Leu His Pro Arg
      50           55           60
Gly Arg Arg Ala Arg Arg Leu Pro Leu Ala Val Leu Trp Arg Pro Ile
      65           70           75           80
Ala His Val Arg Arg Pro Ile Arg Ala Cys Cys Ser Gly Met Gly Pro
      85           90           95
His Arg Asn Ala Pro Arg Gly Thr Ala Cys Arg Thr Arg

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100

105

<210> 95
 <211> 531
 <212> DNA
 <213> Homo sapiens

<400> 95
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 tgcttgatc ctaaaatgga ctggtcttgg gtgtgtaacc ccggtgaagt tatagcctcc
 120
 ccaaattgag gtgacagaag gaagacaaga ggtgtaagct ggagagggaa gggaagaaat
 180
 cagtggcttt ggccagcctc tgtgccaccc agtacgacag aggagtggga actggccctc
 240
 tggggctctg cttggccata ggcactgcac attgtgccac ctgctcatca cctcctctag
 300
 tctcacactg agcatcggag tacctgttgt gcagacagga aaactgagga gctctgagag
 360
 gctgagcatg gagctcaccc catgccatag ggtgtgggaa gagggcacag gaggcctcat
 420
 ccatggggga aagggttgag gatggacatg ggtggggaga gggcatagac atcccttcct
 480
 aatctctgtt cccaccacat tcataggag atgagttagg agatgacagc t
 531

<210> 96
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Pro Val Pro Ser Ser His Thr Leu Trp His Gly Val Ser
 1 5 10 15
 Ser Met Leu Ser Leu Ser Glu Leu Leu Ser Phe Pro Val Cys Thr Thr
 20 25 30
 Gly Thr Pro Met Leu Ser Val Arg Leu Glu Glu Val Met Ser Arg Trp
 35 40 45
 His Asn Val Gln Cys Leu Trp Pro Ser Arg Ala Pro Glu Gly Gln Phe
 50 55 60
 Pro Leu Leu Cys Arg Thr Gly Trp His Arg Gly Trp Pro Lys Pro Leu
 65 70 75 80
 Ile Ser Ser Leu Pro Ser Pro Ala Tyr Thr Ser Cys Leu Pro Ser Val
 85 90 95
 Thr Ser Ile Trp Gly Gly Tyr Asn Phe Thr Gly Val Thr His Pro Arg
 100 105 110
 Pro Val His Phe Arg Ile Gln Ala Lys Phe Pro Glu
 115 120

<210> 97
 <211> 405
 <212> DNA
 <213> Homo sapiens

<400> 97

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 tcgcgggtgcc ttgcgcgcgg gctggttaggt ggagaagccg cgcgagtacg cgccgtagag
 120
 cgacatcgtg tctgagacgt cgaagctcag gccagctttt ggcgtccagg cgcgctcggg
 180
 cggtcgcgcc tcttgccgga attgattcag cgcaatcccg gccatcacat gccagcgctt
 240
 gtccaggggtc atgaaatcct gggcataggg gcgcgaggag cgcagcggcg aattggacag
 300
 gcgctcgata ttgggcgtga tgtccgaaga cgggaacggg acccgggggg agaagacgtt
 360
 gcccgggaaa agatcccccg acgccatcgt ggtgtcgacc gagat
 405

<210> 98

<211> 122

<212> PRT

<213> Homo sapiens

<400> 98

Met	Ala	Ser	Gly	Asp	Leu	Phe	Pro	Gly	Asn	Val	Phe	Ser	Pro	Arg	Val
1				5					10					15	
Pro	Phe	Pro	Ser	Ser	Asp	Ile	Thr	Pro	Asn	Ile	Glu	Arg	Leu	Ser	Asn
			20					25					30		
Ser	Pro	Leu	Arg	Ser	Ser	Arg	Ala	Tyr	Ala	Gln	Asp	Phe	Met	Thr	Leu
		35					40					45			
Asp	Lys	Arg	Trp	His	Val	Met	Ala	Gly	Ile	Ala	Leu	Asn	Gln	Leu	Pro
	50					55					60				
Gln	Glu	Gly	Gly	Pro	Thr	Glu	Arg	Ala	Trp	Thr	Pro	Lys	Leu	Gly	Leu
65					70				75					80	
Ser	Phe	Asp	Val	Ser	Asp	Thr	Met	Ser	Leu	Tyr	Gly	Ala	Tyr	Ser	Arg
			85					90						95	
Gly	Phe	Ser	Thr	Tyr	Gln	Pro	Ala	Arg	Lys	Ala	Pro	Arg	Ala	Tyr	Gly
		100						105					110		
Pro	Ser	Ala	Ala	Arg	Pro	Ser	Lys	Arg	Glu						
		115					120								

<210> 99

<211> 545

<212> DNA

<213> Homo sapiens

<400> 99

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 tgccccgacg acccagcaaa cgtccccggc tgttcctcat tgaccacgcc gaccggatcg
 120
 tcgatcccat cactcgggat ttgctggaat ccctggttcg cgaagccggc gaggctgcgg
 180
 tgatcttggg tgcccagcgt cgcggtcgca tcgattggct ctccccacag atcatccaca
 240

acctggccga acaccatttt gagtcgtcct ctggaggtac tcgatgatga ctgaacgttc
 300
 ccattccacg atcagggttaa ggtggccggc ggtggtggtt ctcgtcctcg ttccgctgct
 360
 ggtggtcgcc ggattggtcc gggacgacct ggcataccac cgaccggttg ggccgggtga
 420
 aagcggccgt cgtcaacgag gacaaggccg tcaaggtgcg tggacaactg gttccgatgg
 480
 gccgccaact caccgccgcc ttgatggact ctggctcgca caccactgat ggccacaccg
 540
 tcgac
 545

<210> 100
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 100
 Met Gly Thr Phe Ser His His Arg Val Pro Pro Glu Asp Asp Ser Lys
 1 5 10 15
 Trp Cys Ser Ala Arg Leu Trp Met Ile Cys Gly Glu Ser Gln Ser Met
 20 25 30
 Arg Pro Arg Arg Trp Ala Pro Lys Ile Thr Ala Ala Ser Pro Ala Ser
 35 40 45
 Arg Thr Arg Asp Ser Ser Lys Ser Arg Val Met Gly Ser Thr Ile Arg
 50 55 60
 Ser Ala Trp Ser Met Arg Asn Ser Arg Gly Arg Leu Leu Gly Arg Arg
 65 70 75 80
 Gly Arg Trp Val Ser Thr Val Ile Ala Glu Arg Ser Ser Ser Thr Thr
 85 90 95
 Ser Gly Ala Asp Ala
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<210> 101
 <211> 619
 <212> DNA
 <213> Homo sapiens

<400> 101
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 tcatgcacga tccggacttc gatccgatcc ccatggtgaa caaggagctt gacgccttcg
 120
 aagctgccgg gggtagctat ctcacccctc ccacggattc cggacgcaag ggatacacga
 180
 ccgcccgtcc tcacgaggcc ggcggaaaac gctattacca acctggacca gatccgcgaa
 240
 gtctgcgcca gccgcaacgt caccgcctgt ctacaccccc attggggaac gatgggtccag
 300
 aaccgtgacg aagtgatccg cgtgctcgag aactcctcga tcgggctgtg cctggacact
 360
 ggtcatctgg cctgtggtgg taccgatgtc gttgagctgg tgcgtaagta cgccaaccgc
 420

gtcgcacattg tccacgccaa agatgtccat aaggagatgg ccgacaagct ttgacctggc
 480
 gagatcacct ggtccgaagg cattcgcgcc gggatgttcg caccatcgg cgacgggtgat
 540
 atcgactttg cagccatcgt gaggctcctt gatgaagccg ggttcgatgg ttattacgtc
 600
 ctagagcagg acatcatga
 619

<210> 102
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 102
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 1 5 10 15
 Ser Pro Arg Ile Pro Asp Ala Arg Asp Thr Arg Pro Pro Val Leu Thr
 20 25 30
 Arg Pro Ala Glu Asn Ala Ile Thr Asn Leu Asp Gln Ile Arg Glu Val
 35 40 45
 Cys Ala Ser Arg Asn Val Thr Ala Cys Leu His Pro His Trp Gly Thr
 50 55 60
 Met Val Gln Asn Arg Asp Glu Val Ile Arg Val Leu Glu Asn Ser Ser
 65 70 75 80
 Ile Gly Leu Cys Leu Asp Thr Gly His Leu Ala Cys Gly Gly Thr Asp
 85 90 95
 Val Val Glu Leu Val Arg Lys Tyr Ala Asn Arg Val Asp Ile Val His
 100 105 110
 Ala Lys Asp Val His Lys Glu Met Ala Asp Lys Leu Leu Pro Gly Glu
 115 120 125
 Ile Thr Trp Ser Glu Gly Ile Arg Ala Gly Met Phe Ala Pro Ile Gly
 130 135 140
 Asp Gly Asp Ile Asp Phe Ala Ala Ile Val Arg Leu Leu Asp Glu Ala
 145 150 155 160
 Gly Phe Asp Gly Tyr Tyr Val Leu Glu Gln Asp Ile Met
 165 170

<210> 103
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 103
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 gccattgggg ggagaccct gccgtgggga aagaccctg ccatggggca gaccctgcc
 120
 actgggggga gaccctgcc gctgggggga gaccgagcc attgggggga gaccctgcc
 180
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<212> PRT
<213> Homo sapiens

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35 40 45
Gly Gly Asp Pro Ser His Trp Gly Glu Thr Pro Ala Met Gly Lys Asp
50 55 60
Pro Cys His Trp Gly Arg Xaa Pro Ala Ile Gly Gly Asp Pro Cys Arg
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Trp Gly Glu Ile Pro Ala Val Gly Gly Arg Xaa Pro Pro Val Gly Glu
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<210> 106
<211> 62
<212> PRT
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Pro Ser Arg Gly Arg Arg Arg Ala Pro Pro Gly Pro Gln Cys Arg His

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<210> 107
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 <212> DNA
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ser Pro His Cys Phe Arg Leu Leu Arg Pro Val Leu Val Thr Asp Arg
 50 55 60
 Ser Arg Gly His Lys Gln Ala Ala Arg Glu Leu Cys Ser Pro Gly Lys
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<210> 109
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<212> DNA

<213> Homo sapiens

<400> 109

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<213> Homo sapiens

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20     25     30
Leu Gln Leu Lys Asp Arg Glu Lys Asn Ala Ala Arg Asp Ser Trp Gln
35     40     45
Lys Lys Val Glu Asp Leu Leu Asn Gln Ile Ser Leu Leu Lys Gln Asn
50     55     60
Leu Glu Ile Gln Leu Ser Gln Ser Gln Thr Ser Leu Gln Gln Leu Gln
65     70     75     80
Ala Gln Phe Thr Gln Glu Arg Gln Arg Leu Thr Gln Glu Leu Glu Glu
85     90     95
Leu Glu Glu Gln His Gln Gln Arg His Lys Ser Leu Lys Glu Ala His
100    105    110
Val Leu Ala Phe Gln Thr Met Glu Glu Glu Lys Glu Lys Glu Gln Arg
115    120    125
Ala Leu Glu Asn His Leu Gln Gln Lys His Ser Ala Glu Leu Gln Ser

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130 135 140
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<210> 112
 <211> 143
 <212> PRT
 <213> Homo sapiens

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 Xaa Thr Leu Ala Glu Ile Ile Ala Pro Phe Gly His Leu Val Met Ile
 50 55 60
 Asp Gly Thr Asp Ser Phe Asp Leu Met Ala Phe Lys Ser Lys Ser Leu
 65 70 75 80
 Thr Val Thr Ser Glu Ser Met Phe Ser Arg Pro Gln Phe Ala Thr Pro
 85 90 95
 Asp Val Ala Glu Gln Gly Arg Ala Leu Ala Ser Ile Ala Asp Leu Val
 100 105 110
 Glu Lys Gly Gln Ile Arg Pro Thr Met Thr Arg His Ile Glu Gly Leu
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<210> 113
 <211> 382

<212> DNA

<213> Homo sapiens

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<210> 114

<211> 125

<212> PRT

<213> Homo sapiens

<400> 114

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			20				25					30			
Ala	Gln	Lys	Glu	Thr	Arg	Arg	Trp	Leu	Pro	Pro	Arg	Asp	Arg	Pro	Ser
		35				40					45				
Ala	Cys	Cys	Cys	Ala	Ser	Ser	Ala	Ile	Ser	Ala	Val	Ser	Tyr	Ser	Ser
	50				55						60				
Thr	Ala	Lys	Pro	Phe	Ser	Cys	Pro	Ser	Trp	Pro	His	Ala	Ser	Trp	Gln
65					70				75					80	
Lys	Val	Gly	Leu	Trp	Thr	Ala	Asp	Ser	Ala	Arg	His	Arg	Ala	Ser	Thr
			85					90					95		
Ser	Leu	Lys	Pro	Gly	Gly	Arg	Arg	Ser	Thr	Gln	Arg	Gln	Gln	Glu	Trp
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<210> 115

<211> 4798

<212> DNA

<213> Homo sapiens

<400> 115

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<210> 116

<211> 1062

<212> PRT

<213> Homo sapiens

<400> 116

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35           40           45
Lys Pro Pro Leu Phe Asn Met Asn Ala Met Ser Ala Leu Tyr His Ile
50           55           60
Ala Gln Asn Glu Ser Pro Val Leu Gln Ser Gly His Trp Ser Glu Tyr
65           70           75           80
Phe Arg Asn Phe Val Asp Ser Cys Leu Gln Lys Ile Pro Gln Asp Arg
85           90           95
Pro Thr Ser Glu Val Leu Leu Lys His Arg Phe Val Leu Arg Glu Arg
100          105          110
Pro Pro Thr Val Ile Met Asp Leu Ile Gln Arg Thr Lys Asp Ala Val
115          120          125
Arg Glu Leu Asp Asn Leu Gln Tyr Arg Lys Met Lys Lys Ile Leu Phe
130          135          140
Gln Glu Ala Pro Asn Gly Pro Gly Ala Glu Ala Pro Glu Glu Glu Glu
145          150          155          160
Glu Ala Glu Pro Tyr Met His Arg Ala Gly Thr Leu Thr Ser Leu Glu
165          170          175
Ser Ser His Ser Val Pro Ser Met Ser Ile Ser Ala Ser Ser Gln Ser
180          185          190
Ser Ser Val Asn Ser Leu Ala Asp Ala Ser Asp Asn Glu Glu Glu Glu
195          200          205
Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly Pro Glu Ala Arg
210          215          220
Glu Met Ala Met Met Gln Glu Gly Glu His Thr Val Thr Ser His Ser
225          230          235          240
Ser Ile Ile His Arg Leu Pro Gly Ser Asp Asn Leu Tyr Asp Asp Pro
245          250          255
Tyr Gln Pro Glu Ile Thr Pro Ser Pro Leu Gln Pro Pro Ala Ala Pro
260          265          270
Ala Pro Thr Ser Thr Thr Ser Ser Ala Arg Arg Arg Ala Tyr Cys Arg
275          280          285
Asn Arg Asp His Phe Ala Thr Ile Arg Thr Ala Ser Leu Val Ser Arg
290          295          300
Gln Ile Gln Glu His Glu Gln Asp Ser Ala Leu Arg Glu Gln Leu Ser
305          310          315          320
Gly Tyr Lys Arg Met Arg Arg Gln His Gln Lys Gln Leu Leu Ala Leu
325          330          335
Glu Ser Arg Leu Arg Gly Glu Arg Glu Glu His Ser Ala Arg Leu Gln
340          345          350
Arg Glu Leu Glu Ala Gln Arg Ala Gly Phe Gly Ala Glu Ala Glu Lys
355          360          365
Leu Ala Arg Arg His Gln Ala Ile Gly Glu Lys Glu Ala Arg Ala Ala
370          375          380
Gln Ala Glu Glu Arg Lys Phe Gln Gln His Ile Leu Gly Gln Gln Lys
385          390          395          400
Lys Glu Leu Ala Ala Leu Leu Glu Ala Gln Lys Arg Thr Tyr Lys Leu
405          410          415
Arg Lys Glu Gln Leu Lys Glu Glu Leu Gln Glu Asn Pro Ser Thr Pro
420          425          430
Lys Arg Glu Lys Ala Glu Trp Leu Leu Arg Gln Lys Glu Gln Leu Gln

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Val	Gly	Gln	Glu	Glu	Ala	Gly	Thr	Trp	Ser	Leu	Trp	Gly	Lys	Glu	Asp	
690					695					700						
Glu	Ser	Leu	Leu	Asp	Glu	Glu	Phe	Glu	Leu	Gly	Trp	Val	Gln	Gly	Pro	
705					710					715					720	
Ala	Leu	Thr	Pro	Val	Pro	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	
725					730					735						
Pro	Ile	Gly	Thr	Pro	Arg	Asp	Pro	Gly	Asp	Gly	Cys	Pro	Ser	Pro	Asp	
740					745					750						
Ile	Pro	Pro	Glu	Pro	Pro	Pro	Thr	His	Leu	Arg	Pro	Cys	Pro	Ala	Ser	
755					760					765						
Gln	Leu	Pro	Gly	Leu	Leu	Ser	His	Gly	Leu	Leu	Ala	Gly	Leu	Ser	Phe	
770					775					780						
Ala	Val	Gly	Ser	Ser	Ser	Gly	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	
785					790					795					800	
Leu	Pro	Leu	Leu	Ala	Ala	Gln	Gly	Gly	Gly	Gly	Leu	Gln	Ala	Ala	Leu	
805					810					815						
Leu	Ala	Leu	Glu	Val	Gly	Leu	Val	Gly	Leu	Gly	Ala	Ser	Tyr	Leu	Leu	
820					825					830						
Leu	Cys	Thr	Ala	Leu	His	Leu	Pro	Ser	Ser	Leu	Phe	Leu	Leu	Leu	Ala	
835					840					845						
Gln	Gly	Thr	Ala	Leu	Gly	Ala	Val	Leu	Gly	Leu	Ser	Trp	Arg	Arg	Gly	
850					855					860						
Leu	Met	Gly	Val	Pro	Leu	Gly	Leu	Gly	Ala	Ala	Trp	Leu	Leu	Ala	Trp	

```
<210> 117
<211> 471
<212> DNA
<213> Homo sapiens
```

```
<210> 118
<211> 157
<212> PRT
<213> Homo sapiens
```

<400> 118
 Xaa Ala Leu Thr Ile Cys Leu Ala Gly Val Val Ile Cys Ala Val Gly
 1 5 10 15
 Val Val Asp Asp Leu Leu Asp Leu Pro Ala Leu Ala Lys Ala Ala Gly
 20 25 30
 Gln Val Leu Ala Ala Gly Ile Val Val Thr Gly Gly Val Arg Met Phe
 35 40 45
 Trp Ile Pro Leu Pro Asn Ser Ile Ile Ala Leu Gly Thr Pro Thr Ser
 50 55 60
 Ile Leu Val Thr Val Phe Phe Ile Val Leu Cys Ala Asn Ala Val Asn
 65 70 75 80
 Phe Ile Asp Gly Leu Asp Gly Leu Ala Ser Gly Val Val Ala Ile Gly
 85 90 95
 Ser Leu Ala Phe Phe Ser Tyr Thr Tyr Leu Leu Ala His Glu Gln Asp
 100 105 110
 Phe Val Val Ala Thr Thr Thr Ser Leu Ile Thr Ala Ala Thr Ala Gly
 115 120 125
 Ala Cys Leu Gly Phe Leu Pro His Asn Trp His Pro Ala Arg Met Phe
 130 135 140
 Met Gly Asp Ser Gly Ala Leu Leu Leu Gly Leu Leu
 145 150 155

<210> 119
 <211> 302
 <212> DNA
 <213> Homo sapiens

<400> 119
 ntcaaacatg agcagtcgtg gcggccgagg ccgcggtggc tattatcgcg agctttatgg
 60
 tagccgaggt cgaggcagta aatctaataa aactttcgca aaaaattcgg atgtctactc
 120
 tcagaaaaag actcgaacag tacgaggcac ctccgaagat ttagcacgat cgctccataa
 180
 gttcatatg cgcccgtacc ctgcgtatca tgacattgag ggtatgtggg ctttcccagc
 240
 ctttactttt tatctggatc atgcacaagc agaccatac gctgccccaa ataaggcacg
 300
 cn
 302

<210> 120
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 120
 Met Ser Ser Arg Gly Gly Arg Gly Arg Gly Gly Tyr Tyr Arg Glu Leu
 1 5 10 15
 Tyr Gly Ser Arg Gly Arg Gly Ser Lys Ser Asn Glu Thr Phe Ala Lys
 20 25 30
 Asn Ser Asp Val Tyr Ser Gln Lys Lys Thr Arg Thr Val Arg Gly Thr
 35 40 45
 Ser Glu Asp Leu Ala Arg Ser Leu His Lys Leu His Met Arg Pro Tyr

```

      50              55              60
Pro Ala Tyr His Asp Ile Glu Gly Met Trp Ala Phe Pro Ala Phe Thr
65              70              75              80
Phe Tyr Leu Asp His Ala Gln Ala Asp Pro Tyr Ala Ala Pro Asn Lys
      85              90              95
Ala Arg

```

<210> 121
 <211> 318
 <212> DNA
 <213> Homo sapiens

```

<400> 121
ngcatggggg gccctgggac cgcacttggtg cccctttttt ttttagggaa aaaattgagc
60
cctaaaggat ttgccgcatt acaggaaagt tttttggtaa gtttgggggtt gtttctgtgc
120
tgtgtgagaa ggagtagaag cagctccagt agagtggggcc ttttcatttt tatccagagg
180
aaattttag gctgtggcta ttacttcctt ttttttcttt tttttttttg ttttagagaca
240
gagtcctgnct ctgtcgccag gctggagtga agtggcacga tctcagctca ctgcaacctc
300
tgctctccag gttcaagc
318

```

<210> 122
 <211> 89
 <212> PRT
 <213> Homo sapiens

```

<400> 122
Xaa Met Gly Gly Pro Gly Thr Ala Leu Val Pro Leu Phe Phe Leu Gly
1      5      10      15
Lys Lys Leu Ser Pro Lys Gly Phe Ala Ala Leu Gln Glu Ser Phe Leu
      20      25      30
Val Ser Leu Gly Leu Phe Leu Cys Cys Val Arg Arg Ser Arg Ser Ser
      35      40      45
Ser Ser Arg Val Gly Leu Phe Ile Phe Ile Gln Arg Lys Phe Val Gly
      50      55      60
Cys Gly Tyr Tyr Phe Leu Phe Phe Leu Phe Phe Cys Leu Glu Thr
65      70      75      80
Glu Ser Xaa Ser Val Ala Arg Leu Glu
      85

```

<210> 123
 <211> 338
 <212> DNA
 <213> Homo sapiens

```

<400> 123
acgcgtctag ggtagaaatc aactccagta actgtcatc aacctcagca atgctgggga
60

```

cgggcagagg cagggcagct gtgtgccaca ttcttgccag ggctgggtcag gccccggctc
 120
 tcaccactcc tctctcctgc tttgaacctg tggaacaaag ggccctgca ccccaactca
 180
 ttctcttttg ccacataagg gcctcaagtc atgctgtccc ctctgcctgg gttgcttttt
 240
 ctccctctgc ttgggtcact gttcacacca ctggccactt tctcaggga agggccctca
 300
 ctgcccacac acctaaacat gccccctgct cctccata
 338

<210> 124

<211> 96

<212> PRT

<213> Homo sapiens

<400> 124

Met	Leu	Gly	Thr	Gly	Arg	Gly	Arg	Ala	Ala	Val	Cys	His	Ile	Pro	Ala
1				5				10					15		
Arg	Ala	Gly	Gln	Ala	Pro	Ala	Leu	Thr	Thr	Pro	Pro	Pro	Cys	Phe	Glu
		20					25					30			
Pro	Val	Glu	Gln	Arg	Ala	Pro	Ala	Pro	Gln	Leu	Ile	Pro	Leu	Cys	His
	35					40					45				
Ile	Arg	Ala	Ser	Ser	His	Ala	Val	Pro	Ser	Ala	Trp	Val	Ala	Phe	Ser
	50				55					60					
Pro	Ser	Ala	Trp	Val	Thr	Val	His	Thr	Thr	Gly	His	Phe	Pro	Gln	Gly
65				70				75						80	
Arg	Ala	Leu	Thr	Ala	His	Thr	Pro	Lys	His	Ala	Pro	Cys	Ser	Ser	Ile
			85					90						95	

<210> 125

<211> 280

<212> DNA

<213> Homo sapiens

<400> 125

ccatggacct ggccagccac catcacctgc ctctgcctc acccaccctg ggtgcctgcc
 60
 ggcaaggatt ggagggcaga ctgctggagc gtgagaccag gccaatctgt ctttctggga
 120
 accttcagcc tccaactgga gctgactgtc aactttcggg tgagaagtca ctttctgca
 180
 ttcccaccac actatctatc tgtgcaatac ggcagcgtga cagcactcac cttattgagg
 240
 gcttctgctg tcttggecca ttctggatag gcctgateta
 280

<210> 126

<211> 92

<212> PRT

<213> Homo sapiens

<400> 126

Met Asp Leu Ala Ser His His His Leu Pro Pro Ala Ser Pro Thr Leu

```

1           5           10           15
Gly Ala Cys Arg Gln Gly Leu Glu Gly Arg Leu Leu Glu Arg Glu Thr
20           25           30
Arg Pro Ile Cys Leu Ser Gly Asn Leu Gln Pro Pro Thr Gly Ala Asp
35           40           45
Cys Gln Leu Ser Gly Glu Lys Ser Leu Phe Cys Ile Pro Thr Thr Leu
50           55           60
Ser Ile Cys Ala Ile Arg Gln Arg Asp Ser Thr His Leu Ile Glu Gly
65           70           75           80
Phe Cys Cys Pro Gly Pro Phe Trp Ile Gly Leu Ile
85           90

```

<210> 127

<211> 444

<212> DNA

<213> Homo sapiens

<400> 127

```

cgcgatgatcg ccgtggcgga gggccgcggc gccgactcga tcgcccagct gacaaccgag
60
ctgcaaagcc gtcactgccc tgcggagcag atcacgtccg tcagcatcga catgtcgcca
120
gcgttcatca ggggctgcgc cgagcacctg cccaacgcgc gcgtcacctt cgacaagttc
180
cacgtcatcg ggcacgcca tgcggccgtg gacaggatgc gccgcatcga gcagcgcagc
240
gacaagtccc tcaaggggat gcgctggtcg ctgctgaaga accgcgccag cctcaagccc
300
gaggctgccg ccgatctgga tgccctgac gccaggatgg ccactgtgcy caccgcgcgc
360
gcctgggtct acaaggagca gctgcgcgag atcctcgcgc gcaagcagat caactgtggc
420
cgcgacatgc tcaagcactg gtgc
444

```

<210> 128

<211> 148

<212> PRT

<213> Homo sapiens

<400> 128

```

Arg Val Ile Ala Val Ala Glu Gly Arg Gly Ala Asp Ser Ile Ala Gln
1           5           10           15
Leu Thr Thr Glu Leu Gln Ser Arg His Cys Pro Ala Glu Gln Ile Thr
20           25           30
Ser Val Ser Ile Asp Met Ser Pro Ala Phe Ile Arg Gly Cys Ala Glu
35           40           45
His Leu Pro Asn Ala Arg Val Thr Phe Asp Lys Phe His Val Ile Gly
50           55           60
His Ala Asn Ala Ala Val Asp Arg Met Arg Arg Ile Glu Gln Arg Ser
65           70           75           80
Asp Lys Ser Leu Lys Gly Met Arg Trp Ser Leu Leu Lys Asn Arg Ala
85           90           95
Ser Leu Lys Pro Glu Ala Ala Ala Asp Leu Asp Ala Leu Ile Ala Arg

```

```

          100          105          110
Met Ala Thr Val Arg Thr Ala Arg Ala Trp Val Tyr Lys Glu Gln Leu
          115          120          125
Arg Glu Ile Leu Ala Arg Lys Gln Ile Asn Val Ala Arg Asp Met Leu
          130          135          140
Lys His Trp Cys
145

```

```

<210> 129
<211> 291
<212> DNA
<213> Homo sapiens

```

```

<400> 129
gaggaggggac gtaccgtccc cgttatagcc aagctcgaga agccgcaagc tatcgagaac
60
ttggacgaga ttattgacgt ctttgacgcc gtcattggtg cccgtggcga tatggccgtc
120
gagtgcccgcc tcgaggaagt tccgctgacg caaaagcaga tcatcgagaa ggctcgttta
180
caggctaagc ccgtcattgt ggccaccagc atgcttgagt cgatgatcca cgctccccgt
240
ccgaccgcgc ctgaggccgc cgacgtcgcg aacgccatcc ttgacggcgc g
291

```

```

<210> 130
<211> 97
<212> PRT
<213> Homo sapiens

```

```

<400> 130
Glu Glu Gly Arg Thr Val Pro Val Ile Ala Lys Leu Glu Lys Pro Gln
1      5      10      15
Ala Ile Glu Asn Leu Asp Glu Ile Ile Asp Val Phe Asp Ala Val Met
20      25      30
Val Ala Arg Gly Asp Met Ala Val Glu Cys Pro Leu Glu Val Pro
35      40      45
Leu Ile Gln Lys Gln Ile Ile Glu Lys Ala Arg Leu Gln Ala Lys Pro
50      55      60
Val Ile Val Ala Thr Gln Met Leu Glu Ser Met Ile His Ala Pro Arg
65      70      75      80
Pro Thr Arg Ala Glu Ala Ala Asp Val Ala Asn Ala Ile Leu Asp Gly
85      90      95
Ala

```

```

<210> 131
<211> 416
<212> DNA
<213> Homo sapiens

```

```

<400> 131
tccggagcgt ccgtggccct catgggtgtg tcagcgtggt tgctgtctcg ggccgcagag
60

```

attccaccgg tgctctacct ggaggccgca gccgtcgggg ttcgattctt cggcatctcc
 120
 cgcgggtgtct tccgctacgc cgaacgtctg gtaggccacg acctggctct gcggatgcag
 180
 ggggcattgc ggatgcgggt ctacgaccgg ctgtcacgta ccnaccctgc tgggnnacgt
 240
 cgccgggggtg acctgctggt acgggttact gccgacgtcg acgcgggtgtt ggacatggtc
 300
 gtgcgggtga tcgttccggc gtgcgcgtca agcctcgtca tcattggcac cacggctcctt
 360
 ctttgtccga gagaagggtg agttttctta gccggattcc aacacagcct gggggc
 416

<210> 132

<211> 126

<212> PRT

<213> Homo sapiens

<400> 132

Ser	Gly	Ala	Ser	Val	Ala	Leu	Met	Gly	Val	Ser	Ala	Trp	Leu	Leu	Ser
1				5					10					15	
Arg	Ala	Ala	Glu	Ile	Pro	Pro	Val	Leu	Tyr	Leu	Glu	Ala	Ala	Ala	Val
			20					25					30		
Gly	Val	Arg	Phe	Phe	Gly	Ile	Ser	Arg	Gly	Val	Phe	Arg	Tyr	Ala	Glu
		35				40					45				
Arg	Leu	Val	Gly	His	Asp	Leu	Ala	Leu	Arg	Met	Gln	Gly	Ala	Leu	Arg
	50					55					60				
Met	Arg	Val	Tyr	Asp	Arg	Leu	Ser	Arg	Thr	Xaa	Pro	Ala	Gly	Xaa	Arg
65				70					75					80	
Arg	Arg	Gly	Asp	Leu	Leu	Val	Arg	Val	Thr	Ala	Asp	Val	Asp	Ala	Val
			85					90						95	
Leu	Asp	Met	Val	Val	Arg	Val	Ile	Val	Pro	Ala	Cys	Ala	Ser	Ser	Leu
		100						105					110		
Val	Ile	Ile	Gly	Thr	Thr	Val	Leu	Leu	Cys	Pro	Arg	Glu	Gly		
		115					120						125		

<210> 133

<211> 327

<212> DNA

<213> Homo sapiens

<400> 133

gccgttgcta tcgctgctgg tatgcgtgca gacgtcactg tttttgatat caatatcgct
 60
 gcgttgaaga gactcgccga catctaccag ggctcgtgttc acacagtagt atccacccgc
 120
 gccgaaattg cgaaggcgct agaaaccgct gacgttgtga tcggttctgt ccttattccg
 180
 ggtagttcta ccccgaagct tgttactacc gatatggttg ctcacatgca gcctgggtct
 240
 gttcttattg atattgctat agaccaaggc ggctgcttcg aggattcgca ccccaccact
 300
 tacgatgacc ccactttcac tgtgcac
 327

<210> 134
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 134
 Ala Val Ala Ile Ala Ala Gly Met Arg Ala Asp Val Thr Val Phe Asp
 1 5 10 15
 Ile Asn Ile Ala Ala Leu Lys Arg Leu Ala Asp Ile Tyr Gln Gly Arg
 20 25 30
 Val His Thr Val Val Ser Thr Arg Ala Glu Ile Ala Lys Ala Leu Glu
 35 40 45
 Thr Ala Asp Val Val Ile Gly Ser Val Leu Ile Pro Gly Ser Ser Thr
 50 55 60
 Pro Lys Leu Val Thr Thr Asp Met Val Ala His Met Gln Pro Gly Ser
 65 70 75 80
 Val Leu Ile Asp Ile Ala Ile Asp Gln Gly Gly Cys Phe Glu Asp Ser
 85 90 95
 His Pro Thr Thr Tyr Asp Asp Pro Thr Phe Thr Val His
 100 105

<210> 135
 <211> 560
 <212> DNA
 <213> Homo sapiens

<400> 135
 taagatgtgg tcctgccctg ttcctgaagg ggctgcagct ctgatggaaa atacagggat
 60
 ttacactcag ggctacagcc acgggggggt gaggcccaag gctgcaatct cgggggaagg
 120
 ggaagtggc ttttcttggg ggattggaaa catcctcttg gaggcaaaga cttttcctgg
 180
 atcttacaga cttcccggga tttttagatt agaattattg gggcaaagga ggctgtcttg
 240
 ttttaaagca atgctacata gacacagtgg ggaagacctg gttcgacggc agataagcag
 300
 tgggtgatgg gcttgaggag gagagtcagg gcaaagtcta agactgagca gaaaggaatt
 360
 ccccatctc ccatggataa gtacgttcta gaacattctc tttgggtcta atactctgaa
 420
 atgacatctt gtcttcatgc tcgagagaga attacttcac tggctccact tggagtgcc
 480
 gtgttcagac accaagcctg actgggaggg ttccggtttc ttaacacctt cccaccgccg
 540
 acttccaagt cccacgcgt
 560

<210> 136
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 136

```

Met Trp Ser Cys Pro Val Pro Glu Gly Ala Ala Ala Leu Met Glu Asn
 1           5           10           15
Thr Gly Ile Tyr Thr Gln Gly Tyr Ser His Gly Gly Leu Arg Pro Lys
           20           25           30
Ala Ala Ile Ser Gly Glu Gly Glu Val Gly Phe Ser Trp Trp Ile Gly
           35           40           45
Asn Ile Leu Leu Glu Ala Lys Thr Phe Pro Gly Ser Tyr Arg Leu Pro
           50           55           60
Gly Ile Phe Arg Leu Glu Tyr Trp Gly Gln Arg Arg Leu Ser Cys Phe
           65           70           75           80
Lys Ala Met Leu His Arg His Ser Gly Glu Asp Leu Val Arg Arg Gln
           85           90           95
Ile Ser Ser Gly
           100

```

<210> 137

<211> 429

<212> DNA

<213> Homo sapiens

<400> 137

```

accggttgga tggcctgcag gccaaagcgt tcctgcaaac tcagcaggcc ttcagcgcaa
60
gaggcaaaca gctggtcgcg cacctgcttg aggtccaccg attgcgcatt gcccttgagc
120
aaggcgcgcc agttggtttt gtcggccact tggctgcgga acaggtcttc gacaaaaccg
180
gactgctggc gggctcgcaac gcgcatgatt ggcagcgcct ggctggcgcc ctggctcgagc
240
cagcgcgtcg gcagttgggt ggcccgggtg ataccgacct tgatccccga cgaattggcc
300
aggtacacca catggtcggc catgcagaat gtttcgcccc agccgggatc acggcaagtg
360
ccggcgtcgt aatggcaacg ttcggggctc atgatgcaca ggtcacactg ggccagcttg
420
gtcatgccc
429

```

<210> 138

<211> 141

<212> PRT

<213> Homo sapiens

<400> 138

```

Met Thr Lys Leu Ala Gln Cys Asp Leu Cys Ile Met Ser Pro Glu Arg
 1           5           10           15
Cys His Tyr Asp Ala Gly Thr Cys Arg Asp Pro Gly Trp Gly Glu Thr
           20           25           30
Phe Cys Met Thr Asp His Val Val Tyr Leu Ala Asn Ser Ser Gly Ile
           35           40           45
Lys Val Gly Ile Thr Arg Ala Thr Gln Leu Pro Thr Arg Trp Leu Asp
           50           55           60
Gln Gly Ala Ser Gln Ala Leu Pro Ile Met Arg Val Ala Thr Arg Gln

```

```

65              70              75              80
Gln Ser Gly Phe Val Glu Asp Leu Phe Arg Ser Gln Val Ala Asp Lys
              85              90              95
Thr Asn Trp Arg Ala Leu Leu Lys Gly Asp Ala Gln Ser Val Asp Leu
              100              105              110
Lys Gln Val Arg Asp Gln Leu Phe Ala Ser Cys Ala Glu Gly Leu Leu
              115              120              125
Ser Leu Gln Glu Arg Phe Gly Leu Gln Ala Ile Gln Pro
              130              135              140

```

<210> 139
 <211> 341
 <212> DNA
 <213> Homo sapiens

```

<400> 139
acgcgtcgtt tgaaggcttg atccgcacgt ccaattcgct ttgcgccaat gcgccgcagc
60
ttgtgaacag cagaatcaag ccgctggtaa atcttctctg gagcttcata ggcggggatg
120
ctacacgagc tgggggagaca ctttgaaccc ggaattgtct gaataattct gtctcaaacc
180
tttgcagcct gtaacgactg agggttcgga tggaaaaaca catgctccag gatgggaccg
240
acggccactt caccgatctc ttcatagccc tggcgtttgt agaaatccag gtagcgcgaa
300
tcgccagcgt cgagcacgac gcctgatgag tgcgggtcat t
341

```

<210> 140
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 140
Met Thr Arg Thr His Gln Ala Ser Cys Ser Thr Leu Ala Ile Arg Ala
1      5      10      15
Thr Trp Ile Ser Thr Asn Ala Arg Ala Met Lys Arg Ser Val Lys Trp
20     25     30
Pro Ser Val Pro Ser Trp Ser Met Cys Phe Ser Ile Arg Thr Leu Ser
35     40     45
Arg Tyr Arg Leu Gln Arg Phe Glu Thr Glu Leu Phe Arg Gln Phe Arg
50     55     60
Val Gln Ser Val Ser Pro Ala Arg Val Ala Ser Pro Pro Met Lys Leu
65     70     75     80
Pro Gly Arg Phe Thr Ser Gly Leu Ile Leu Leu Phe Thr Ser Cys Gly
85     90     95
Ala Leu Ala Gln Ser Glu Leu Asp Val Arg Ile Lys Pro Ser Asn Asp
100    105    110
Ala

```

<210> 141
 <211> 324

<212> DNA

<213> Homo sapiens

<400> 141

```

gaattcctct tggatagctt cgggtaaagt ggtacagcaa atatcaggag cgcaaccgca
60
acctttactt actggtacat gaacaccatt tacattacag ctatcgtact caccacacgt
120
catgtgaaca gacacataac tgaaagggtt ataaaccaca gtctcacggt acgtatgacc
180
gtcaactgtg aacaccgcta agtaatagcc tgcgggggct tgcattgaact cctttgacca
240
tgcgtaataa atacgtccgt cattagtcac acctgatggg gcgaaacaaa aagaacggca
300
gcagttatca ccgcccatac gcgt
324

```

<210> 142

<211> 106

<212> PRT

<213> Homo sapiens

<400> 142

```

Met Gly Gly Asp Asn Cys Cys Arg Ser Phe Cys Phe Ala Pro Ser Gly
1      5      10      15
Val Thr Asn Asp Gly Arg Ile Tyr Tyr Ala Trp Ser Lys Glu Phe Met
20     25     30
Gln Ala Pro Ala Gly Tyr Tyr Leu Ala Val Phe Thr Val Asp Gly His
35     40     45
Thr Tyr Arg Glu Thr Val Val Tyr Lys Pro Phe Ser Tyr Val Ser Val
50     55     60
His Met Thr Trp Gly Glu Tyr Asp Ser Cys Asn Val Asn Gly Val His
65     70     75     80
Val Pro Val Ser Lys Gly Cys Gly Cys Ala Pro Asp Ile Cys Cys Thr
85     90     95
His Leu Pro Glu Ala Ile Gln Glu Glu Phe
100    105

```

<210> 143

<211> 1325

<212> DNA

<213> Homo sapiens

<400> 143

```

naccgctgga tctgccagct gagcctggag ctgtgcaggc agctgccctg ctacgatgag
60
gcaccccagg agaagaactt cctgtacaaa tgcattaggca ccaccctggg tgctgcttca
120
agtaaggagg tggtaggaa gcaccttcaa gagctgctgg agacggccag ataccaggag
180
gaggcagaac gcgagggcct cgctgctgc ttccgggatct gtgccatctc ccacctcgag
240
gacacgctgg ccagctgga ggacttcgtg aggtcagagg tcttcagaaa atccattggc
300

```

attctcaaca tttttaagga tcgaagtga aacgaagtgg agaaggtgaa gagtgcctctg
 360
 atcctgtgct atgggcacgt ggcggcccg gcccccgagg agctggtgct ggccaaggta
 420
 gagtcagaca tcctccggaa catcntgcca gcacttcagc acnncaagga cccagccctg
 480
 aagctgtgcc ttgtccagag tgtgtgcatg gtcagccgag ccatctgcag cagcaccag
 540
 gctggctcct tccacttcac ccggaaagca gagctggtgg cacagatgat ggagttcatc
 600
 agggcagagc ccccggaactc cttgaggaca cctattcgga agaaagccat gctcacctgc
 660
 acttacttgg tctccgtgga gccagcgctg gacgagcagg cccgggaggga tgtgatccat
 720
 ggctgcctgc acagcatcat ggccctgctg cctgagccca aggaggagga cggaggctgc
 780
 cagaagtcce tgtatctgga gacactgcac gcccttgagg atctgctgac gagcctcctg
 840
 cagcgggaaca tgacccccca aggctgcag atcatgattg agcacctgag cccatggatc
 900
 aagtccecaa gaggtcacgt agcggcgctg gccctaggcc tgagcgccct cctcgtgcgc
 960
 tacttcttgg agcacctgcg tgtcagtggc gcccaagtag ataccaggtt tccatctgag
 1020
 cccaggatcc tgtgcaatgg cctggtgccc cttccacaac ctgggccttc tcatcggcct
 1080
 cttctcccca cgggtgtgcg acctgtggcc tgccaccgag caggaggccg tggactgtgt
 1140
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<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

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Cys	Tyr	Asp	Glu	Ala	Pro	Gln	Glu	Lys	Asn	Phe	Leu	Tyr	Lys	Cys	Ile
			20					25					30		
Gly	Thr	Thr	Leu	Gly	Ala	Ala	Ser	Ser	Lys	Glu	Val	Val	Arg	Lys	His
			35				40					45			
Leu	Gln	Glu	Leu	Leu	Glu	Thr	Ala	Arg	Tyr	Gln	Glu	Glu	Ala	Glu	Arg
			50			55				60					
Glu	Gly	Leu	Ala	Cys	Cys	Phe	Gly	Ile	Cys	Ala	Ile	Ser	His	Leu	Glu
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<210> 145
<211> 802
<212> DNA
<213> Homo sapiens
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240
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<210> 146

<211> 151

<212> PRT

<213> Homo sapiens

<400> 146

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Thr	Ile	Ser	Pro	Arg	Arg	Thr	Arg	His	His	Ala	Pro	Tyr	Leu	Asp	Arg
			20					25					30		
Met	Ser	Asp	Met	Ser	Met	Pro	Arg	Arg	Ala	Ala	Pro	Glu	Asp	Asp	Thr
		35					40					45			
Asp	Leu	Ala	Asp	Ala	Ala	Arg	Ser	Trp	Arg	Arg	Tyr	Leu	Ile	Leu	Val
	50					55					60				
Ile	Cys	Gly	Val	Ile	Val	Ala	Val	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Tyr
65					70				75					80	
Leu	Ala	Trp	Trp	Ser	Leu	Cys	Asp	Gln	Ala	Ala	Gly	Val	Cys	Gln	Arg
			85					90					95		
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			100					105					110		
Gly	Leu	Ile	Ile	Gly	Val	Leu	Thr	Gln	Ile	Trp	Leu	Glu	Lys	Arg	Trp
		115					120					125			
Trp	His	Met	Leu	Ala	Ile	Val	Ile	Pro	Ala	Val	Phe	Ile	Val	Ala	Gly
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145						150									

<210> 147

<211> 368

<212> DNA

<213> Homo sapiens

<400> 147

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368

<210> 148
<211> 117
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<213> Homo sapiens

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35 40 45
Glu Lys Val Leu His Lys Lys Asp Tyr Trp Asp Leu Ala Thr Pro Met
50 55 60
Pro Ile Ala Trp Gly Thr Thr Asp Arg Thr Val Ile Ala Asp Ala Arg
65 70 75 80
Arg Thr Ile Pro Thr Thr Glu Trp Asp Ile Leu Ala Arg Leu Arg Pro
85 90 95
Arg Leu Glu Glu Val Arg Lys Gln Arg Asn Asp Val Leu Leu Leu Asn
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Glu Glu Asp Pro Pro
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<211> 407
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<210> 150
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 <212> PRT
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 35 40 45
 Ser Ala Asp Glu Gly Lys Ser Trp Ala Pro Ile Lys Gly Pro Glu Gln
 50 55 60
 Gly Gln Ala His Leu Phe Val Leu His Pro Tyr Asp Lys Thr Gln Ala
 65 70 75 80
 Tyr Ile Leu Thr Arg Ser Thr Gln His Trp Arg Thr Ser Asn Arg Gly
 85 90 95
 Glu Thr Trp Gln Ser Phe Ser Thr Pro His Pro Pro Thr Thr Leu Lys
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 Ala Met Pro Leu Asp Phe His Pro Thr His His Asp Trp Ile Leu Phe
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<210> 151
 <211> 448
 <212> DNA
 <213> Homo sapiens

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<210> 152

<211> 149
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 35 40 45
 Cys Pro Val Ser Ala Pro Pro Ser Ser Pro Pro Glu Gly Lys Thr Trp
 50 55 60
 Ala Leu Arg Glu Pro Cys Gly Met Phe Phe Val Ile Asn Cys Thr Ser
 65 70 75 80
 Ala Ser Thr Ala Arg Pro Arg Ala Lys Ser Arg Val Ser Gly Pro Trp
 85 90 95
 Ser Lys Leu Arg Leu Ser Ala Ala Thr Ser Gly Gly Gln Gly Glu Gly
 100 105 110
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 130 135 140
 Cys Met Asp Ile Arg
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<210> 153
 <211> 440
 <212> DNA
 <213> Homo sapiens

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<210> 154
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 154
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 Gly Pro Cys Ile Cys Val Tyr Ile Cys Gly Asp Met Tyr Met Cys Val
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 Cys Met Asn Arg Cys Lys Trp Gly Ala Leu Arg Cys Val Cys Val Cys
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 Ser Cys Thr Arg Val
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<210> 155
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 <212> DNA
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<210> 156
 <211> 92
 <212> PRT
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<400> 156
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 20 25 30
 Gln Arg His Ser Asp Asn Ala Pro Gln Glu Val Lys Ser Ser Leu Ser
 35 40 45
 Asp His Gly Arg Arg Ala Ser Ala Gln Gly Glu Leu Gly Thr Ser Gln
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6420

cacatgggct tatgcattaa gtttaattgt gataaatttg tgctgttcca gtatatgcaa
 6480
 tacacttttaa tgttttattc ttgtacataa aaatgtgcaa tatggagatg tatacagtct
 6540
 ttactatatt aggtttataa acagttttta gaatttcac cttttgccaa aatgggtggag
 6600
 tatgtaattg gtaaatcata aatcctgtgg tgaatgggtgg tgtactttta agctgtcacc
 6660
 atgttatatt ttcttttaag acattaattt agtaatttta tatttgggaa aataaagggt
 6720
 tttaatttta tttaactgga atcactgccc tgctgtaatt aaacattctg taccacatct
 6780
 gtattaaaaa gacattgctg accattaaaa aaaaaa
 6816

<210> 158
 <211> 1572
 <212> PRT
 <213> Homo sapiens

<400> 158
 Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
 1 5 10 15
 Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
 20 25 30
 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
 35 40 45
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
 50 55 60
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
 65 70 75 80
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
 85 90 95
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
 100 105 110
 Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
 115 120 125
 Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
 130 135 140
 Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
 145 150 155 160
 Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
 165 170 175
 Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
 180 185 190
 Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
 195 200 205
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
 210 215 220
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
 225 230 235 240
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
 245 250 255
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly

Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr
		275					280					285			
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu
	290					295					300				
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser
305					310					315					320
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile
				325					330					335	
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val
			340					345					350		
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His
		355					360					365			
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr
	370					375					380				
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu
385					390					395					400
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu
				405					410					415	
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu
			420					425					430		
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu
		435					440					445			
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr
	450					455					460				
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn
465					470					475					480
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys
				485					490					495	
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn
			500					505					510		
Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu
		515					520					525			
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile
	530					535					540				
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr
545					550					555					560
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn
			565						570					575	
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln
			580					585					590		
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu
		595					600					605			
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Glu
	610					615									

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        690                695                700
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser
705                710                715                720
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu
        725                730                735
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
        740                745                750
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
        755                760                765
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Ala Leu
        770                775                780
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785                790                795                800
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
        805                810                815
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
        820                825                830
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
        835                840                845
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
        850                855                860
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865                870                875                880
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
        885                890                895
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
        900                905                910
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
        915                920                925
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
        930                935                940
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945                950                955                960
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
        965                970                975
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
        980                985                990
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
        995                1000                1005
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
        1010                1015                1020
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025                1030                1035                1040
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
        1045                1050                1055
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
        1060                1065                1070
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
        1075                1080                1085
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
        1090                1095                1100
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105                1110                1115                1120
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg

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				1125				1130				1135			
Arg	Ser	Arg	Gly	Gly	Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val
			1140					1145					1150		
Ile	Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly
			1155					1160					1165		
Met	Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu
			1170					1175					1180		
Gln	Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala
1185															
Asp	Ile	Tyr	Lys	Leu	Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe
Glu	Arg	Leu	Ala	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Ala	Tyr	Ser	Lys
Val	Thr	Glu	Val	Met	His	Ser	Gly	Arg	Arg	Leu	Leu	Gly	Thr	Tyr	Phe
Arg	Val	Ala	Phe	Phe	Gly	Gln	Ala	Ala	Gln	Tyr	Gln	Phe	Thr	Asp	Ser
Glu	Thr	Asp	Val	Glu	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr
1265															
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Ile	Pro	Phe	Phe	Asp	Glu	Lys	Glu
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Ser	His	Asn	Ile	Arg	Arg
1345															
Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val
Ala	Glu	Leu	Arg	Gln	Leu	Cys	Ser	Ser	Ala	Glu	Val	Asp	Met	Ile	Lys
1425															
Leu	Gln	Leu	Lys	Leu	Gln	Gly	Ser	Val	Ser	Val	Gln	Val	Asn	Ala	Gly
Pro	Leu	Ala	Tyr	Ala	Arg	Ala	Phe	Leu	Asp	Asp	Thr	Asn	Thr	Lys	Arg
Tyr	Pro	Asp	Asn	Lys	Val	Lys	Leu	Leu	Lys	Glu	Val	Phe	Arg	Gln	Phe
Val	Glu	Ala	Cys	Gly	Gln	Ala	Leu	Ala	Val	Asn	Glu	Arg	Leu	Ile	Lys
Glu	Asp	Gln	Leu	Glu	Tyr	Gln	Glu	Glu	Met	Lys	Ala	Asn	Tyr	Arg	Glu
1505															
Met	Ala	Lys	Glu	Leu	Ser	Glu	Ile	Met	His	Glu	Gln	Ile	Cys	Pro	Leu
Glu	Glu	Lys	Thr	Ser	Val	Leu	Pro	Asn	Ser	Leu	His	Ile	Phe	Asn	Ala
Ile	Ser	Gly	Thr	Pro	Thr	Ser	Thr	Met	Val	His	Gly	Met	Thr	Ser	Ser

1555
Ser Ser Val Val
1570

1560

1565

<210> 159
<211> 540
<212> DNA
<213> Homo sapiens

<400> 159
gccggctctg ccattgtgctt actctgagcc acctaacctc ggcgtgcttc agtttactca
60
tccgctcatc tgcagaatgg gtgatgctgt cggctacttcg tggcatacag gaaagtgcgc
120
agcatgggtca gcctcagtga gaggtggcca gtgggggagtg gtggccactg tacacctggc
180
acagcccaga gatgcatgtg ccactctgtt gtgtgcttca accaaggggc gctctggcag
240
ggcttgggtg ggacttccca aagggcatgg aaaagttccc agtcaatgag atccatggag
300
acccatggga gtgggggtca gcccagcct aagaggaccc ccagccctgc cctgtgcccc
360
aggacacacc aggactgtc ccttgctgcc ttcccagaca acctgtaccc tccaggccac
420
cagttctcgt ccatgacaaa gaaaggagcc ttctaaataa gtgcccgcga gaggctgcac
480
gcttccctgc cccttccggg tggacctggg tttcaaagag aagctgccag tgcaacgcgt
540

<210> 160
<211> 110
<212> PRT
<213> Homo sapiens

<400> 160
Met Val Ser Leu Ser Glu Arg Trp Pro Val Gly Ser Gly Gly His Cys
1 5 10 15
Thr Pro Gly Thr Ala Gln Arg Cys Met Cys His Ser Val Val Cys Phe
20 25 30
Asn Gln Gly Ala Leu Trp Gln Gly Leu Gly Gly Thr Ser Gln Arg Ala
35 40 45
Trp Lys Ser Ser Gln Ser Met Arg Ser Met Glu Thr His Gly Ser Gly
50 55 60
Gly Gln Pro Gln Pro Lys Arg Thr Pro Ser Pro Ala Leu Cys Pro Arg
65 70 75 80
Thr His Gln Ala Leu Ser Leu Val Ala Phe Pro Asp Asn Leu Tyr Pro
85 90 95
Pro Gly His Gln Phe Ser Ser Met Thr Lys Lys Gly Ala Phe
100 105 110

<210> 161
<211> 351
<212> DNA
<213> Homo sapiens

<400> 161

nnacgcgtac gtcttttcggc cgaagaagga acgtgggcag gggcctcctt cgctggccgc
 60
 cgcgcttgcc tgcagcgcac gatgaagggc gacgacagca gcaagatcac ccacaagatc
 120
 gcccgggcga agcgcgaggg ccgcgtatgg tggagctttg agtacttccc gccgcgcacg
 180
 ccgcagggca tgcagaattt gtatgaccgt atcgagcgca tgagtcagct gggccccgag
 240
 tttgtggaca ttacgtggaa tgccgggggc cggacgtcgg atatgacgac gcagctggtc
 300
 aagacggtgc atgcgtactt tggtgtcgag acgtgcatgc atctgacgtg c
 351

<210> 162

<211> 117

<212> PRT

<213> Homo sapiens

<400> 162

Xaa	Arg	Val	Arg	Leu	Ser	Ala	Glu	Glu	Gly	Thr	Trp	Ala	Gly	Ala	Ser
1				5					10					15	
Phe	Ala	Gly	Arg	Arg	Ala	Trp	Leu	Ala	Ala	Thr	Met	Lys	Gly	Asp	Asp
			20				25						30		
Ser	Ser	Lys	Ile	Thr	His	Lys	Ile	Ala	Arg	Ala	Lys	Arg	Glu	Gly	Arg
		35				40					45				
Val	Trp	Trp	Ser	Phe	Glu	Tyr	Phe	Pro	Pro	Arg	Thr	Pro	Gln	Gly	Met
	50					55				60					
Gln	Asn	Leu	Tyr	Asp	Arg	Ile	Glu	Arg	Met	Ser	Gln	Leu	Gly	Pro	Glu
65				70					75					80	
Phe	Val	Asp	Ile	Thr	Trp	Asn	Ala	Gly	Gly	Arg	Thr	Ser	Asp	Met	Thr
			85					90					95		
Thr	Gln	Leu	Val	Lys	Thr	Val	His	Ala	Tyr	Phe	Gly	Val	Glu	Thr	Cys
		100					105						110		
Met	His	Leu	Thr	Cys											
		115													

<210> 163

<211> 360

<212> DNA

<213> Homo sapiens

<400> 163

gcgtgctcca tcggcacctt gcagatgggc gaattcgctg aaaacgtcgc cgggtggcgtc
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 gacacctaca ccctgcgtca gcccatcggc gtatgcgcag gcatcactcc gttcaacttc
 120
 ccggcgatga ttccactgtg gatgttcccg atggcgattg cctgcggtaa cactttcgtg
 180
 ctcaaaccgt ccgaacaaga ccctctgtcg acgatgctgc tggtagaact ggcgctggaa
 240
 gccggtgtgc cggccggcgt gctcaacgtg gtgcacggcg gcaaggatgt ggtggatgcg
 300

ctgtgcaccc ataaagatat caaggcagtt tctttcgctg gttcgaccgc cgttggtacc
360

<210> 164

<211> 120

<212> PRT

<213> Homo sapiens

<400> 164

Ala	Cys	Ser	Ile	Gly	Thr	Leu	Gln	Met	Gly	Glu	Phe	Ala	Glu	Asn	Val
1				5					10					15	
Ala	Gly	Gly	Val	Asp	Thr	Tyr	Thr	Leu	Arg	Gln	Pro	Ile	Gly	Val	Cys
			20					25					30		
Ala	Gly	Ile	Thr	Pro	Phe	Asn	Phe	Pro	Ala	Met	Ile	Pro	Leu	Trp	Met
		35				40					45				
Phe	Pro	Met	Ala	Ile	Ala	Cys	Gly	Asn	Thr	Phe	Val	Leu	Lys	Pro	Ser
	50					55					60				
Glu	Gln	Asp	Pro	Leu	Ser	Thr	Met	Leu	Leu	Val	Glu	Leu	Ala	Leu	Glu
65					70					75				80	
Ala	Gly	Val	Pro	Ala	Gly	Val	Leu	Asn	Val	Val	His	Gly	Gly	Lys	Asp
				85				90						95	
Val	Val	Asp	Ala	Leu	Cys	Thr	His	Lys	Asp	Ile	Lys	Ala	Val	Ser	Phe
			100					105						110	
Val	Gly	Ser	Thr	Ala	Val	Gly	Thr								
		115					120								

<210> 165

<211> 728

<212> DNA

<213> Homo sapiens

<400> 165

gctagcagcc ttcacccctcc tagaggggca ggctcggcga caaggggagg ggggtgccccg
60
tcccagcgag ggacgcccgg ggctgggggt gccggtcgag cccggggcaa cagcttcacc
120
aagtttgga accgcaacgt cttcatgaag gacaacagct cttcttccag cacagactcc
180
cgctcccgt cctcctccag gtccccgacg cgccacttcc gcagaagtga ctcccactca
240
gactccgaca gtcctactc aggggaatgag tgtcaccctg tgggcgcgag gaaccgcccc
300
cctaagggcc ggggcggctg agggggccat atggatcggg gccgaggcag ggcgcagcgt
360
gggaagaggc acgatctggc gccaccaag cgcagtcgaa agaagatggc ggcgctggag
420
tgtgaggacc cggagcgaga gctgaagaag cagaagcggg cagcccgtt ccagcacgga
480
cactcccgcc gcctgcgect cgagcccctg gtgctgcaga tgagcagcct ggagagcagt
540
ggggctgacc ctgactggca ggagctgcag atcgtgggca cctgccctga catcaccaag
600
cactacctgc gcctcacctg tgccccgac ccgtccaccg tgcgcctgt ggcattccct
660

gtggcaggtt ttgaaaaagt cgctgtgcat ggtcaagtgc cactggaaag agaagcagga
 720
 ctacgcgt
 728

<210> 166
 <211> 242
 <212> PRT
 <213> Homo sapiens

<400> 166
 Ala Ser Ser Leu His Pro Pro Arg Gly Ala Gly Ser Ala Thr Arg Gly
 1 5 10 15
 Gly Gly Ala Pro Ser Gln Arg Gly Thr Pro Gly Ala Gly Gly Ala Gly
 20 25 30
 Arg Ala Arg Gly Asn Ser Phe Thr Lys Phe Gly Asn Arg Asn Val Phe
 35 40 45
 Met Lys Asp Asn Ser Ser Ser Ser Thr Asp Ser Arg Ser Arg Ser
 50 55 60
 Ser Ser Arg Ser Pro Thr Arg His Phe Arg Arg Ser Asp Ser His Ser
 65 70 75 80
 Asp Ser Asp Ser Ser Tyr Ser Gly Asn Glu Cys His Pro Val Gly Arg
 85 90 95
 Arg Asn Pro Pro Pro Lys Gly Arg Gly Gly Arg Gly Ala His Met Asp
 100 105 110
 Arg Gly Arg Gly Arg Ala Gln Arg Gly Lys Arg His Asp Leu Ala Pro
 115 120 125
 Thr Lys Arg Ser Arg Lys Lys Met Ala Ala Leu Glu Cys Glu Asp Pro
 130 135 140
 Glu Arg Glu Leu Lys Lys Gln Lys Arg Ala Ala Arg Phe Gln His Gly
 145 150 155 160
 His Ser Arg Arg Leu Arg Leu Glu Pro Leu Val Leu Gln Met Ser Ser
 165 170 175
 Leu Glu Ser Ser Gly Ala Asp Pro Asp Trp Gln Glu Leu Gln Ile Val
 180 185 190
 Gly Thr Cys Pro Asp Ile Thr Lys His Tyr Leu Arg Leu Thr Cys Ala
 195 200 205
 Pro Asp Pro Ser Thr Val Arg Pro Val Ala Phe Pro Val Ala Gly Phe
 210 215 220
 Glu Lys Val Ala Val His Gly Gln Val Pro Leu Glu Arg Glu Ala Gly
 225 230 235 240
 Leu Arg

<210> 167
 <211> 510
 <212> DNA
 <213> Homo sapiens

<400> 167
 nnacgcgtgg aaccagaact caggcccgtg tgaggagtct ggtttggaac acacggggcc
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 gcaacacaga attgtcaggt cctgtgccgt gaccaccaac cctcggggcca tgccaggtgc
 120

tgggtgagggg caggtggctc ccgccaggcg cctgctggcc tgaccgcact ccgtccacag
 180
 gtcctcatgg ggcctcctcg gctgggcttc gtgtccgect acctctcaca gccactgctc
 240
 gatggctttg ccatgggggc ctccgtgacc atcctgacct cgcagctcaa acacctgctg
 300
 ggcgtgcgga tcccgcggca ccagggggccc ggcatgggtg tcttcacatg gctgagcctg
 360
 ctgcgcggcg ccgggcaggc caacgtgtgc gacgtggtca ccagcacggt gtgcctggcg
 420
 gtgctgctag ccgcgaagga gctctcagac cgctaccgac accgcctgag ggtgccgctg
 480
 cccacggagc tgctgggtcat cgtgggtggcc
 510

<210> 168

<211> 128

<212> PRT

<213> Homo sapiens

<400> 168

Gly	Ala	Gly	Gly	Ser	Arg	Gln	Ala	Pro	Ala	Gly	Leu	Thr	Ala	Leu	Arg
1				5					10					15	
Pro	Gln	Val	Leu	Met	Gly	Val	Leu	Arg	Leu	Gly	Phe	Val	Ser	Ala	Tyr
			20					25					30		
Leu	Ser	Gln	Pro	Leu	Leu	Asp	Gly	Phe	Ala	Met	Gly	Ala	Ser	Val	Thr
		35					40					45			
Ile	Leu	Thr	Ser	Gln	Leu	Lys	His	Leu	Leu	Gly	Val	Arg	Ile	Pro	Arg
	50					55					60				
His	Gln	Gly	Pro	Gly	Met	Val	Val	Leu	Thr	Trp	Leu	Ser	Leu	Leu	Arg
65					70				75					80	
Gly	Ala	Gly	Gln	Ala	Asn	Val	Cys	Asp	Val	Val	Thr	Ser	Thr	Val	Cys
			85					90						95	
Leu	Ala	Val	Leu	Leu	Ala	Ala	Lys	Glu	Leu	Ser	Asp	Arg	Tyr	Arg	His
		100						105					110		
Arg	Leu	Arg	Val	Pro	Leu	Pro	Thr	Glu	Leu	Leu	Val	Ile	Val	Val	Ala
		115					120						125		

<210> 169

<211> 537

<212> DNA

<213> Homo sapiens

<400> 169

gaattccacc gcatgtcgtg tctggacgta tgtaggtcgc ggtagtgtgc gaccgccggt
 60
 gccttaaagg agagcgggca tcggcggttc agtacgagag gggaagggtg gcggatactt
 120
 attgtcgggtg cggcatcgtc catccacacc gttcgatggg tcaatggact ggtcaagcgg
 180
 ggtcacgagg ttacactggc atcagtccat ccggcggggc gtcactccat tgatccccga
 240
 gtccggatcc acctggcccc acacggcggg aaggcaaaat acgtcgtcaa tgccgggtgg
 300

ctgcgatcag tggcggctgg ggtgcaacct gacatcgtea acgtccacta tgcgaccggt
 360
 tatggtctgc tcgctcgtct tgcccatatt gacgccccga cgctgctgtc ggtgtgggga
 420
 agtgacgttt acgattcccc ccgggcaaatt cccctcatgc gtcacatggt ccgatccaac
 480
 ttggtctcag ctactcggat cgcacgcaca agccactgca tggcgcggtgt cacgcgt
 537

<210> 170
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 170
 Cys Ala Thr Ala Gly Ala Leu Lys Glu Ser Gly His Arg Arg Cys Ser
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 Thr Arg Gly Glu Gly Val Arg Ile Leu Ile Val Gly Ala Ala Ser Ser
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Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala	Leu					
	610					615					620									
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala	Ile					
625					630					635					640					
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg	Lys					
				645					650					655						
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro	Ala					
			660					665					670							
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val	Pro					
	675					680						685								
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg	Thr					
	690				695						700									
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr	Leu					
705					710					715					720					
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe	His					
			725						730					735						
Arg	Glu	Ser	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr	Leu						
			740				745					750								
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe	Leu					
	755						760					765								
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser	Met					
	770				775						780									
Pro	Trp	Ile	Leu	Thr	Asp	His	Ile	Leu	Glu	Thr	Lys	Glu	Ala	Ser	Met					
785					790					795					800					
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Asp	Leu	Tyr	Asn	Asp	Ser	Ala	His					
			805						810					815						
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile	Glu					
			820					825					830							
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala	Asp					
	835						840					845								
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu	Asp					
	850					855					860									
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His	Leu					
865					870					875					880					
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val	Gln					

980										985					990				
Pro	Asn	Tyr	Cys	Tyr	Asn	Gly	Ser	Thr	Asn	Arg	Phe	Val	Arg	Thr	Val				
995			1000					1005											
Leu	Pro	Phe	Ser	Gln	Glu	Phe	Gln	Arg	Asp	Lys	Gln	Pro	Asn	Ala	Gln				
1010			1015					1020											
Pro	Gln	Tyr	Leu	His	Gly	Ser	Lys	Ala	Leu	Asn	Leu	Ala	Tyr	Ser	Ser				
1025			1030					1035					1040						
Ile	Tyr	Gly	Ser	Tyr	Arg	Asn	Phe	Val	Gly	Pro	Pro	His	Phe	Gln	Val				
1045			1050					1055											
Ile	Cys	Arg	Leu	Leu	Gly	Tyr	Gln	Gly	Ile	Ala	Val	Val	Met	Glu	Glu				
1060			1065					1070											
Leu	Leu	Lys	Val	Val	Lys	Ser	Leu	Leu	Gln	Gly	Thr	Ile	Leu	Gln	Tyr				
1075			1080					1085											
Val	Lys	Thr	Leu	Met	Glu	Val	Met	Pro	Lys	Ile	Cys	Arg	Leu	Pro	Arg				
1090			1095					1100											
His	Glu	Tyr	Gly	Ser	Pro	Gly	Ile	Leu	Glu	Phe	Phe	His	His	Gln	Leu				
1105			1110					1115					1120						
Lys	Asp	Ile	Val	Glu	Tyr	Ala	Glu	Leu	Lys	Thr	Val	Cys	Phe	Gln	Asn				
1125			1130					1135											
Leu	Arg	Glu	Val	Gly	Asn	Ala	Ile	Leu	Phe	Cys	Leu	Leu	Ile	Glu	Gln				
1140			1145					1150											
Ser	Leu	Ser	Leu	Glu	Glu	Val	Cys	Asp	Leu	Leu	His	Ala	Ala	Pro	Phe				
1155			1160					1165											
Gln	Asn	Ile	Leu	Pro	Arg	Val	His	Val	Lys	Glu	Gly	Glu	Arg	Leu	Asp				
1170			1175					1180											
Ala	Lys	Met	Lys	Arg	Leu	Glu	Ser	Lys	Tyr	Ala	Pro	Leu	His	Leu	Val				
1185			1190					1195					1200						
Pro	Leu	Ile	Glu	Arg	Leu	Gly	Thr	Pro	Gln	Gln	Ile	Ala	Ile	Ala	Arg				
1205			1210					1215											
Glu	Gly	Asp	Leu	Leu	Thr	Lys	Glu	Arg	Leu	Cys	Cys	Gly	Leu	Ser	Met				
1220			1225					1230											
Phe	Glu	Val	Ile	Leu	Thr	Arg	Ile	Arg	Ser	Phe	Leu	Asp	Asp	Pro	Ile				
1235			1240					1245											
Trp	Arg	Gly	Pro	Leu	Pro	Ser	Asn	Gly	Val	Met	His	Val	Asp	Glu	Cys				
1250			1255					1260											
Val	Glu	Phe	His	Arg	Leu	Trp	Ser	Ala	Met	Gln	Phe	Val	Tyr	Cys	Ile				
1265			1270					1275					1280						
Pro	Val	Gly	Thr	His	Glu	Phe	Thr	Val	Glu	Gln	Cys	Phe	Gly	Asp	Gly				
1285			1290					1295											
Leu	His	Trp	Ala	Gly	Cys	Met	Ile	Ile	Val	Leu	Leu	Gly	Gln	Gln	Arg				
1300			1305					1310											
Arg	Phe	Ala	Val	Leu	Asp	Phe	Cys	Tyr	His	Leu	Leu	Lys	Val	Gln	Lys				
1315			1320					1325											
His	Asp	Gly	Lys	Asp	Glu	Ile	Ile	Lys	Asn	Val	Pro	Leu	Lys	Lys	Met				
1330			1335					1340											
Val	Glu	Arg	Ile	Arg	Lys	Phe	Gln	Ile	Leu	Asn	Asp	Glu	Ile	Ile	Thr				
1345			1350					1355					1360						
Ile	Leu	Asp	Lys	Tyr	Leu	Lys	Ser	Gly	Asp	Gly	Glu	Gly	Thr	Pro	Val				
1365			1370					1375											
Glu	His	Val	Arg	Cys	Phe	Gln	Pro	Pro	Ile	His	Gln	Ser	Leu	Ala	Ser				
1380			1385					1390											
Ser																			

<210> 177
 <211> 417
 <212> DNA
 <213> Homo sapiens

<400> 177
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 60
 gcagttcgtg gcgcgcatag tttctggcat gcttcgcgca tcttgagac cgatcccgcc
 120
 gctgccgtga aaccgcctaa aaatgtgaag cgattgcca aagccgtgtc cgtggagcaa
 180
 atgcaaaagc tccttgccat acccagtctt aagactccta ccggcctgcg taatcgagcg
 240
 atacttgagt tcttatatgc taccggcgcg cgctgagcg agatgctggc aacagacctg
 300
 gacgatatac acctgggcca aaaaccccgcg gatgaaaacg gggaatctat tgcacttccc
 360
 ggggtatgtgc gccttttttg aaagggaggt aaagagcggt tagtcccttt gggatcc
 417

<210> 178
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 178
 Thr Arg Asp Val Thr Leu Pro Leu Pro Leu Gly Pro Asn Ser Ile Ala
 1 5 10 15
 Arg Thr Met Ala Ala Val Arg Gly Ala His Ser Phe Trp His Ala Ser
 20 25 30
 Arg Ile Leu Glu Thr Asp Pro Ala Ala Val Lys Pro Pro Lys Asn
 35 40 45
 Val Lys Arg Leu Pro Lys Ala Val Ser Val Glu Gln Met Gln Lys Leu
 50 55 60
 Leu Ala Ile Pro Ser Leu Lys Thr Pro Thr Gly Leu Arg Asn Arg Ala
 65 70 75 80
 Ile Leu Glu Phe Leu Tyr Ala Thr Gly Ala Arg Val Ser Glu Met Leu
 85 90 95
 Ala Thr Asp Leu Asp Asp Ile His Leu Gly Glu Lys Pro Arg Asp Glu
 100 105 110
 Asn Gly Glu Ser Ile Ala Leu Pro Gly Tyr Val Arg Leu Phe Gly Lys
 115 120 125
 Gly Gly Lys Glu Arg Leu Val Pro Leu Gly Ser
 130 135

<210> 179
 <211> 362
 <212> DNA
 <213> Homo sapiens

<400> 179
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 60

aggtgattgc ccgtgggttg atggtggaag atcccccatc cccaagaatc cgggaattcg
 120
 ccattggggcc gggcagcccg aatccaaaat gtcggggcac gccagtgagg agtatggtaa
 180
 gggggcggca ccgatgttgg nggcagcata cggatggaag tgctgggcga ggcctgggt
 240
 ttgccggcag agcaactggg gcagctcaag gcgggcgggg tgatcgagca gttggattga
 300
 gcaatggcgg ccgcgaagcc cgccatttac cttgatgact gtttagcgcg cggattcttt
 360
 aa
 362

<210> 180
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Ala Gly Phe Ala Ala Ala Ile Ala Gln Ser Asn Cys Ser Ile Thr
 1 5 10 15
 Pro Pro Ala Leu Ser Cys Pro Ser Cys Ser Ala Gly Lys Pro Arg Arg
 20 25 30
 Ser Pro Ser Thr Ser Ile Arg Met Leu Pro Pro Thr Ser Val Pro Ala
 35 40 45
 Pro Tyr His Thr Pro Thr Gly Arg Ala Pro Thr Phe Trp Ile Arg Ala
 50 55 60
 Ala Arg Pro Asn Gly Glu Phe Pro Asp Ser Trp Gly Cys Gly Ile Phe
 65 70 75 80
 His His Gln Pro Thr Gly Asn His Leu Arg Leu Phe Gln Gly Leu Arg
 85 90 95
 Asp Val Ile Asp Arg Pro His Arg His Leu Arg Arg
 100 105

<210> 181
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 181
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 60
 ccgattcact tgtcgggtaca ggccaatacg gtgaattggg ccagcgtcga gttctggcaa
 120
 cagcaaggta tctgccgggt aatcctgtcg cgggaattgt cactggaaga aatcggcgaa
 180
 atccgccaac aggtgccggc catggagctg gaagtgtttg tgcacgggtg cctgtacatg
 240
 gcctattccg ggcgctgttt gttgtccggc tatatgaaca agcgcgatgc caaccaa
 297

<210> 182
 <211> 99
 <212> PRT

<213> Homo sapiens

<400> 182

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Ala Leu Ile Met Ser Asp Pro Gly Leu Ile Met Leu Val Arg Arg His
 1             5             10             15
Phe Pro Cys Met Pro Ile His Leu Ser Val Gln Ala Asn Thr Val Asn
      20             25             30
Trp Ala Ser Val Glu Phe Trp Gln Gln Gly Ile Cys Arg Val Ile
      35             40             45
Leu Ser Arg Glu Leu Ser Leu Glu Glu Ile Gly Glu Ile Arg Gln Gln
      50             55             60
Val Pro Ala Met Glu Leu Glu Val Phe Val His Gly Ala Leu Tyr Met
      65             70             75             80
Ala Tyr Ser Gly Arg Cys Leu Leu Ser Gly Tyr Met Asn Lys Arg Asp
      85             90             95
Ala Asn Gln

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<210> 183

<211> 351

<212> DNA

<213> Homo sapiens

<400> 183

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cgggacgtca ccatgaagcc gaccggctcg ggggatgtgg cgaacaaggt catcacccat
60
attccgttta acatcgcttc ccaggcgact catccattcc ttcgtacctt ggacgatgtc
120
aagcgcattc ctttggcgac cgacgggctc ggccaccagg tcttgetcaa gggctaccag
180
gccgagggcc acgactacgc acaccccgac tacggcggca acgtctccca cctgcccggc
240
gggatgaagg atctcgagaa gtcaccgag tcgggcaggc agtggaacac cgatttcggc
300
attcacgtca acctggtgga gtcctatcct gaggcgaatc acttcggcga c
351

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<210> 184

<211> 117

<212> PRT

<213> Homo sapiens

<400> 184

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Arg Asp Val Thr Met Lys Pro Thr Gly Ser Gly Asp Val Ala Asn Lys
 1             5             10             15
Val Ile Thr His Ile Pro Phe Asn Ile Val Ser Gln Ala Thr His Pro
      20             25             30
Phe Leu Arg Thr Leu Asp Asp Val Lys Arg Ile Ser Leu Ala Thr Asp
      35             40             45
Gly Leu Gly His Gln Val Leu Leu Lys Gly Tyr Gln Ala Glu Gly His
      50             55             60
Asp Tyr Ala His Pro Asp Tyr Gly Gly Asn Val Ser His Arg Ala Gly
      65             70             75             80
Gly Met Lys Asp Leu Glu Lys Leu Thr Glu Ser Gly Arg Gln Trp Asn

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			85					90				95			
Thr	Asp	Phe	Gly	Ile	His	Val	Asn	Leu	Val	Glu	Ser	Tyr	Pro	Glu	Ala
			100					105					110		
Asn	His	Phe	Gly	Asp											
			115												

<210> 185
 <211> 396
 <212> DNA
 <213> Homo sapiens

<400> 185
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 gctgttggtg gcattgtggt ttatgcaggc catgaaacca aagcaatgct gaacaacagt
 120
 gggccacggt ataagcgcag caaattagaa agaagagcaa acacagatgt cctctggtgt
 180
 gtcattgcttc tggtcataat gtgcttaact ggcgagtag gtcattggaat ctggctgagc
 240
 aggtatgaaa agatgcattt tttcaatgtt cccgagcctg atggacatat catatcacca
 300
 ctggtggcag gattttatat gttttggacc gtgatcattt tgttacaggt cttgattcct
 360
 atttctctct atgtttccat cgaaattgtg aagctt
 396

<210> 186
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 186
 Arg Val Gly Leu Ser Lys Glu Asn Leu Leu Arg Gly Cys Thr Ile
 1 5 10 15
 Arg Asn Thr Glu Ala Val Val Gly Ile Val Val Tyr Ala Gly His Glu
 20 25 30
 Thr Lys Ala Met Leu Asn Asn Ser Gly Pro Arg Tyr Lys Arg Ser Lys
 35 40 45
 Leu Glu Arg Arg Ala Asn Thr Asp Val Leu Trp Cys Val Met Leu Leu
 50 55 60
 Val Ile Met Cys Leu Thr Gly Ala Val Gly His Gly Ile Trp Leu Ser
 65 70 75 80
 Arg Tyr Glu Lys Met His Phe Phe Asn Val Pro Glu Pro Asp Gly His
 85 90 95
 Ile Ile Ser Pro Leu Leu Ala Gly Phe Tyr Met Phe Trp Thr Val Ile
 100 105 110
 Ile Leu Leu Gln Val Leu Ile Pro Ile Ser Leu Tyr Val Ser Ile Glu
 115 120 125
 Ile Val Lys Leu
 130

<210> 187
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 187

cgagtgtca ccgcgtcagc cgtcatgcgt cccactgagg ctgttgtctc tcggtcggca
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 gaacctcgac gagttcagcg gatcctggac cagcgcgagt gggctggcgt cttcgttgct
 120
 gatgagcatc gtcgtttgct tggcacggtc ggcgatcaag aggtcatcga ggctgctcgc
 180
 cgcgagatc gcagtattgc tgacgcggtg gaaactaacg gcatactcac ggcgcgagacc
 240
 gacactccgt tgtccgagct cttcgtcccg accagcaacg ccagggtgcc gttggccggt
 300
 gtcgacgagg acttccacct catgggtgtc atctctcggg tgaccctgct cgacgcgatg
 360
 tcacgagctc gcgacgaggc aggagagggg tctgtcatgt ccttgagaga caccggaag
 420
 ctt
 423

<210> 188

<211> 141

<212> PRT

<213> Homo sapiens

<400> 188

Arg	Val	Leu	Thr	Ala	Ser	Ala	Val	Met	Arg	Pro	Thr	Glu	Ala	Val	Val
1				5				10					15		
Ser	Arg	Ser	Ala	Glu	Pro	Arg	Arg	Val	Gln	Arg	Ile	Leu	Asp	Gln	Arg
		20					25					30			
Glu	Trp	Ala	Gly	Val	Phe	Val	Val	Asp	Glu	His	Arg	Arg	Leu	Leu	Gly
	35					40					45				
Thr	Val	Gly	Asp	Gln	Glu	Val	Ile	Glu	Ala	Ala	Arg	Arg	Gly	Asp	Arg
	50				55					60					
Ser	Ile	Ala	Asp	Ala	Val	Glu	Thr	Asn	Gly	Ile	Leu	Thr	Ala	Arg	Thr
65				70				75					80		
Asp	Thr	Pro	Leu	Ser	Glu	Leu	Phe	Ala	Pro	Thr	Ser	Asn	Ala	Arg	Val
			85					90					95		
Pro	Leu	Ala	Val	Val	Asp	Glu	Asp	Phe	His	Leu	Met	Gly	Val	Ile	Ser
		100						105					110		
Arg	Val	Thr	Leu	Leu	Asp	Ala	Met	Ser	Arg	Ala	Arg	Asp	Glu	Ala	Gly
		115				120						125			
Glu	Gly	Ser	Val	Met	Ser	Leu	Glu	Asn	Thr	Gly	Lys	Leu			
	130					135					140				

<210> 189

<211> 429

<212> DNA

<213> Homo sapiens

<400> 189

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aaatgtttga agatgccggc gtttccggcc tcaacttggt tcgatgccgt ggttccaccg
 120
 atttcgccga tgcggctcat cgcacgggta agaagtttcg tccagataac ccaggacaga
 180
 gcaaggtata tcaggctcag aaccaggaaa agcagggcct taccctcagtg ccccatatag
 240
 accgcgctag ctacggcaaa aggcgcgccc agtgggggtcc aggacagcac tttcatggct
 300
 gaagggagcg catcccnagc ttcgcctagc cccagagcta acccagcgac cagtggacca
 360
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 420
 ctgatttcn
 429

<210> 190
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Met Gly Ala Gly Pro Leu Val Ala Gly Leu Ala Leu Gly Leu Gly
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 Glu Ala Xaa Asp Ala Leu Pro Ser Ala Met Lys Val Leu Ser Trp Thr
 20 25 30
 Pro Leu Gly Ala Pro Phe Ala Val Ala Ser Ala Val Tyr Met Gly His
 35 40 45
 Trp Gly Lys Ala Leu Leu Phe Leu Val Leu Ser Leu Ile Tyr Leu Ala
 50 55 60
 Leu Ser Trp Val Ile Trp Thr Lys Leu Leu Asn Arg Ala Met Ser Arg
 65 70 75 80
 Ile Gly Glu Ile Gly Gly Thr Thr Ala Ser Lys Gln Val Glu Ala Gly
 85 90 95
 Asn Ala Gly Ile Phe Lys His Phe Thr Ala Ser Pro Arg Gly Ala Ile
 100 105 110
 Ala Ala Arg Thr Val His Met Leu Val Asn His
 115 120

<210> 191
 <211> 4845
 <212> DNA
 <213> Homo sapiens

<400> 191
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 60
 cctccggcct ctgcctccgg ccaggagttc tggcccgagc aatcggcggc cgatattctg
 120
 tcggggggcg cttcccgagc acggtatctt ctgtatgacg tcaaccccc ggaaggcttc
 180
 aacctgcgca gggatgtcta tatccgaatc gcctctctcc tgaagactct gctgaagacg
 240
 gaggagtggg tgcttgctct gcctccatgg ggccgctct atcactggca gagtcctgac
 300

atccaccagg tccggattcc ctggtctgag ttttttgatc ttccaagtct caataaaaac
360
atccccgtca tcgagtatga gcagttcatc gcagaatctg gtggggccctt tattgaccag
420
gttttacgtcc tgcaaagtta cgcagagggg tggaaagaag ggacctggga agagaagggtg
480
gacgagcggc cgtgtattga tcagctcctg tactcccagg acaagcacga gtactacaga
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660
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720
cgtcgcagca tgggtgtttgc caggcacctg cgggaggtgg gagacgagtt caggagcaga
780
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900
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960
cgcagcctca tgaagaccca ccggctggac aagggtgtttg tggccacaga tgccgtcaga
1020
aaggaatatg aagagctaaa aaagctgtta cccgagatgg tgaggtttga acccacgtgg
1080
gaggagctgg agctctacaa ggacggaggc gttgctgatta ttgaccagtg gatctgcgca
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1200
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1320
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1380
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1620
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1680
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1740
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1800
aaagacctgc ctgcccattc gcataggaga tgaaggctgg ggtaggggtg aaacgggttg
1860
agttaaatgg aaaatgaaag tagagggaaat gatcttccc gtgggttagca ctgtgcacac
1920

gcgtgcgtct ctgtgggtta gtctgtctct ctctgcccc aggaatgctg agcgccctga
1980
gccggtgcct cttcacacat ctgctatttc ctgtggtgtt ctgggcatgg tgtataagac
2040
ccacagaggc tccgggtgat gctgtctgct ggggtgtgggt ccctttccct gttaagcaga
2100
caggatgcag cgctgacttc ttaggtcagg gcggaggtgt gcaggagccc agtcacgagc
2160
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2220
ccgcagccca ggaagcctgc tgtggggagg ctctgcactg agctctcagc ctctgcccc
2280
cagctgcgcg aagcgctcgg ccagctcac tgaagctgcc ctgcctccgg gccggcgcgg
2340
cctgctctgg caggccctg tgtgtgggggt ggtgagggtc tccccaccag tgctgcaccc
2400
cgcagcagca tacaggcctg tgtggcctgc tggcctgtg gctctgtgta cagcgctgtg
2460
catgttacat ttgctctgga aacatctctg gggtttgctt gttcacgaag ttcataaagt
2520
gccgctggag agccagagac cagctgcgca ggagccggag gaacgggcag gccgctgacc
2580
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2640
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2700
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<210> 192
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 192
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 Ala Val Ser Trp Pro Pro Ala Ser Ala Ser Gly Gln Glu Phe Trp Pro
 20 25 30
 Gly Gln Ser Ala Ala Asp Ile Leu Ser Gly Ala Ala Ser Arg Arg Arg

	35						40						45					
Tyr	Leu	Leu	Tyr	Asp	Val	Asn	Pro	Pro	Glu	Gly	Phe	Asn	Leu	Arg	Arg			
	50					55					60							
Asp	Val	Tyr	Ile	Arg	Ile	Ala	Ser	Leu	Leu	Lys	Thr	Leu	Leu	Lys	Thr			
65					70					75					80			
Glu	Glu	Trp	Val	Leu	Val	Leu	Pro	Pro	Trp	Gly	Arg	Leu	Tyr	His	Trp			
				85					90					95				
Gln	Ser	Pro	Asp	Ile	His	Gln	Val	Arg	Ile	Pro	Trp	Ser	Glu	Phe	Phe			
			100					105					110					
Asp	Leu	Pro	Ser	Leu	Asn	Lys	Asn	Ile	Pro	Val	Ile	Glu	Tyr	Glu	Gln			
		115					120					125						
Phe	Ile	Ala	Glu	Ser	Gly	Gly	Pro	Phe	Ile	Asp	Gln	Val	Tyr	Val	Leu			
	130					135					140							
Gln	Ser	Tyr	Ala	Glu	Gly	Trp	Lys	Glu	Gly	Thr	Trp	Glu	Glu	Lys	Val			
145					150					155					160			
Asp	Glu	Arg	Pro	Cys	Ile	Asp	Gln	Leu	Leu	Tyr	Ser	Gln	Asp	Lys	His			
				165					170					175				
Glu	Tyr	Tyr	Arg	Gly	Trp	Phe	Trp	Gly	Tyr	Glu	Glu	Thr	Arg	Gly	Leu			
			180					185					190					
Asn	Val	Ser	Cys	Leu	Ser	Val	Gln	Gly	Ser	Ala	Ser	Ile	Val	Ala	Pro			
		195					200					205						
Leu	Leu	Leu	Arg	Asn	Thr	Ser	Ala	Arg	Ser	Val	Met	Leu	Asp	Arg	Ala			
	210					215					220							
Glu	Asn	Leu	Leu	His	Asp	His	Tyr	Gly	Gly	Lys	Glu	Tyr	Trp	Asp	Thr			
225					230					235					240			
Arg	Arg	Ser	Met	Val	Phe	Ala	Arg	His	Leu	Arg	Glu	Val	Gly	Asp	Glu			
				245					250					255				
Phe	Arg	Ser	Arg	His	Leu	Asn	Ser	Thr	Asp	Asp	Ala	Asp	Arg	Ile	Pro			
			260					265					270					
Phe	Gln	Glu	Asp	Trp	Met	Lys	Met	Lys	Val	Lys	Leu	Gly	Ser	Ala	Leu			
	275						280					285						
Gly	Gly	Pro	Tyr	Leu	Gly	Val	His	Leu	Arg	Arg	Lys	Asp	Phe	Ile	Trp			
	290					295					300							
Gly	His	Arg	Gln	Asp	Val	Pro	Ser	Leu	Glu	Gly	Ala	Val	Arg	Lys	Ile			
305					310					315					320			
Arg	Ser	Leu	Met	Lys	Thr	His	Arg	Leu	Asp	Lys	Val	Phe	Val	Ala	Thr			
				325					330					335				
Asp	Ala	Val	Arg	Lys	Glu	Tyr	Glu	Glu	Leu	Lys	Lys	Leu	Leu	Pro	Glu			
			340					345					350					
Met	Val	Arg	Phe	Glu	Pro	Thr	Trp	Glu	Glu	Leu	Glu	Leu	Tyr	Lys	Asp			
		355					360					365						
Gly	Gly	Val	Ala	Ile	Ile	Asp	Gln	Trp	Ile	Cys	Ala	His	Ala	Arg	Cys			
	370					375					380							
Leu	Pro	Thr	Ser	Leu	Ser	Ala	Glu	Ser	Gly	Ser	Gly	Gly	Phe	Gln	Arg			
385					390					395								

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<210> 193
<211> 350
<212> DNA
<213> Homo sapiens
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<400> 193

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gcgcagctgt acgacgagcc cttcgtcgte gcgctgcggg cgtcgcaccc gctggccgac
120
cgtgccagca tcagccccga ggaggtcaag ggcgagacca tgttgatgtt gggcacgggc
180
ccctggtttc cccggggcccg cgggtgggggt ttggcccga tttggcgcgt ttctccagcg
240
ccgttaaggg catacgccgc agtttcgagg gctcgtcgct ggagaccatc aagcacatcg
300
tggcttcggg catggcgtga cgggtggtgcc gcagctgtcc gtgccgcgcg
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<210> 194

<211> 116

<212> PRT

<213> Homo sapiens

<400> 194

Ala	Gly	Glu	Leu	Asp	Cys	Ala	Ile	Met	Ala	Glu	Pro	Phe	Pro	Asp	Thr
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Gly	Leu	Ala	Thr	Ala	Gln	Leu	Tyr	Asp	Glu	Pro	Phe	Val	Val	Ala	Leu
			20					25						30	
Arg	Ala	Ser	His	Pro	Leu	Ala	Asp	Arg	Ala	Ser	Ile	Ser	Pro	Glu	Glu
		35					40					45			
Val	Lys	Gly	Glu	Thr	Met	Leu	Met	Leu	Gly	Thr	Gly	Pro	Trp	Phe	Pro
	50					55					60				
Arg	Ala	Arg	Gly	Gly	Gly	Leu	Ala	Arg	Ile	Trp	Arg	Val	Ser	Pro	Ala
65					70				75					80	
Pro	Leu	Arg	Ala	Tyr	Ala	Ala	Val	Ser	Arg	Ala	Arg	Arg	Trp	Arg	Pro
			85					90						95	
Ser	Ser	Thr	Ser	Trp	Leu	Arg	Ala	Trp	Arg	Asp	Gly	Gly	Ala	Ala	Ala
			100					105						110	
Val	Arg	Ala	Ala												
			115												

<210> 195

<211> 495

<212> DNA

<213> Homo sapiens

<400> 195

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gaaatggttc gcttcgacga aagcgagact ctcgaccgcc ttgcatcggg cgtccttgaa
120
ccagaacttg gcgacgattt ggccgcccgc ctgctcgatt ctcacgggt tgcgtgcac
180
agcgagggat cgaactggct tgcctcgcta cccgtgatcg taggtcgcaa cacggaacag
240
tttcgcagca taccagacct tgcccgcgac cggatcgaca aactgcacca gttgagccat
300

cgcgaaatag cacgaaatcg cgagctcctg cgtgcccgcg ctgcgtcggg gcaggtgcgg
 360
 cactgccacg gcgacgcaca cctcggcaac atcgtcatga ttgacggcaa gccggtcctg
 420
 ttcgacgcga tcgaatttga tcctgatatc gcgacaacgg atgtgctgta cgatttcgcg
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 ttccctctga tggat
 495

<210> 196

<211> 165

<212> PRT

<213> Homo sapiens

<400> 196

Thr	Arg	Glu	Arg	Asp	Gly	Leu	Ala	Ile	Gly	Gly	Val	Gly	Pro	Val	Val
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Glu	Trp	Ala	Val	Glu	Met	Val	Arg	Phe	Asp	Glu	Ser	Glu	Thr	Leu	Asp
			20					25					30		
Arg	Leu	Ala	Ser	Gly	Val	Leu	Glu	Pro	Glu	Leu	Gly	Asp	Asp	Leu	Ala
		35					40					45			
Ala	Val	Leu	Leu	Asp	Ser	His	Arg	Val	Ala	Val	Ile	Ser	Glu	Gly	Ser
	50					55					60				
Asn	Trp	Leu	Ala	Ser	Leu	Pro	Val	Ile	Val	Gly	Arg	Asn	Thr	Glu	Gln
65					70					75				80	
Phe	Arg	Ser	Ile	Pro	Asp	Leu	Ala	Arg	Asp	Arg	Ile	Asp	Lys	Leu	His
				85					90					95	
Gln	Leu	Ser	His	Arg	Glu	Ile	Ala	Arg	Asn	Arg	Glu	Leu	Leu	Arg	Ala
			100					105					110		
Arg	Ala	Ala	Ser	Gly	Gln	Val	Arg	His	Cys	His	Gly	Asp	Ala	His	Leu
	115						120					125			
Gly	Asn	Ile	Val	Met	Ile	Asp	Gly	Lys	Pro	Val	Leu	Phe	Asp	Ala	Ile
	130					135					140				
Glu	Phe	Asp	Pro	Asp	Ile	Ala	Thr	Thr	Asp	Val	Leu	Tyr	Asp	Phe	Ala
145					150					155					160
Phe	Pro	Leu	Met	Asp											
					165										

<210> 197

<211> 402

<212> DNA

<213> Homo sapiens

<400> 197

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 120
 tcttcattag cattcaaaat tgcaactgac ccattcgtag gtaacttaac cttcttcctg
 180
 gtgtactcag gtgtaattaa ctctggtgat acagtattaa actctgtacg tcaaaaacgt
 240
 gaacgttttg gtcgtatcgt acagatgcac gctaataaac gtgaagaaat taaagaagtt
 300

cgtgcgggcg atatcgctgc agcaatcggc ttaaaagatg taactacggg tgaaccatta
 360
 tgtgctgtcg atgcaccaat cattcttgag cgtatggaat tc
 402

<210> 198
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 198
 Gln Ala Met Leu Asp Ala Val Val Glu Tyr Leu Pro Ala Pro Thr Asp
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 Ile Pro Ala Ile Lys Gly Ile Asn Pro Asp Glu Thr Glu Gly Glu Arg
 20 25 30
 His Ala Ser Asp Asp Glu Pro Phe Ser Ser Leu Ala Phe Lys Ile Ala
 35 40 45
 Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe Arg Val Tyr Ser Gly
 50 55 60
 Val Ile Asn Ser Gly Asp Thr Val Leu Asn Ser Val Arg Gln Lys Arg
 65 70 75 80
 Glu Arg Phe Gly Arg Ile Val Gln Met His Ala Asn Lys Arg Glu Glu
 85 90 95
 Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala Ala Ile Gly Leu Lys
 100 105 110
 Asp Val Thr Thr Gly Glu Pro Leu Cys Ala Val Asp Ala Pro Ile Ile
 115 120 125
 Leu Glu Arg Met Glu Phe
 130

<210> 199
 <211> 507
 <212> DNA
 <213> Homo sapiens

<400> 199
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 tatcgacaaa agaccaagcg accctggacg ttctagacag aactctgcta cgaggcctga
 120
 caatagtga atccccgaga acccagctat ggaagggttt ccagatgctc gaaggcctgt
 180
 cataccagag gttagggttaa actgtatgga gactttcgag gtgaaagttg actcgccggt
 240
 aaagcctgct cctaaagagg atttagatct gatagatcta tcctcagatt caacctcggt
 300
 gcctgaaaaa cactctatac tctcaacctc cgacagcgac tctcttgat ttgagcctct
 360
 tccctctctc agaatagtcg agagtgaaga agaagaggag acgatgaacc aaggcgatga
 420
 cggccctccc ggtaaaaatg ctgcctcttc tccctccatc cccagccatc cctccgtcct
 480
 cagcctgagc acagctccgc ttgtaca
 507

<210> 200
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 200
 Met Glu Gly Glu Glu Ala Ala Phe Leu Pro Glu Gly Pro Ser Ser Pro
 1 5 10 15
 Trp Phe Ile Val Ser Ser Ser Ser Ser Leu Ser Thr Ile Leu Arg Glu
 20 25 30
 Gly Arg Gly Ser Asn Thr Arg Glu Ser Leu Ser Glu Val Glu Ser Ile
 35 40 45
 Glu Cys Phe Ser Gly Pro Glu Val Glu Ser Glu Asp Arg Ser Ile Arg
 50 55 60
 Ser Lys Ser Ser Leu Gly Ala Gly Phe Thr Gly Glu Ser Thr Phe Thr
 65 70 75 80
 Ser Lys Val Ser Ile Gln Phe Asn Leu Thr Ser Gly Met Thr Gly Leu
 85 90 95
 Arg Ala Ser Gly Asn Pro Ser Ile Ala Gly Phe Ser Gly Ile Ser Leu
 100 105 110
 Leu Ser Gly Leu Val Ala Glu Phe Cys Leu Glu Arg Pro Gly Ser Leu
 115 120 125
 Gly Leu Cys Ala Ile Tyr Ala Ala Trp Val Gly Gly Phe Ser Met Ser
 130 135 140
 His Arg Ser Met His Asp Phe Thr Arg
 145 150

<210> 201
 <211> 527
 <212> DNA
 <213> Homo sapiens

<400> 201
 gatgtggcta ttatccctgt ttcccaggtg agaaacaggg tcagtgatag agctgggatg
 60
 tgtgacctgca ggctcaccag ccagtcccct cctcaccaag gatgatgttc tccgtggtga
 120
 gctggtcctt ggtctcctgg aactcgtggc gcacctgggc cagctgcgcc tcgaaggcat
 180
 ccttctccat ctctttggct agctgcaagt tctggagctg ctcgttgagg tctgtgatct
 240
 catccacctg ctgggtgagc gtgcgcttga ggaaggccac aatctccttc ttgttattgg
 300
 ccagctgctc aaactcctgg cggaacatct tctcctgcac agccagctca tcccacttcc
 360
 gctggtaccg ggctagccgg tcctccaggt ctcgatctg gatgtggtag aactccttca
 420
 tctccttggc cagaggcggc tccacggcca ccaccggctc cttcttgccc cttttcttct
 480
 tgacttcaag ctcttgcct gccttgetca cactcttttt gggaggc
 527

<210> 202

<211> 70
 <212> PRT
 <213> Homo sapiens

<400> 202
 Gly Arg Pro Gln Ser Pro Ser Cys Tyr Trp Pro Ala Ala Gln Thr Pro
 1 5 10 15
 Gly Gly Thr Ser Ser Pro Ala Gln Pro Ala His Pro Thr Ser Ala Gly
 20 25 30
 Thr Gly Leu Ala Gly Pro Pro Gly Leu Gly Ser Gly Cys Gly Arg Thr
 35 40 45
 Pro Ser Ser Pro Trp Pro Glu Ala Ala Pro Arg Pro Pro Pro Ala Pro
 50 55 60
 Ser Cys Pro Leu Ser Ser
 65 70

<210> 203
 <211> 304
 <212> DNA
 <213> Homo sapiens

<400> 203
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 cgacccaagg gagttgtcgt caccacacacc ggactcgaca gcttcgcact cgaccagcag
 120
 cgtcgattcc acgcagatca ccactctcga accctgcact tcgccacccc cagcttcgac
 180
 ggagccgtct tcgagtacct gcaggcattc ggtgtcggag ccaccatggt gatcgctccc
 240
 accgacatct acggcggcgc cgaactggca agtctcatcc gccgcgaaca cgtcactcac
 300
 gcgt
 304

<210> 204
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 204
 Xaa Ala Pro Val Val Met Asp Asn Ala Ala Tyr Val Val Tyr Thr Ser
 1 5 10 15
 Gly Ser Thr Gly Arg Pro Lys Gly Val Val Val Thr His Thr Gly Leu
 20 25 30
 Asp Ser Phe Ala Leu Asp Gln Gln Arg Arg Phe His Ala Asp His His
 35 40 45
 Ser Arg Thr Leu His Phe Ala Thr Pro Ser Phe Asp Gly Ala Val Phe
 50 55 60
 Glu Tyr Leu Gln Ala Phe Gly Val Gly Ala Thr Met Val Ile Val Pro
 65 70 75 80
 Thr Asp Ile Tyr Gly Gly Ala Glu Leu Ala Ser Leu Ile Arg Arg Glu
 85 90 95
 His Val Thr His Ala

100

<210> 205
 <211> 356
 <212> DNA
 <213> Homo sapiens

<400> 205
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 gcacaattaa atacagtgtt aactttatctt tcaccacaat caaaagataa agattttaatc
 120
 atgccagatc aacaagaaga aatagatatt ctgattgcaa ccgactgtat ttcagaagga
 180
 cagaacttac aagattgtga ttacttaata aactatgaca ttcattggaa tccagttcgt
 240
 atcattcaaa gatttggacg gattgatcga attgggtcga agaataaatg tgtacaatta
 300
 gttaactttt ggccagatat tacattagat gaatatattg atctaaaggg acgcgt
 356

<210> 206
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 206
 Xaa Asn Ser Ala Met Ile Thr Gly Ser Ile Glu Gly Lys Thr Thr Ile
 1 5 10 15
 Glu Gly Ile Asn Ala Gln Leu Asn Thr Val Leu Thr Leu Phe Ser Pro
 20 25 30
 Gln Ser Lys Asp Lys Asp Leu Ile Met Pro Asp Gln Gln Glu Glu Ile
 35 40 45
 Asp Ile Leu Ile Ala Thr Asp Cys Ile Ser Glu Gly Gln Asn Leu Gln
 50 55 60
 Asp Cys Asp Tyr Leu Ile Asn Tyr Asp Ile His Trp Asn Pro Val Arg
 65 70 75 80
 Ile Ile Gln Arg Phe Gly Arg Ile Asp Arg Ile Gly Ser Lys Asn Lys
 85 90 95
 Cys Val Gln Leu Val Asn Phe Trp Pro Asp Ile Thr Leu Asp Glu Tyr
 100 105 110
 Ile Asp Leu Lys Gly Arg
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<210> 207
 <211> 324
 <212> DNA
 <213> Homo sapiens

<400> 207
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 catggtgtgt gcacgtgtng cactgtgtgt ggatgcatgg taatgtgcac gtgtgcactg
 120

tgtgtggtgt gtatgcatgg tgtgtgcacg tgtgcactgt gtgtgtgtgt atgcatgtgt
 180
 gtgcacatgt gcactgtgtg gtgtgtatgc atggtgtgtg cacgtgtgca ctgtgtatgc
 240
 atgngtgtgt gcatgtgtgc actgtgtatg catagtgtgc acgtgtgcac tgtgtggtgt
 300
 gtatgcatgg taatgtgcac gtgt
 324

<210> 208
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 208
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met His Gly Val Cys Thr Cys Xaa Thr Val Cys Gly Cys
 20 25 30
 Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val
 35 40 45
 Cys Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Met Cys
 50 55 60
 Thr Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys
 65 70 75 80
 Met Xaa Val Cys Met Cys Ala Leu Cys Met His Ser Val His Val Cys
 85 90 95
 Thr Val Trp Cys Val Cys Met Val Met Cys Thr Cys
 100 105

<210> 209
 <211> 168
 <212> DNA
 <213> Homo sapiens

<400> 209
 nntccagag gttatgaggt tggaagcccg gtttttttca ggtgcagaaa aggtaccat
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 attcaagggt ccacgactcg cacctgcctt gccaatTTaa catggagtgg gatacagacc
 120
 gaatgtatac ctcatgcctg cagacagcca gaaaccccg cacacgcg
 168

<210> 210
 <211> 56
 <212> PRT
 <213> Homo sapiens

<400> 210
 Xaa Ser Arg Gly Tyr Glu Val Gly Ser Pro Val Phe Phe Arg Cys Arg
 1 5 10 15
 Lys Gly Tyr His Ile Gln Gly Ser Thr Thr Arg Thr Cys Leu Ala Asn
 20 25 30
 Leu Thr Trp Ser Gly Ile Gln Thr Glu Cys Ile Pro His Ala Cys Arg

35 40 45
 Gln Pro Glu Thr Pro Ala His Ala
 50 55

<210> 211
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 211
 tacatgggct ttgacacagt ggtggctgaa gctgcactaa ggggtgttgg aggcaatgct
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 cagctggcag ctcagaccct tgcacaccat ggaggaagcc tcccaccga cctgcagttc
 120
 tcaggagagg actcctcccc cacaccgtcc acatcccat ctgactctgc agggacctct
 180
 agtgcctcga cagatgaaga catggagacg gaggctgtca acgaaatcct ggaggacatt
 240
 ccggagcacg aggaggacta cctggactcc acgctggagg atgaagaagt cattattgct
 300
 gaatacttgt cctgcgttga aagtataagt tctgccngca aagaacaact gatc
 354

<210> 212
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 212
 Tyr Met Gly Phe Asp Thr Val Val Ala Glu Ala Ala Leu Arg Val Phe
 1 5 10 15
 Gly Gly Asn Val Gln Leu Ala Ala Gln Thr Leu Ala His His Gly Gly
 20 25 30
 Ser Leu Pro Pro Asp Leu Gln Phe Ser Gly Glu Asp Ser Ser Pro Thr
 35 40 45
 Pro Ser Thr Ser Pro Ser Asp Ser Ala Gly Thr Ser Ser Ala Ser Thr
 50 55 60
 Asp Glu Asp Met Glu Thr Glu Ala Val Asn Glu Ile Leu Glu Asp Ile
 65 70 75 80
 Pro Glu His Glu Glu Asp Tyr Leu Asp Ser Thr Leu Glu Asp Glu Glu
 85 90 95
 Val Ile Ile Ala Glu Tyr Leu Ser Cys Val Glu Ser Ile Ser Ser Ala
 100 105 110
 Xaa Lys Glu Gln Leu Ile
 115

<210> 213
 <211> 669
 <212> DNA
 <213> Homo sapiens

<400> 213
 attgcccaat ctcagagtgt ccaggaaagc ctggagagcc tggtgcagtc tattggggaa
 60

gttgaacaaa acctggaagg gaaacaggtg tcatcactct catcaggagt catccaggaa
 120
 gccttagcca caaatatgaa attgaagcag gacattgctc ggcaaaagag cagcttggag
 180
 gccacccgtg agatggtgac ccgattcatg gagacagcag acagtactac agcagcagtg
 240
 ctgcagggca aactggcaga ggtgagccag cggttcgaac agctctgtct acagcagcaa
 300
 gaaaaggaga gctccctaaa gaagcttcta ccccaggcag agatgtttga acacctctct
 360
 ggtaagctgc agcagttcat ggaaaacaaa agtcggatgc tggcctctgg aaatcagcca
 420
 gatcaagata ttacacattt cttccaacag atccaggagc tcaatttgga aatggaagac
 480
 caacaggaga acctagatac tcttgagcac ctggtcactg aactgagctc ttgtggcttt
 540
 gcgctggact tgtgccagca tcaggacagg gtacagaatc taagaaaaga cttcacagag
 600
 ctacagaaga cagttaaaga gagagagaaa gatgcatcat cttgccagga acagttggat
 660
 gaattccgg
 669

<210> 214
 <211> 223
 <212> PRT
 <213> Homo sapiens

<400> 214
 Ile Ala Gln Ser Gln Ser Val Gln Glu Ser Leu Glu Ser Leu Leu Gln
 1 5 10 15
 Ser Ile Gly Glu Val Glu Gln Asn Leu Glu Gly Lys Gln Val Ser Ser
 20 25 30
 Leu Ser Ser Gly Val Ile Gln Glu Ala Leu Ala Thr Asn Met Lys Leu
 35 40 45
 Lys Gln Asp Ile Ala Arg Gln Lys Ser Ser Leu Glu Ala Thr Arg Glu
 50 55 60
 Met Val Thr Arg Phe Met Glu Thr Ala Asp Ser Thr Thr Ala Ala Val
 65 70 75 80
 Leu Gln Gly Lys Leu Ala Glu Val Ser Gln Arg Phe Glu Gln Leu Cys
 85 90 95
 Leu Gln Gln Gln Glu Lys Glu Ser Ser Leu Lys Lys Leu Leu Pro Gln
 100 105 110
 Ala Glu Met Phe Glu His Leu Ser Gly Lys Leu Gln Gln Phe Met Glu
 115 120 125
 Asn Lys Ser Arg Met Leu Ala Ser Gly Asn Gln Pro Asp Gln Asp Ile
 130 135 140
 Thr His Phe Phe Gln Gln Ile Gln Glu Leu Asn Leu Glu Met Glu Asp
 145 150 155 160
 Gln Gln Glu Asn Leu Asp Thr Leu Glu His Leu Val Thr Glu Leu Ser
 165 170 175
 Ser Cys Gly Phe Ala Leu Asp Leu Cys Gln His Gln Asp Arg Val Gln
 180 185 190
 Asn Leu Arg Lys Asp Phe Thr Glu Leu Gln Lys Thr Val Lys Glu Arg

195 200 205
 Glu Lys Asp Ala Ser Ser Cys Gln Glu Gln Leu Asp Glu Phe Arg
 210 215 220

<210> 215
 <211> 814
 <212> DNA
 <213> Homo sapiens

<400> 215
 aaatttcgta cccgctccgg cacagtacga gcccttgacg atgtgagcct ggctattaag
 60
 agagggttcca tctcagccgt tatcggggcac tccggagccg gcaaattccac cctgggttcgc
 120
 ctcatcaacg gattagagac tcccacgcgt ggccgcgtct tggtagacgg caccgacgtc
 180
 tcgcagctct cggacaaagc gatgcgcccc ctacgcgcag acatcgggat gatcttccaa
 240
 cagttcaacc tattcggctc aaggaccatc tacgacaacg ttgcctatcc actcaagctg
 300
 gtcattgga agaaagcaga cgagaagaag cgcgtcaccg aattgctgag cttcgtcggg
 360
 ttgacgagca aagcctggga ccatccagac cagctctcgg gcggacagaa acagcgggtt
 420
 ggtattgccc gagcgctagc aactaaacca tcgattttgt tggctgacga gtccacctcg
 480
 gcgctggatc cagaaacgac agctgatgtc ctatccctgc tcaagcgggt caatgcggaa
 540
 ctaggggtga cggtcgtcgt catcaccac gagatggagg tcgtccgctc gattgccag
 600
 caggtctcgg tactagcagc tggccatctc gtcgagtctg gaagcgcccc ccaggtcttc
 660
 gtcattccac agtcagagac caccacgcgt ttcttggcga cgattatcgg ccagcaccgc
 720
 agtggggagg aacaggcacg gttgcagtcg gaaaaccag atgcacgact cgtcgacgtc
 780
 agttcgggtg ccagtcactc gttcggtgac gcgt
 814

<210> 216
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 216
 Lys Phe Arg Thr Arg Ser Gly Thr Val Arg Ala Leu Asp Asp Val Ser
 1 5 10 15
 Leu Ala Ile Lys Arg Gly Ser Ile Ser Ala Val Ile Gly His Ser Gly
 20 25 30
 Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Glu Thr Pro
 35 40 45
 Thr Arg Gly Arg Val Leu Val Asp Gly Thr Asp Val Ser Gln Leu Ser
 50 55 60
 Asp Lys Ala Met Arg Pro Leu Arg Ala Asp Ile Gly Met Ile Phe Gln

65					70					75				80
Gln	Phe	Asn	Leu	Phe	Gly	Ser	Arg	Thr	Ile	Tyr	Asp	Asn	Val	Ala Tyr
				85					90					95
Pro	Leu	Lys	Leu	Ala	His	Trp	Lys	Lys	Ala	Asp	Glu	Lys	Lys	Arg Val
			100					105					110	
Thr	Glu	Leu	Leu	Ser	Phe	Val	Gly	Leu	Thr	Ser	Lys	Ala	Trp	Asp His
		115					120					125		
Pro	Asp	Gln	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Val	Gly	Ile	Ala Arg
	130					135					140			
Ala	Leu	Ala	Thr	Lys	Pro	Ser	Ile	Leu	Leu	Ala	Asp	Glu	Ser	Thr Ser
145					150					155				160
Ala	Leu	Asp	Pro	Glu	Thr	Thr	Ala	Asp	Val	Leu	Ser	Leu	Leu	Lys Arg
				165				170					175	
Val	Asn	Ala	Glu	Leu	Gly	Val	Thr	Val	Val	Val	Ile	Thr	His	Glu Met
			180					185				190		
Glu	Val	Val	Arg	Ser	Ile	Ala	Gln	Gln	Val	Ser	Val	Leu	Ala	Ala Gly
	195						200					205		
His	Leu	Val	Glu	Ser	Gly	Ser	Ala	Arg	Gln	Val	Phe	Ala	His	Pro Gln
	210					215					220			
Ser	Glu	Thr	Thr	Gln	Arg	Phe	Leu	Ala	Thr	Ile	Ile	Gly	Gln	His Pro
225					230					235				240
Ser	Gly	Glu	Glu	Gln	Ala	Arg	Leu	Gln	Ser	Glu	Asn	Pro	Asp	Ala Arg
				245				250					255	
Leu	Val	Asp	Val	Ser	Ser	Val	Ala	Ser	His	Ser	Phe	Gly	Asp	Ala
			260					265					270	

<210> 217
 <211> 500
 <212> DNA
 <213> Homo sapiens

<400> 217
 nnacgcgtcg cgatgaaaga ggcgctgaaa ggtgccatcc agattccaac agtgactttt
 60
 agctctgaga agtccaatac tacagccctg gctgagttcg gaaaatacat tcataaagtc
 120
 ttctctacag tggtcagcac cagctttatc cagcatgaag tcgtggaaga gtatagccac
 180
 ctgttcacta tccaaggctc ggaccccgagc ttgcagccct acctgctgat ggctcacttt
 240
 gatgtggtgc ctgcccctga agaaggctgg gaggtgcccc cattctcttg gttggagcgt
 300
 gatggcggtca tctatggttg gggcacactg gacgacaaga actctgtgat ggcattactg
 360
 caggccttgg agtcctgct gatcaggaag tacatcccc gaagatcttt cttcatttct
 420
 ctgggccatg atgaggagtc atcagggaca ggggctcaga ggatctcagc cctgctacag
 480
 tcaaggggcg tccagctagc
 500

<210> 218
 <211> 166
 <212> PRT

<213> Homo sapiens

<400> 218

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Xaa Arg Val Ala Met Lys Glu Ala Leu Lys Gly Ala Ile Gln Ile Pro
 1           5           10           15
Thr Val Thr Phe Ser Ser Glu Lys Ser Asn Thr Thr Ala Leu Ala Glu
      20           25           30
Phe Gly Lys Tyr Ile His Lys Val Phe Pro Thr Val Val Ser Thr Ser
      35           40           45
Phe Ile Gln His Glu Val Val Glu Glu Tyr Ser His Leu Phe Thr Ile
      50           55           60
Gln Gly Ser Asp Pro Ser Leu Gln Pro Tyr Leu Leu Met Ala His Phe
65           70           75           80
Asp Val Val Pro Ala Pro Glu Glu Gly Trp Glu Val Pro Pro Phe Ser
      85           90           95
Gly Leu Glu Arg Asp Gly Val Ile Tyr Gly Trp Gly Thr Leu Asp Asp
      100          105          110
Lys Asn Ser Val Met Ala Leu Leu Gln Ala Leu Glu Leu Leu Leu Ile
      115          120          125
Arg Lys Tyr Ile Pro Arg Arg Ser Phe Phe Ile Ser Leu Gly His Asp
      130          135          140
Glu Glu Ser Ser Gly Thr Gly Ala Gln Arg Ile Ser Ala Leu Leu Gln
145          150          155          160
Ser Arg Gly Val Gln Leu
      165

```

<210> 219

<211> 361

<212> DNA

<213> Homo sapiens

<400> 219

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acgcgttgaa acgggtatat tggggatgac gccgctgtgc aatatgcgca aggccataca
60
caagggtccgc acgctcccat gtccctcggt ttcgacagtt cttttgcgcc gcattatggc
120
gaagccgtcg agattgcgcc tgatatcaag cgcatacacgg tcaacaaccc cagccccttc
180
acttttttcg gcaccaacag ttatctgatc ggccgcgata cgctggcatt gatcgatccc
240
ggtccgcttg acgaggccca tcacgcggcg ctgctgcgtg ccattgccgg ccggccggtc
300
agccatatct ttgtcagcca cacacaccgg gaccactcgc cagtcgcgac ggttttgaaa
360
g
361

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<210> 220

<211> 102

<212> PRT

<213> Homo sapiens

<400> 220

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Met Ala Asp Arg Pro Ala Gly Asn Gly Thr Gln Gln Arg Arg Val Met

```

```

1           5           10           15
Gly Leu Val Lys Arg Thr Gly Ile Asp Gln Cys Gln Arg Ile Ala Ala
20           25           30
Asp Gln Ile Thr Val Gly Ala Glu Lys Ser Glu Gly Ala Gly Val Val
35           40           45
Asp Arg Asp Ala Leu Asp Ile Arg Arg Asn Leu Asp Gly Phe Ala Ile
50           55           60
Met Arg Arg Lys Arg Thr Val Glu Asn Glu Gly His Gly Ser Val Arg
65           70           75           80
Thr Leu Cys Met Ala Leu Arg Ile Leu His Ser Gly Val Ile Pro Asn
85           90           95
Ile Pro Val Ser Thr Arg
100

```

<210> 221
 <211> 401
 <212> DNA
 <213> Homo sapiens

```

<400> 221
agatctctgt gtcgtcgggt gcaaagagga tgagcccaga tgcatatcag gggctccctc
60
ccacatccca cctgctcggg cagcccacgg cagccccaca ctgctgcagc acacctcgct
120
gcagctctgg ttctctctca gaaatatccc tgccaccctg ctaagccttg gccaacactg
180
caccctgtcc caatgcgggt ccagtgacca cacccccagg gcataaccctc ctacagagca
240
ttcccaaaaa aggctagagt agacaccagc ctgctccgta gggggcctcc accccattct
300
ccaaggcctc caccagggga cgcttggtga accagcatcc aggctgggcc cacctccctg
360
ctcagagtcc atgttctgtg acaagggtgg caactgggat t
401

```

<210> 222
 <211> 124
 <212> PRT
 <213> Homo sapiens

```

<400> 222
Met Asp Ser Glu Gln Gly Gly Gly Pro Gly Leu Asp Ala Gly Ser Pro
1           5           10           15
Gly Val Pro Gly Trp Arg Pro Trp Arg Met Gly Trp Arg Pro Pro Thr
20           25           30
Glu Gln Ala Gly Val Tyr Ser Ser Leu Phe Trp Glu Cys Ser Val Gly
35           40           45
Gly Tyr Ala Leu Gly Val Trp Ser Leu Glu Pro His Trp Asp Arg Val
50           55           60
Gln Cys Trp Pro Arg Leu Ser Arg Val Ala Gly Ile Phe Leu Arg Arg
65           70           75           80
Asn Gln Ser Cys Ser Glu Val Cys Cys Ser Ser Val Gly Leu Pro Trp
85           90           95
Ala Ala Arg Ala Gly Gly Met Trp Glu Gly Ala Pro Asp Met His Leu

```

100 105 110
 Gly Ser Ser Ser Leu Gln Pro Thr Thr Gln Arg Ser
 115 120

<210> 223
 <211> 331
 <212> DNA
 <213> Homo sapiens

<400> 223
 tcatgaaatc tgtgggcagt gaccaggag ggtatgggca ggccaacca ggttggtgtg
 60
 cccttgaagc cccacagacc tgccagggca gcagggcagt tgggagccgg agaacctgag
 120
 aaccaagcca ggctgcatgc aggaggctgg cacgtgaacg ctgcaggtgt tgccggcagc
 180
 cgtgggtgcct ggcagatagt gttegacccc cnaggacctt cttgctgggc agcccagtcc
 240
 aaaagctgtt cccgcttaag ccacccccac cgccttggcc acacctggca catgggtgaa
 300
 gcaagggcat ttcccggggc ttcctgttcc c
 331

<210> 224
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 224
 Met Pro Leu Leu His Pro Cys Ala Arg Cys Gly Gln Gly Gly Gly Gly
 1 5 10 15
 Gly Leu Ser Gly Asn Ser Phe Trp Thr Gly Leu Pro Ser Lys Lys Val
 20 25 30
 Leu Gly Gly Arg Thr Leu Ser Ala Arg His His Gly Cys Arg Gln His
 35 40 45
 Leu Gln Arg Ser Arg Ala Ser Leu Leu His Ala Ala Trp Leu Gly Ser
 50 55 60
 Gln Val Leu Arg Leu Pro Thr Ala Leu Leu Pro Trp Gln Val Cys Gly
 65 70 75 80
 Ala Ser Arg Ala His Gln Pro Gly Trp Ala Cys Pro Tyr Pro Pro Gly
 85 90 95
 Ser Leu Pro Thr Asp Phe Met
 100

<210> 225
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 225
 tgatcacggg cgtgagccac cagcccagca tcccttgcct ttcattcgca cctccacctc
 60
 cagaatgacc ctcattccct cctgcacaga cggtgacagc agtaactcct acaaacacca
 120

ccagactgat cttcaagagc agaggaactc ccaatcacga ttccaccccc gccgggctct
 180
 caaatcctcc agggctgcct gctatggggg agggaggcac actttgcttg gctctcaagg
 240
 cctcagccag cggggtccaa accaactccc agcctggcct caccatccca ccgccaaacc
 300
 tttgctcaca ctggccctc ttcttgaac atgggctn
 339

<210> 226
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Thr Leu Ile Pro Ser Cys Thr Asp Gly Asp Ser Ser Asn Ser Tyr
 1 5 10 15
 Lys His His Gln Thr Asp Leu Gln Glu Gln Arg Asn Ser Gln Ser Arg
 20 25 30
 Phe His Pro Arg Arg Ala Leu Lys Ser Ser Arg Ala Ala Cys Tyr Gly
 35 40 45
 Gly Gly Arg His Thr Leu Leu Gly Ser Gln Gly Leu Ser Gln Pro Gly
 50 55 60
 Pro Asn Gln Leu Pro Ala Trp Pro His His Pro Thr Ala Lys Pro Leu
 65 70 75 80
 Leu Thr Leu Ala Pro Leu Pro Gly Thr Trp Ala
 85 90

<210> 227
 <211> 353
 <212> DNA
 <213> Homo sapiens

<400> 227
 gtcgaccct tcgattgtgg cgaactccat ggctgctgcg ggcttgcgta ggctctcgag
 60
 tagctcgacg tcgggttcgc gagggctcgc agcgtggcca tgctgcttct tggatggttc
 120
 gggcaactcc tcgggggatt cgagcagttc ttggcgcacc tgctctggcg tcatcccga
 180
 ggccaggccg acaagtgctg cctcctgcc cccgtgagc gacgctgcc tgttgagtac
 240
 ggcgtcttca ctggtcaggg cgagcgcggt atcgaccagg ttggcgcca ggccgagaga
 300
 cagcatgtct gctcagtcgc ggtgatgact ggagtggcgg tctcctgcac ggg
 353

<210> 228
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 228
 Met Leu Ser Leu Gly Leu Asp Ala Asn Leu Val Asp Thr Ala Leu Ala

1		5		10		15									
Leu	Thr	Ser	Glu	Asp	Ala	Val	Leu	Asn	Met	Ala	Ala	Ser	Leu	Ser	Gly
		20						25					30		
Trp	Gln	Glu	Ala	Ala	Leu	Val	Gly	Leu	Ala	Ser	Gly	Met	Thr	Pro	Glu
		35					40					45			
Gln	Val	Arg	Gln	Glu	Leu	Leu	Glu	Ser	Pro	Glu	Glu	Leu	Pro	Glu	Pro
		50				55					60				
Ser	Lys	Lys	Gln	His	Gly	His	Ala	Ala	Ser	Pro	Arg	Glu	Pro	Asp	Val
65				70					75					80	
Glu	Leu	Leu	Glu	Ser	Leu	Arg	Arg	Pro	Ala	Ala	Ala	Met	Glu	Phe	Ala
			85					90					95		
Thr	Ile	Glu	Gly	Val	Asp										
			100												

<210> 229
 <211> 743
 <212> DNA
 <213> Homo sapiens

<400> 229
 nnggctaggg acacggcctc ctcctcaaca ggcagtgcct gtgcaggctc aggggcatca
 60
 tcaaagataa cacagggtcg gtcaggggct gctggctgct cctgccccag gactggctcc
 120
 aggatgggca aggctgcctc cctggtagcc agggggagag ggggaaggag caccagggag
 180
 tgggccagca ggtgtggcat cggccaggag gagatggagg ccagcagcag ccaagaccag
 240
 agtaaagtgt ctgccccagg ggtgctcaca gcccaggacc gggtagttgg aaagccagcc
 300
 cagcttggca ctcagcggag ccaggaggca gatgttcagg actgggagtt cagaaagagg
 360
 gattcccagg gcacttactc cagccgggat gcagaactcc aggaccagga attcggaaag
 420
 agagattcac tgggtacctc cagtagtcga gatgtaagcc ttggggactg ggaatttggg
 480
 aagagagatt ctctgggtgc ttatgccagc caagatgcc aacgagcagg ccaagatttg
 540
 gggaagaggg accaccatgg taggtacagc agccaggatg ccgatgagca ggactgggag
 600
 ttccagaaga gagatgtgtc actcggcacc tatggcagcc gggctgcgga gccacaggaa
 660
 caggagtttg ggaagagcgc ttggataagg gactacagca gtggtggcag ctccaggacc
 720
 cttgacgccc aggacagaag ctt
 743

<210> 230
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 230
 Xaa Ala Arg Asp Thr Ala Ser Ser Ser Thr Gly Ser Ala Cys Ala Gly

1				5					10					15					
Ser	Gly	Ala	Ser	Ser	Lys	Ile	Thr	Gln	Gly	Trp	Ser	Gly	Ala	Ala	Gly				
			20					25					30						
Cys	Ser	Cys	Pro	Arg	Thr	Gly	Ser	Arg	Met	Gly	Lys	Ala	Ala	Ser	Leu				
		35				40					45								
Val	Ala	Arg	Gly	Arg	Gly	Glu	Gly	Ser	Thr	Arg	Glu	Trp	Ala	Ser	Arg				
	50				55					60									
Cys	Gly	Ile	Gly	Gln	Glu	Met	Glu	Ala	Ser	Ser	Ser	Gln	Asp	Gln					
65				70				75					80						
Ser	Lys	Val	Ser	Ala	Pro	Gly	Val	Leu	Thr	Ala	Gln	Asp	Arg	Val	Val				
			85					90					95						
Gly	Lys	Pro	Ala	Gln	Leu	Gly	Thr	Gln	Arg	Ser	Gln	Glu	Ala	Asp	Val				
		100						105					110						
Gln	Asp	Trp	Glu	Phe	Arg	Lys	Arg	Asp	Ser	Gln	Gly	Thr	Tyr	Ser	Ser				
	115					120						125							
Arg	Asp	Ala	Glu	Leu	Gln	Asp	Gln	Glu	Phe	Gly	Lys	Arg	Asp	Ser	Leu				
	130				135						140								
Gly	Thr	Tyr	Ser	Ser	Arg	Asp	Val	Ser	Leu	Gly	Asp	Trp	Glu	Phe	Gly				
145				150						155					160				
Lys	Arg	Asp	Ser	Leu	Gly	Ala	Tyr	Ala	Ser	Gln	Asp	Ala	Asn	Glu	Gln				
			165					170					175						
Gly	Gln	Asp	Leu	Gly	Lys	Arg	Asp	His	His	Gly	Arg	Tyr	Ser	Ser	Gln				
	180							185					190						
Asp	Ala	Asp	Glu	Gln	Asp	Trp	Glu	Phe	Gln	Lys	Arg	Asp	Val	Ser	Leu				
	195						200					205							
Gly	Thr	Tyr	Gly	Ser	Arg	Ala	Ala	Glu	Pro	Gln	Glu	Gln	Glu	Phe	Gly				
	210				215						220								
Lys	Ser	Ala	Trp	Ile	Arg	Asp	Tyr	Ser	Ser	Gly	Gly	Ser	Ser	Arg	Thr				
225				230						235					240				
Leu	Asp	Ala	Gln	Asp	Arg	Ser													
			245																

<210> 231

<211> 431

<212> DNA

<213> Homo sapiens

<400> 231

acgcgttggc caccgagagg ctggcgaggg tgtgcagcac ggcgcagtgt ggcagggtcc
 60
 cagggtgcag cctgcgcage agctcctcca tcaccttgcg gatgaactgt cttcccacgg
 120
 ccaccaggac gccactcgcc gectgctgcc agtcccagac caggtccttc gtcttggtca
 180
 tctcgctgga ggccaggagg atgatggtgc tggctgtgtc cttgtccage tcaactggcg
 240
 gactgctcag gaccctctcc atggcctcca ggaccgctgc tcggtatggg tgtgccagct
 300
 tgtcatgctg ccgcagatac tcctcgagg cacggagcgt ctccaccctg ctggacgcc
 360
 tcaccgataa ggacccccctg gtgcaggagc aggtctgcag tgccctgtgc tccctcgggg
 420
 aggtgcggcc g
 431

<210> 232
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 232
 Met Ala Ser Ser Arg Val Glu Thr Leu Arg Ala Cys Glu Glu Tyr Leu
 1 5 10 15
 Arg Gln His Asp Lys Leu Ala His Pro Tyr Arg Ala Ala Val Leu Arg
 20 25 30
 Ala Met Glu Arg Val Leu Ser Ser Arg Ala Ser Glu Leu Asp Lys Asp
 35 40 45
 Thr Ala Ser Thr Ile Ile Leu Leu Ala Ser Ser Glu Met Thr Lys Thr
 50 55 60
 Lys Asp Leu Val Trp Asp Trp Gln Gln Ala Ala Ser Gly Val Leu Val
 65 70 75 80
 Ala Val Gly Arg Gln Phe Ile Ser Lys Val Met Glu Glu Leu Leu Arg
 85 90 95
 Arg Leu His Pro Gly Thr Leu Pro His Cys Ala Val Leu His Thr Leu
 100 105 110
 Ala Ser Leu Ser Val Ala Asn Ala
 115 120

<210> 233
 <211> 606
 <212> DNA
 <213> Homo sapiens

<400> 233
 acgcgttcag ggatgccaga aatctaactg ggtaataaaa agctgggaga acattccaga
 60
 aaggtgggca cccttagcat tcccaaaaag caccagccct cctcatcctt cccagcttct
 120
 gtgctggaat gcacccccat cggaaaggct cgaaaactca ggacacatta ggatcacctg
 180
 gaaagcattt gtcaaaacgc atctccctgc gggtcagggt ccaagttaaa atcaaacttc
 240
 aggtgatgct gactcagggt gctccagaaa cacctgggga agcagcactt tggaggctgc
 300
 ctctcacatc caccacacag caagtgggca gggagctagg taaatctcct tcccagttga
 360
 gaaggggctc ggagcaggca cagagaagag atacccttag aatgcaagtt gttcagctgc
 420
 gaaagtccag cctgcaggct tcctgggcaa gctagtgggc tgaagtatgc cacagcaaca
 480
 ggcttctaga gccggctgcc cagctcctac tctgcctctg ccactcactg actgtgtggt
 540
 cttgagcagg tcacctgtct gacttggtga gagctgacag gcacacactg ttagaggctt
 600
 acgcgt
 606

<210> 234

<211> 108
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met His Pro His Arg Lys Gly Ser Lys Thr Gln Asp Thr Leu Gly Ser
 1 5 10 15
 Pro Gly Lys His Leu Ser Lys Arg Ile Ser Leu Arg Val Arg Val Gln
 20 25 30
 Val Lys Ile Lys Leu Gln Val Met Leu Thr Gln Val Ala Pro Glu Thr
 35 40 45
 Pro Gly Glu Ala Ala Leu Trp Arg Leu Pro Leu Thr Ser Thr Pro Gln
 50 55 60
 Gln Val Gly Arg Glu Leu Gly Lys Ser Pro Ser Gln Leu Arg Arg Gly
 65 70 75 80
 Ser Glu Gln Ala Gln Arg Arg Asp Thr Leu Arg Met Gln Val Val Gln
 85 90 95
 Leu Arg Lys Ser Ser Leu Gln Ala Ser Trp Ala Ser
 100 105

<210> 235
 <211> 328
 <212> DNA
 <213> Homo sapiens

<400> 235
 cgaccgttga ctattctcta caaaccacaa agacaatgat tgatttaact gaatttagaa
 60
 atagcaaaca cttaaaacag cagcagtaca gagctgaaaa ccagattctt ttgaaagaga
 120
 ttgaaagtct agaggaagaa cgacttgatc tgaaaaaaaa aattcgccaa atggctcaag
 180
 aaagaggaaa aagaagggca acttcaggat taaccactgg ggacctgaac ctaactgaaa
 240
 acatttctca aggagataga ataagtgaag gaaaattgga tttattgagc ctcaaaaata
 300
 tgagtgaagc acaatcaaag aatgaatt
 328

<210> 236
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ile Asp Leu Thr Glu Phe Arg Asn Ser Lys His Leu Lys Gln Gln
 1 5 10 15
 Gln Tyr Arg Ala Glu Asn Gln Ile Leu Leu Lys Glu Ile Glu Ser Leu
 20 25 30
 Glu Glu Glu Arg Leu Asp Leu Lys Lys Lys Ile Arg Gln Met Ala Gln
 35 40 45
 Glu Arg Gly Lys Arg Arg Ala Thr Ser Gly Leu Thr Thr Gly Asp Leu
 50 55 60
 Asn Leu Thr Glu Asn Ile Ser Gln Gly Asp Arg Ile Ser Glu Arg Lys

65		70		75		80
Leu	Asp	Leu	Leu	Ser	Leu	Lys
		85		90		95
Glu						

<210> 237
 <211> 2059
 <212> DNA
 <213> Homo sapiens

<400> 237
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 gagcacgaag ccggcggtcca tagctacggc ccatacggtc atgtctgcca tggctccggt
 120
 gatgtcagac tgcacatgaa atcgggttacg gtaccccagg atcatcgcta ccgagtacac
 180
 cccgaacagc acccgctggg cgccgatcag cgtgagggag tgccccacca gtggcacttt
 240
 tcttagatag cggaacccat ccaccacatc cccagtcacc gttctcatcg tccgggaacg
 300
 atccaccagt ggcgggccaa gctcccgaag tgaaaactgc agcccctagg cgaccgagac
 360
 tgccaagagg gctgcggaga tgcagaaaat gatcgtgtcg gcgtgggtgca caggaatatg
 420
 gcgtccggca atcatgcgca ctgctgcagc aacaaccgca ccgatcatga gccctagcgg
 480
 ccaatcgttg gcatgattga cgatgccgtc aggtagtcgc gcttgctgat ggtgtattcc
 540
 aaccagcga ccaaggcggg gagcaaaaac cggttcaggc tcatcgcgat gagcaacca
 600
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 660
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 720
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 780
 cccgagccca gaacctgcca cagtcccctg agaacaccga cctgcagggt attccaggca
 840
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 900
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 960
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 1260

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 1380
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 1440
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 1560
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 1920
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 2040
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 2059

<210> 238
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 238
 Ala Glu Gln Lys Phe Cys Ala Arg Leu Pro Pro Ser Pro Pro Gly His
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 Val Leu Asp Gly Pro Cys Ser Cys Gly Ser Trp Val Ser Ser Glu Leu
 20 25 30
 Asp Ile Asn Ala Trp Ile Leu Gln Pro Ala Leu Pro Ser Phe Arg Arg
 35 40 45
 Gln Glu Ser Pro Gly His Ser Pro Pro Gly Pro Pro Gln Glu Gly Met
 50 55 60
 Lys Gly Met Pro Ser Ser Leu Val Pro Arg Ala Gln Pro Ser Pro Ser
 65 70 75 80
 Pro Pro Gly Gln Gly Gln Cys Gly Ile Phe Arg Phe Arg Pro Leu Trp
 85 90 95
 Ala Glu Pro Pro Cys Glu Cys Ser Tyr Cys Leu Cys Val Ala Val Thr
 100 105 110
 Ser Ile Cys Leu Leu Leu Ile Cys Gln Pro Ile Ala Ala Gly Ser Thr
 115 120 125
 Phe

<210> 239
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 239
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 ggtcagctgc ccctcctcca cttctgcttc tcggcggttac cccataccgt attggccgcg
 180
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 240
 atgccgacct cagcatcggc atctgcagtg atgagtgcgt atcgcgccac acgaaacgcc
 300
 cagcgcaacc gtgtcctcgc acgatacgaa gtgcttgggt atctcagctc tgggtacctat
 360
 ggtcgtgtat ataaagcaaa ggaacttn
 388

<210> 240
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 240
 Met Val Asp Trp Met Ser Gln Val Leu Val Val Ala Ala Ala Val Gly
 1 5 10 15
 Gln Leu Pro Leu Leu His Phe Cys Phe Ser Ala Leu Pro His Thr Val
 20 25 30
 Leu Ala Ala Cys Ser Pro Leu Asn Ala Ala Met Ser Ser Ser Pro Tyr
 35 40 45
 Arg Asn Asp Val Pro Ser Lys Met Pro Thr Ser Ala Ser Ala Ser Ala
 50 55 60
 Val Met Ser Ala Tyr Arg Ala Thr Arg Asn Ala Gln Arg Asn Arg Val
 65 70 75 80
 Leu Ala Arg Tyr Glu Val Leu Gly Tyr Leu Ser Ser Gly Thr Tyr Gly
 85 90 95
 Arg Val Tyr Lys Ala Lys Glu Leu
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<210> 241
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 241
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 tcccatctgg gggcccttag cacagtcctt gggacccac atgctgcctt tcaggctgat
 180

gtgggcaaac tcggcagccc agcctactcc cgggccatgg gccaccatct cagcttccct
 240
 ggggctaagc cgtgtgctct gaatcaaaag cagtagtggc atcggcggca ctggcgccat
 300
 gggaaacggg ttgacttgca caaccagcac
 330

<210> 242
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ala Pro Val Pro Pro Met Pro Leu Leu Leu Leu Ile Gln Ser Thr
 1 5 10 15
 Arg Leu Ser Pro Arg Glu Ala Glu Met Val Ala His Gly Pro Gly Val
 20 25 30
 Gly Trp Ala Ala Glu Phe Ala His Ile Ser Leu Lys Gly Ser Met Trp
 35 40 45
 Gly Pro Arg Asp Cys Ala Lys Gly Pro Gln Met Gly Arg Ala Lys Gly
 50 55 60
 Ala Trp Glu Gly Arg Cys Phe Pro Gln Ala Arg Pro Gly Ser Ser Ile
 65 70 75 80
 Pro Arg Ser Glu Ala Ser Ser Thr Ala Ser Val Pro Ala Ala Phe Asn
 85 90 95
 Ser Ala Pro Arg
 100

<210> 243
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 243
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 cacacaggcc accccgcccc cactgcgctc gtcgctaate ttccctataa cggtgcggta
 120
 cccgtactgc tacacatgct agatattctc ccctccttgc ggactacagt ggtgatgggtg
 180
 caggcagaag tagccgatcg attggctgcc acaccaggca gccgcattta cgggtgtcccc
 240
 agcgtcaaag tcaactttta cgggactgtc tcgcgtgcgg gagcaattgg acgcaatgtc
 300
 ttctggccgg ctcccaatgt tgattctggn
 330

<210> 244
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 244
 Xaa Pro Ser Leu Arg Val Ile Thr Lys Asp Ala Met His Val Thr Ala

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Glu Glu Ile Leu His Thr Gly His Pro Ala Pro Thr Ala Leu Val Ala
      20           25           30
Asn Leu Pro Tyr Asn Val Ala Val Pro Val Leu Leu His Met Leu Asp
      35           40           45
Ile Leu Pro Ser Leu Arg Thr Val Val Met Val Gln Ala Glu Val
      50           55           60
Ala Asp Arg Leu Ala Ala Thr Pro Gly Ser Arg Ile Tyr Gly Val Pro
65      70           75           80
Ser Val Lys Val Asn Phe Tyr Gly Thr Val Ser Arg Ala Gly Ala Ile
      85           90           95
Gly Arg Asn Val Phe Trp Pro Ala Pro Asn Val Asp Ser Gly
      100           105           110

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<210> 245
 <211> 355
 <212> DNA
 <213> Homo sapiens

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<400> 245
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120
gcgtgttgca gaaacagaag ttgaccgtcg gaggtaggcg gcattcgctt cggatcgaag
180
cgtccccagg catccatctc gagttgacga cgaaaatctt tccagtccac gccgtagggg
240
ganttggcaa ccacagcatc gaatttgtcc agaaggaagt ggtcgttggt gagggtattg
300
ccccattcaa tacgcgcac tccccggaag cgcgcctcta ttgcggccaa cgcgt
355

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<210> 246
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 246
Met Arg Val Leu Asn Gly Ala Ile Pro Ser Pro Thr Thr Thr Ser Phe
1           5           10           15
Trp Thr Asn Ser Met Leu Trp Leu Pro Xaa Pro Pro Thr Ala Trp Thr
      20           25           30
Gly Lys Ile Phe Val Val Asn Ser Arg Trp Met Pro Arg Asp Ala Ser
      35           40           45
Ile Arg Ser Glu Cys Arg Leu Pro Pro Thr Val Asn Phe Cys Phe Cys
      50           55           60
Asn Thr Leu His Ser Thr Phe Pro Arg Trp Val Trp Leu Pro Ser Ser
65      70           75           80
Ile Arg Ala Arg His Cys Phe Gln Val Thr Pro Ala Glu Val Asn Pro
      85           90           95
Lys Leu Gly Gly Gly
      100

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<210> 247
 <211> 333
 <212> DNA
 <213> Homo sapiens

<400> 247
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 gcctgggaca ccagcgctcgt gtccgagatc aagatgggag acaggtacga gacggtcagg
 120
 ttcttccact gctacaagcg cggagtggac cgcggtgttcg ttgaccaccc actgttcctg
 180
 gagaggggttt ggggaaagac cgaggagaag atctacgggc ctgacgctgg aacggactac
 240
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 300
 ctgagcctca acaacaaccc atacttctcc gga
 333

<210> 248
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 248
 Met Ala Ala Asn Gly His Arg Val Met Val Val Ser Pro Arg Tyr Asp
 1 5 10 15
 Gln Tyr Lys Asp Ala Trp Asp Thr Ser Val Val Ser Glu Ile Lys Met
 20 25 30
 Gly Asp Arg Tyr Glu Thr Val Arg Phe Phe His Cys Tyr Lys Arg Gly
 35 40 45
 Val Asp Arg Val Phe Val Asp His Pro Leu Phe Leu Glu Arg Val Trp
 50 55 60
 Gly Lys Thr Glu Glu Lys Ile Tyr Gly Pro Asp Ala Gly Thr Asp Tyr
 65 70 75 80
 Arg Asp Asn Gln Leu Arg Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu
 85 90 95
 Ala Pro Arg Ile Leu Ser Leu Asn Asn Asn Pro Tyr Phe Ser Gly
 100 105 110

<210> 249
 <211> 5503
 <212> DNA
 <213> Homo sapiens

<400> 249
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 120
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 180
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 240

cagaagttcg tcatgttcta cgacagcgag tatgatatcc gtgggcttca aagctttctg
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360
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420
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480
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 5503

<210> 250

<211> 927

<212> PRT

<213> Homo sapiens

<400> 250

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			20					25					30		
Phe	Val	Gln	Arg	Asn	Pro	Gly	Gly	Ser	Pro	Arg	Thr	Ala	Cys	His	Leu
		35					40					45			
Asn	Pro	Ser	Pro	Asp	Gly	Glu	Ala	Tyr	Thr	Leu	Ala	Ser	Arg	Pro	Pro
	50				55					60					
Val	Arg	Leu	Asn	Asp	Val	Met	Leu	Arg	Leu	Val	Thr	Glu	Leu	Arg	Trp
65				70					75					80	
Gln	Lys	Phe	Val	Met	Phe	Tyr	Asp	Ser	Glu	Tyr	Asp	Ile	Arg	Gly	Leu
			85					90					95		
Gln	Ser	Phe	Leu	Asp	Gln	Ala	Ser	Arg	Leu	Gly	Leu	Asp	Val	Ser	Leu
			100					105					110		
Gln	Lys	Val	Asp	Lys	Asn	Ile	Ser	His	Val	Phe	Thr	Ser	Leu	Phe	Thr
		115					120					125			
Thr	Met	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Tyr	Arg	Asp	Thr	Leu	Arg	Arg
	130					135					140				
Ala	Ile	Leu	Leu	Leu	Ser	Pro	Gln	Gly	Ala	His	Ser	Phe	Ile	Asn	Glu
145					150					155					160
Ala	Val	Glu	Thr	Asn	Leu	Ala	Ser	Lys	Asp	Ser	His	Trp	Val	Phe	Val
			165					170						175	
Asn	Glu	Glu	Ile	Ser	Asp	Pro	Glu	Ile	Leu	Asp	Leu	Val	His	Ser	Ala
		180					185					190			
Leu	Gly	Arg	Met	Thr	Val	Val	Arg	Gln	Ile	Phe	Pro	Ser	Ala	Lys	Asp
	195						200					205			
Asn	Gln	Lys	Cys	Thr	Arg	Asn	Asn	His	Arg	Ile	Ser	Ser	Leu	Leu	Cys
	210					215					220				
Asp	Pro	Gln	Glu	Gly	Tyr	Leu	Gln	Met	Leu	Gln	Ile	Ser	Asn	Leu	Tyr
225				230						235					240
Leu	Tyr	Asp	Ser	Val	Leu	Met	Leu	Ala	Asn	Ala	Phe	His	Arg	Lys	Leu
			245					250						255	
Glu	Asp	Arg	Lys	Trp	His	Ser	Met	Ala	Ser	Leu	Asn	Cys	Ile	Arg	Lys

														260				265				270				
Ser	Thr	Lys	Pro	Trp	Asn	Gly	Gly	Arg	Ser	Met	Leu	Asp	Thr	Ile	Lys											
														275				280				285				
Lys	Gly	His	Ile	Thr	Gly	Leu	Thr	Gly	Val	Met	Glu	Phe	Arg	Glu	Asp											
														290				295				300				
Ser	Ser	Asn	Pro	Tyr	Val	Gln	Phe	Glu	Ile	Leu	Gly	Thr	Thr	Tyr	Ser											
305															310				315				320			
Glu	Thr	Phe	Gly	Lys	Asp	Met	Arg	Lys	Leu	Ala	Thr	Trp	Asp	Ser	Glu											
														325				330				335				
Lys	Gly	Leu	Asn	Gly	Ser	Leu	Gln	Glu	Arg	Pro	Met	Gly	Ser	Arg	Leu											
														340				345				350				
Gln	Gly	Leu	Thr	Leu	Lys	Val	Val	Thr	Val	Leu	Glu	Glu	Pro	Phe	Val											
														355				360				365				
Met	Val	Ala	Glu	Asn	Ile	Leu	Gly	Gln	Pro	Lys	Arg	Tyr	Lys	Gly	Phe											
														370				375				380				
Ser	Ile	Asp	Val	Leu	Asp	Ala	Leu	Ala	Lys	Ala	Leu	Gly	Phe	Lys	Tyr											
385															390				395				400			
Glu	Ile	Tyr	Gln	Ala	Pro	Asp	Gly	Arg	Tyr	Gly	His	Gln	Leu	His	Asn											
														405				410				415				
Thr	Ser	Trp	Asn	Gly	Met	Ile	Gly	Glu	Leu	Ile	Ser	Lys	Arg	Ala	Asp											
														420				425				430				
Leu	Ala	Ile	Ser	Ala	Ile	Thr	Ile	Thr	Pro	Glu	Arg	Glu	Ser	Val	Val											
														435				440				445				
Asp	Phe	Ser	Lys	Arg	Tyr	Met	Asp	Tyr	Ser	Val	Gly	Ile	Leu	Ile	Lys											
														450				455				460				
Lys	Pro	Glu	Glu	Lys	Ile	Ser	Ile	Phe	Ser	Leu	Phe	Ala	Pro	Phe	Asp											
465															470				475				480			
Phe	Ala	Val	Trp	Ala	Cys	Ile	Ala	Ala	Ala	Ile	Pro	Val	Val	Gly	Val											
														485				490				495				
Leu	Ile	Phe	Val	Leu	Asn	Arg	Ile	Gln	Ala	Val	Arg	Ala	Gln	Ser	Ala											
														500				505				510				
Ala	Gln	Pro	Arg	Pro	Ser	Ala	Ser	Ala	Thr	Leu	His	Ser	Ala	Ile	Trp											
														515				520				525				
Ile	Val	Tyr	Gly	Ala	Phe	Val	Gln	Gln	Gly	Gly	Glu	Ser	Ser	Val	Asn											
														530				535				540				
Ser	Met	Ala	Met	Arg	Ile	Val	Met	Gly	Ser	Trp	Trp	Leu	Phe	Thr	Leu											
545															550				555				560			
Ile	Val	Cys	Ser	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Thr	Val											
														565				570				575				
Ser	Arg	Met	Asp	Asn	Pro	Ile	Arg	Thr	Phe	Gln	Asp	Leu	Ser	Lys	Gln											
														580				585				590				
Val	Glu	Met	Ser	Tyr	Gly	Thr	Val	Arg	Asp	Ser	Ala	Val	Tyr	Glu	Tyr											
														595				600				605				
Phe	Arg	Ala	Lys	Gly	Thr	Asn	Pro	Leu	Glu	Gln	Asp	Ser	Thr	Phe	Ala											
														610				615				620				
Glu	Leu	Trp	Arg	Thr	Ile	Ser	Lys	Asn	Gly	Gly	Ala	Asp	Asn	Cys	Val											
625															630				635				640			
Ser	Ser	Pro	Ser	Glu	Gly	Ile	Arg	Lys	Ala	Lys	Lys	Gly	Asn	Tyr	Ala											
														645				650				655				
Phe	Leu	Trp	Asp	Val	Ala	Val	Val	Glu	Tyr	Ala	Ala	Leu	Thr	Asp	Asp											
														660				665				670				
Asp	Cys	Ser	Val	Thr	Val	Ile	Gly	Asn	Ser	Ile	Ser	Ser	Lys	Gly	Tyr											

690	695	700
Arg Ile Leu Glu Leu Gln Asp Thr Gly Asp Leu Asp Val Leu Lys Gln		
705	710	715
Lys Trp Trp Pro His Met Gly Arg Cys Asp Leu Thr Ser His Ala Ser		720
	725	730
Ala Gln Ala Asp Gly Lys Ser Leu Lys Leu His Ser Phe Ala Gly Val		735
	740	745
Phe Cys Ile Leu Ala Ile Gly Leu Leu Leu Ala Cys Leu Val Ala Ala		750
	755	760
Leu Glu Leu Trp Trp Asn Ser Asn Arg Cys His Gln Glu Thr Pro Lys		765
	770	775
Glu Asp Lys Glu Val Asn Leu Glu Gln Val His Arg Arg Met Asn Ser		780
785	790	795
Leu Met Asp Glu Asp Ile Ala His Lys Gln Ile Ser Pro Ala Ser Ile		800
	805	810
Glu Leu Ser Ala Leu Glu Met Gly Gly Leu Ala Pro Thr Gln Thr Leu		815
	820	825
Glu Pro Thr Arg Glu Tyr Gln Asn Thr Gln Leu Ser Val Ser Thr Phe		830
	835	840
Leu Pro Glu Gln Ser Ser His Gly Thr Ser Arg Thr Leu Ser Ser Gly		845
	850	855
Pro Ser Ser Asn Leu Pro Leu Pro Leu Ser Ser Ser Ala Thr Met Pro		860
865	870	875
Ser Met Gln Cys Lys His Arg Ser Pro Asn Gly Gly Leu Phe Arg Gln		880
	885	890
Ser Pro Val Lys Thr Pro Ile Pro Met Ser Phe Gln Pro Val Pro Gly		895
	900	905
Gly Val Leu Pro Glu Ala Leu Asp Thr Ser His Gly Thr Ser Ile		910
	915	920
		925

<210> 251
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 251
 nngatcagcc gcggggtccg cgccctcgat tcggcggtgg agaccgagag tctgcgtgag
 60
 gacgtcaacg cgctcgaacg gctgcggttg gccgtgcgcg ccagcgtggt catcctcatc
 120
 gattaccacc attcgggtgac cctgctgctg cgggtgcgcg ggaactcacc tctggaacga
 180
 gagccctcg agggccgccc ccgtatcgat gcaagggttc ccgctctcgt cgagagcgcc
 240
 atcgccgagg gtggtctgcg ctccgatttc actcccgggc tcatcacgcg t
 291

<210> 252
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 252
 Xaa Ile Ser Arg Gly Val Arg Ala Leu Asp Ser Ala Val Glu Thr Glu

```

      1           5           10           15
Ser Leu Arg Glu Asp Val Asn Ala Leu Glu Arg Leu Arg Leu Ala Val
      20           25           30
Arg Ala Ser Val Val Ile Leu Ile Glu Tyr His His Ser Val Thr Leu
      35           40           45
Leu Leu Arg Val Arg Gly Asn Ser Pro Leu Glu Arg Glu Ala Leu Glu
      50           55           60
Ala Arg Arg Arg Ile Asp Ala Lys Val Pro Ala Leu Val Glu Ser Ala
65           70           75           80
Ile Ala Glu Gly Gly Leu Arg Ser Asp Phe Thr Pro Gly Leu Ile Thr
      85           90           95
Arg

```

<210> 253
 <211> 327
 <212> DNA
 <213> Homo sapiens

```

<400> 253
gtgcacggat gggagcgcctc gcgcgcgtgc tggcgccttc acagcccggc gagcggcgtg
60
cgctcacggg cctgtaccga ccgatctcgc aaccttcgcg agaccgatcc accaaccgcg
120
cccacatgtc ggcagtgatg gcgggcacct tgcgggagaa ggccgggaag gtcgagcgag
180
ccaatgaccg tcgcacgggc ggcacgctcc acgagcggga cgagaagctc gcggcaggac
240
gctcactcgt cgcgggtgtcc tccgcggtct ccataccggt ccctgcgaca tggaacgccc
300
acgacttcgg acggcgactc gacgcgt
327

```

<210> 254
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 254
Met Gly Ala Leu Ala Arg Val Leu Val Pro Ser Gln Pro Gly Glu Arg
      1           5           10           15
Arg Ala Leu Thr Val Leu Tyr Arg Pro Ile Ser Gln Pro Ser Ala Asp
      20           25           30
Arg Ser Thr Asn Arg Ala His Met Ser Ala Val Met Ala Gly Thr Leu
      35           40           45
Arg Glu Lys Ala Gly Lys Val Glu Arg Ala Asn Asp Arg Arg Thr Val
      50           55           60
Gly Thr Leu His Glu Arg Asp Glu Lys Leu Ala Ala Gly Arg Ser Leu
65           70           75           80
Val Ala Val Ser Ser Ala Val Ser Ile Thr Val Pro Ala Thr Trp Asn
      85           90           95
Ala His Asp Phe Gly Arg Arg Leu Asp Ala
      100           105

```

<210> 255
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 255
 ctagaaatgg ctggctacga atacatggaa gctgaaaata gccacaagc ccacgaaatt
 60
 atcgtggacc atagacctga cttaatctta tgtgattgga tgatgccagg agggagtggc
 120
 atcgagctaa ctcgtcgctt aaagaaagac agcacgacag cagaaatcgc tggtatttta
 180
 ctaacggcca aaagtgaaga agacaataaa attcaaggct tagaagtcgg tgcagatgac
 240
 tacatcacta aacctttctc tcctcgtgaa ctagtagcac gcctcaaggc ggtattacgc
 300
 cgagcgactc cacaaggtat tgatgatcct attgaaattg atggtttaac gcttgatccc
 360
 attagccaac gc
 372

<210> 256
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 256
 Leu Glu Met Ala Gly Tyr Glu Tyr Met Glu Ala Glu Asn Ser Gln Gln
 1 5 10 15
 Ala His Glu Ile Val Asp His Arg Pro Asp Leu Ile Leu Cys Asp
 20 25 30
 Trp Met Met Pro Gly Gly Ser Gly Ile Glu Leu Thr Arg Arg Leu Lys
 35 40 45
 Lys Asp Ser Thr Thr Ala Glu Ile Pro Val Ile Leu Leu Thr Ala Lys
 50 55 60
 Ser Glu Glu Asp Asn Lys Ile Gln Gly Leu Glu Val Gly Ala Asp Asp
 65 70 75 80
 Tyr Ile Thr Lys Pro Phe Ser Pro Arg Glu Leu Val Ala Arg Leu Lys
 85 90 95
 Ala Val Leu Arg Arg Ala Thr Pro Gln Gly Ile Asp Asp Pro Ile Glu
 100 105 110
 Ile Asp Gly Leu Thr Leu Asp Pro Ile Ser Gln Arg
 115 120

<210> 257
 <211> 639
 <212> DNA
 <213> Homo sapiens

<400> 257
 nnacgcgtag cggtcgaggt tgcggacacc atgcccgaa cgggcctgct cgccatcgag
 60
 gcacccatgg gacacggcaa gaccgaggcc gccctcatgt gcgcacaggt gctcgcggaa
 120

cggttcgggc tcggcgcat cttcttcggt ctaccgacga tggccacgtc caatcccatg
 180
 ttcggtcgag ttcgggaatg gctggacgct gtgccagcca aggaccgtc aagcatttcc
 240
 ctggctcact cgaaagctgg actcaacgag gagtaccagc agtcatgcc gtggaacgcc
 300
 accatggccg tctacgacga aggtgccggc acgcagcgtg aagcttcggc gatcgtccat
 360
 gagtggttct tgggcccga ggcgcgcgac ctggccgacc acgtcgtcgg gaccatcgac
 420
 caggcactgt tcaccggtct caaagccaag catgtggtgt tacgccacct cggctctggcg
 480
 agcaaggctc tcattcattga tgaggtccac gccgccgacg tctatatgcg cgaataacct
 540
 aaggtcgtcc tcgaatggct cggcgcctac cgcacgccag tcattcctcat gtccgcgacg
 600
 ctgccaccgg cccaacgtca tgaactcgcg ctagcgtac
 639

<210> 258

<211> 213

<212> PRT

<213> Homo sapiens

<400> 258

Xaa	Arg	Val	Ala	Val	Glu	Val	Ala	Asp	Thr	Met	Pro	Glu	Pro	Gly	Leu
1				5					10					15	
Leu	Ala	Ile	Glu	Ala	Pro	Met	Gly	His	Gly	Lys	Thr	Glu	Ala	Ala	Leu
			20					25					30		
Met	Cys	Ala	Gln	Val	Leu	Ala	Glu	Arg	Phe	Gly	Leu	Gly	Gly	Ile	Phe
		35					40					45			
Phe	Gly	Leu	Pro	Thr	Met	Ala	Thr	Ser	Asn	Pro	Met	Phe	Gly	Arg	Val
	50					55					60				
Arg	Glu	Trp	Leu	Asp	Ala	Val	Pro	Ala	Lys	Asp	Pro	Ser	Ser	Ile	Ser
65				70					75					80	
Leu	Ala	His	Ser	Lys	Ala	Gly	Leu	Asn	Glu	Glu	Tyr	Gln	Gln	Leu	Met
			85					90						95	
Pro	Trp	Asn	Ala	Thr	Met	Ala	Val	Tyr	Asp	Glu	Gly	Ala	Gly	Thr	Gln
		100						105					110		
Arg	Glu	Ala	Ser	Ala	Ile	Val	His	Glu	Trp	Phe	Leu	Gly	Arg	Lys	Arg
		115					120					125			
Ala	Ile	Leu	Ala	Asp	His	Val	Val	Gly	Thr	Ile	Asp	Gln	Ala	Leu	Phe
	130					135					140				
Thr	Gly	Leu	Lys	Ala	Lys	His	Val	Val	Leu	Arg	His	Leu	Gly	Leu	Ala
145				150					155					160	
Ser	Lys	Val	Val	Ile	Ile	Asp	Glu	Val	His	Ala	Ala	Asp	Val	Tyr	Met
		165						170						175	
Arg	Glu	Tyr	Leu	Lys	Val	Val	Leu	Glu	Trp	Leu	Gly	Ala	Tyr	Arg	Thr
	180							185					190		
Pro	Val	Ile	Leu	Met	Ser	Ala	Thr	Leu	Pro	Pro	Ala	Gln	Arg	His	Glu
	195						200					205			
Leu	Ala	Leu	Ala	Tyr											
	210														

<210> 259
 <211> 252
 <212> DNA
 <213> Homo sapiens

<400> 259
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
 60
 ncatgggtgtg tgcacgtgtg cnaactgtgta tgcattggtaa tgtgcacgtg tgcancgtgtg
 120
 tgtnggtgtg tatgcatgng tgtgtgcacg tgtgcactgn agtgtgggggt gtatgcatgg
 180
 tgtgtgcaca tgagcactgt gtgggtgtgta tgcattggtn ggtgcacgtg tgcactgtgt
 240
 atgcaatgggt gt
 252

<210> 260
 <211> 84
 <212> PRT
 <213> Homo sapiens

<400> 260
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Xaa Val Cys Xaa Cys Val Cys Met Xaa Val
 35 40 45
 Cys Thr Cys Ala Leu Xaa Cys Gly Val Tyr Ala Trp Cys Val His Met
 50 55 60
 Ser Thr Val Trp Cys Val Cys Met Val Xaa Cys Thr Cys Ala Leu Cys
 65 70 75 80
 Met Gln Trp Cys

<210> 261
 <211> 1202
 <212> DNA
 <213> Homo sapiens

<400> 261
 gctagcccgg tcgcgttcgt cgtcgatttg ctggcggcag tcccctcgat cgtcttcgggt
 60
 ctgtggggcg gcatcgtctt cggatcgtcg ggaatcatca acggttacgc gggggcctta
 120
 ttcaaagcgc tcggctggat tccgatcttt tccgaagatc cgtcgtggtc ctccggtact
 180
 ggacaggctc accttgccag tctcgtcctg gccatcatga tccctgccaat taccactgct
 240
 gttagccgcg acgtcatgcc ccgaacgcc catgatcaag tcgaggccgc gctcgccctc
 300
 ggatcgacgc gctgggaggt catcaagctt gcagtgttcc cccactcgcg gtccggcatc
 360

atttccggat ccatgttggg tctaggacgc gccctcggcg agaccctggc tgtcacccctc
 420
 atcctgcaga cgatgagccc catggcgctc aaacagaacc tcaacctgtc gatcttcgtc
 480
 ggtgggtgaga cattcgcgtc gaagattgcc ggtaacttct ccgaggccat tagcgatccc
 540
 acctcgctgg gtgcctcgt ggcgtcggcc ctggccctgt tcgtcattac cttcgtggtc
 600
 aacgcgactg cccggttgat tgcggcgaag ggggttaagc gatgagcgcc accaccctg
 660
 accacatcac ccaccatggc gacaacacgc ccggacagct agatctctcc cgcccgtctg
 720
 gtaaaccggac tatcaagagc ggctgcgcct caacattcat gatcgtggcc accgtactgg
 780
 ctgttatccc actggcctgg ctgctcttcg cggcgcgtccg gcgcggcatc ggatcactat
 840
 tccacgcgtc gtggtggacc cactcgatgg atccctcctt cgacttggcc gagcagggcg
 900
 ccateccacgc tatcgtcgga acccttgaaa ttggccttat tacatcgatt atctcggtag
 960
 cgatcgctct gatgaccgcg atcttcctag tcgagtacgc ccgcggaact aagatcgcca
 1020
 aggtcattag cttcgcgcgtc gacgtgctaa ccggtgtacc ttcaatcgtc gcggccctct
 1080
 tcgtcttcgc cgtagtcgtt accaccttcg gtggcaccca atccgcgtgg gcctcctcgt
 1140
 tggccctcat gatcctcatg gttccgacgg tgctgcgata aaccgaggaa atgctcaagc
 1200
 tt
 1202

<210> 262
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 262
 Ala Ser Pro Val Ala Phe Val Val Asp Leu Leu Ala Ala Val Pro Ser
 1 5 10 15
 Ile Val Phe Gly Leu Trp Gly Gly Ile Val Phe Gly Ser Ser Gly Ile
 20 25 30
 Ile Asn Gly Tyr Ala Gly Ala Leu Phe Lys Ala Leu Gly Trp Ile Pro
 35 40 45
 Ile Phe Ser Glu Asp Pro Ser Trp Ser Ser Ala Thr Gly Thr Val Tyr
 50 55 60
 Leu Ala Ser Leu Val Leu Ala Ile Met Ile Leu Pro Ile Ile Thr Ala
 65 70 75 80
 Val Ser Arg Asp Val Met Pro Arg Thr Pro His Asp Gln Val Glu Ala
 85 90 95
 Ala Leu Ala Leu Gly Ser Thr Arg Trp Glu Val Ile Lys Leu Ala Val
 100 105 110
 Phe Pro His Ser Arg Ser Gly Ile Ile Ser Gly Ser Met Leu Gly Leu
 115 120 125
 Gly Arg Ala Leu Gly Glu Thr Leu Ala Val Thr Leu Ile Leu Gln Thr

```

      130              135              140
Met Ser Pro Met Ala Leu Lys Gln Asn Leu Asn Leu Ser Ile Phe Val
145              150              155              160
Gly Gly Glu Thr Phe Ala Ser Lys Ile Ala Gly Asn Phe Ser Glu Ala
      165              170              175
Ile Ser Asp Pro Thr Ser Leu Gly Ala Leu Val Ala Ser Ala Leu Ala
      180              185              190
Leu Phe Val Ile Thr Phe Val Val Asn Ala Thr Ala Arg Leu Ile Ala
      195              200              205
Ala Lys Gly Val Lys Arg
      210

```

<210> 263
 <211> 424
 <212> DNA
 <213> Homo sapiens

```

<400> 263
acgcgtgagt gctctgcgct ggaaacaacg gtgatagagc ccatccgcgc tgaactttcc
60
gacgtggtgc tcgtgaacaa gctcgaaaag tatgtacgcg aacgtacctc ggaagacggt
120
gcgcacatgg aagaggatgc ggaccagacg ggcaacgaca tcctcacgac gatcctgctg
180
tcgaactggg atccactatt ggatatgacg acgcaggatc atgtgctggc catgcaaaag
240
gcttatatgg cctcgccatt ccgtgccaat ttggacctgg catacccatc ttcgacgcca
300
caggcccagt cccagccggc gatgccgcgc tgggagacag ggacctcagc cagtagcatg
360
gcggatgctc gtgaatttgc gctgctgaag ctgtacctgc gtagcttgct gcagaagcac
420
gann
424

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<210> 264
 <211> 99
 <212> PRT
 <213> Homo sapiens

```

<400> 264
Met Glu Glu Asp Ala Asp Gln Thr Gly Asn Asp Ile Leu Thr Thr Ile
1      5      10      15
Leu Leu Ser Asn Trp Asp Pro Leu Leu Asp Met Thr Thr Gln Asp His
      20      25      30
Val Leu Ala Met Gln Lys Ala Tyr Met Ala Ser Pro Phe Arg Ala Asn
      35      40      45
Leu Asp Leu Ala Tyr Pro Ser Ser Thr Pro Gln Ala Gln Ser Gln Pro
      50      55      60
Ala Met Pro Pro Trp Glu Thr Gly Thr Ser Ala Ser Ser Met Ala Asp
65      70      75      80
Ala Arg Glu Phe Ala Leu Leu Lys Leu Tyr Leu Arg Ser Leu Leu Gln
      85      90      95
Lys His Xaa

```

<210> 265
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 265
 ncgtacggcc ctggcgtccg catggacgag ggataccatt ccggcatgac ggtgccgggt
 60
 gccttcgact ccctcatcgg caagctcatc atcactggtg atagccgtga gcaagccctg
 120
 gctcgagctg cccgcgccct cgacgaaatc gtcacgcacg gcatgccgac ggtcattccc
 180
 tttcaccagg cggtggttca cgaccgggt ttcactgccg ccgacggctg cttcggcgtc
 240
 tttaccgact ggatcgaaac cgagtccgac aacaagatcg agccatacac cgggtctctg
 300
 ggcgagtctg ccaattccga gcctcctcgt gaggtcgtcg tcgagggtcaa cggtaaaccg
 360

<210> 266
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 266
 Xaa Tyr Gly Pro Gly Val Arg Met Asp Glu Gly Tyr His Ser Gly Met
 1 5 10 15
 Thr Val Pro Gly Ala Phe Asp Ser Leu Ile Gly Lys Leu Ile Ile Thr
 20 25 30
 Gly Asp Ser Arg Glu Gln Ala Leu Ala Arg Ala Ala Leu Asp
 35 40 45
 Glu Ile Val Ile Asp Gly Met Pro Thr Val Ile Pro Phe His Gln Ala
 50 55 60
 Val Val His Asp Pro Ala Phe Thr Ala Ala Asp Gly Cys Phe Gly Val
 65 70 75 80
 Phe Thr Asp Trp Ile Glu Thr Glu Phe Asp Asn Lys Ile Glu Pro Tyr
 85 90 95
 Thr Gly Ser Leu Gly Glu Ser Ala Asn Ser Glu Pro Pro Arg Glu Val
 100 105 110
 Val Val Glu Val Asn Gly Lys Arg
 115 120

<210> 267
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 267
 natcctcaac gtgtgttcag ttccacgcga aagatcatgt tcgtcatcgg atcgatgccg
 60
 ttaacgcac ctagtcaatc caccgatggc gaccctggca aaaaatacga ggtgacttgg
 120

ctagatctcg ggcaccttca ccctagtcgg ccgggactcg tcactatcac cacaactgtc
 180
 gatgatgacg tcatcacctc ttcccaggta aatgtcggca acctccaccg cggggatgaa
 240
 aaacttttcg aagctcgca ttaccgccag attccgatgc ttgcatcacg tcatggctgg
 300
 acagctccat tcattggtga gaccggcgca gcccatgcca tcgaggatgc gatgggcatt
 360
 accatcccaa ctgcgtggc atggatacga accctgctcg ctgagttcag cagaatcacc
 420
 tcacatttca ctttttgtc atgggtaggc catcactgtg atgatgccg c
 471

<210> 268
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 268
 Xaa Pro Gln Arg Val Phe Ser Ser Thr Arg Lys Ile Met Phe Val Ile
 1 5 10 15
 Gly Ser Met Pro Leu Thr His Pro Ser Gln Ser Thr Asp Gly Asp Pro
 20 25 30
 Gly Lys Lys Tyr Glu Val Thr Trp Leu Asp Leu Gly His Leu His Pro
 35 40 45
 Ser Arg Pro Gly Leu Val Thr Ile Thr Thr Thr Val Asp Asp Asp Val
 50 55 60
 Ile Thr Ser Ser Gln Val Asn Val Gly Asn Leu His Arg Gly Asp Glu
 65 70 75 80
 Lys Leu Phe Glu Ala Arg Asp Tyr Arg Gln Ile Pro Met Leu Ala Ser
 85 90 95
 Arg His Gly Trp Thr Ala Pro Phe Ile Gly Glu Thr Gly Ala Ala His
 100 105 110
 Ala Ile Glu Asp Ala Met Gly Ile Thr Ile Pro Thr Arg Val Ala Trp
 115 120 125
 Ile Arg Thr Leu Leu Ala Glu Phe Ser Arg Ile Thr Ser His Phe Thr
 130 135 140
 Phe Leu Ser Trp Val Gly His His Cys Asp Asp Ala Gly
 145 150 155

<210> 269
 <211> 387
 <212> DNA
 <213> Homo sapiens

<400> 269
 acgctgtcg tgtttccaga aaaaaccaat aaattagagt ttatggtaga agtgattgct
 60
 gatatgacgg taatcaatcc atttgatttc tttgtggaaa gctacgcaga agactaccca
 120
 ttgcttatg acaaagctct taaaaaagag ttagaacctt atttacaggt ttctgaacct
 180
 tgttcgttac tcgacaaatg gctgtctggt gttgatcgtg aaaaaacacc gatcaatgat
 240

tttctagtcg caataaacag tcgccttgcc ggtgatattg gctatggat tcgcttagaa
 300
 ccgggcgttc agtcacctga agaaacgctc acattaatga aaggctcttg tcgcgatacc
 360
 tcgggggttat tggttcaaact actacgc
 387

<210> 270
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 270
 Thr Arg Val Val Phe Pro Glu Lys Thr Asn Lys Leu Glu Phe Met Val
 1 5 10 15
 Glu Val Ile Ala Asp Met Thr Val Ile Asn Pro Phe Asp Phe Phe Val
 20 25 30
 Glu Ser Tyr Ala Glu Asp Tyr Pro Phe Ala Tyr Asp Lys Ala Leu Lys
 35 40 45
 Lys Glu Leu Glu Pro Tyr Leu Gln Val Ser Glu Pro Cys Ser Leu Leu
 50 55 60
 Asp Lys Trp Leu Ser Gly Val Asp Arg Glu Lys Thr Pro Ile Asn Asp
 65 70 75 80
 Phe Leu Val Ala Ile Asn Ser Arg Leu Ala Gly Asp Ile Gly Tyr Gly
 85 90 95
 Ile Arg Leu Glu Pro Gly Val Gln Ser Pro Glu Glu Thr Leu Thr Leu
 100 105 110
 Met Lys Gly Ser Cys Arg Asp Thr Ser Gly Leu Leu Val Gln Ile Leu
 115 120 125
 Arg

<210> 271
 <211> 443
 <212> DNA
 <213> Homo sapiens

<400> 271
 gccggcacca acggaaagtc ctctaccgcg cgcattggctg attcgctttt gcgtgccttc
 60
 caccgcccag tgggtttggt aaccagccca cacctgcagc gcgttactga gcgcacggc
 120
 attgatggcc agcccattca cccgcgcgat tatgtacgca tctggcacga gattaagcca
 180
 tttgtggaaa tggtcgatgc cgaatcggac gtgcctatgt ctaagtctga ggtcttcgtg
 240
 ggctgtcct atgctgcgtt tgccgacgcc cccggggacg tcgctgtcgt cgaagtcggc
 300
 cttggcggac gttgggacgc taccaatgtg gtcaacgcgg atgtctctgt cattaccccg
 360
 gtgggcatgg accacacgga ttacctgggg gagacgatca ctgaaatcgc aggcgagaaa
 420
 gctggcatta ttaagccacg cgt
 443

<210> 272
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 272
 Ala Gly Thr Asn Gly Lys Ser Ser Thr Ala Arg Met Val Asp Ser Leu
 1 5 10 15
 Leu Arg Ala Phe His Arg Arg Val Gly Leu Val Thr Ser Pro His Leu
 20 25 30
 Gln Arg Val Thr Glu Arg Ile Gly Ile Asp Gly Gln Pro Ile His Pro
 35 40 45
 Arg Asp Tyr Val Arg Ile Trp His Glu Ile Lys Pro Phe Val Glu Met
 50 55 60
 Val Asp Ala Glu Ser Asp Val Pro Met Ser Lys Phe Glu Val Phe Val
 65 70 75 80
 Gly Leu Ser Tyr Ala Ala Phe Ala Asp Ala Pro Gly Asp Val Ala Val
 85 90 95
 Val Glu Val Gly Leu Gly Gly Arg Trp Asp Ala Thr Asn Val Val Asn
 100 105 110
 Ala Asp Val Ser Val Ile Thr Pro Val Gly Met Asp His Thr Asp Tyr
 115 120 125
 Leu Gly Glu Thr Ile Thr Glu Ile Ala Gly Glu Lys Ala Gly Ile Ile
 130 135 140
 Lys Pro Arg
 145

<210> 273
 <211> 864
 <212> DNA
 <213> Homo sapiens

<400> 273
 caaagtaaga ctgcttcaaa ttttgtgttc tgctctgcag ctgcgtcccc cctgctgtcg
 60
 aagagaagcc aaagcccccc cccccacct caaaggctcg gaagtctggc atccctactt
 120
 ccgagcctgg atcccagtaa ggatcttgcc ctccctgcaa caccgagtgc cttagacagc
 180
 tgctgcctga gaactggcct ccagccggtg tcctcattcc atggggctcc ctgctgactg
 240
 catttctga tctgggatga tgtttaccag cccaaaacca gtcattgttct tccaaaagct
 300
 tctctttgat agaattttga ggccatgcc cctcccttcc agtccacatg gaattccaga
 360
 atcagtcaca gcctctgatt ttttccaaga agagattgcc ttcaccattg ttaaatgtca
 420
 gcctgtacgg cagagacatg gtggtctgca caagcctgga caagttcttc catattgatg
 480
 gtgggagcaa cccctgtaat ctactccttg gaaggatttt ttgctttgct tatgaaaage
 540
 tgtgcttgag acttaggtac ttttctcacg tggacacact gatcccatcc catattgcat
 600

ctttgaagag atggatatca agtacacttt ggtagctgaa ataatcatat ctttctgatg
 660
 tctattgtat ctcctttgag gaaaagaaca cacattttta atggagattg gctgctttca
 720
 ggtatgtgtg tctatcattg aaagagcatg gactcaaaca tcagccctga gttcttgagt
 780
 ccacccaact cccatcttct tgtggcacag gaaagctgcc ctctccctct cccaccacac
 840
 tcctgactaa tgcccttcac gcgt
 864

<210> 274
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 274
 Met Trp Thr Gly Arg Glu Val Ala Trp Pro Gln Asn Ser Ile Lys Glu
 1 5 10 15
 Lys Leu Leu Glu His Asp Trp Phe Trp Ala Gly Lys His His Pro
 20 25 30
 Arg Ser Gly Asn Ala Val Ser Arg Glu Pro His Gly Met Arg Thr Pro
 35 40 45
 Ala Gly Gly Gln Phe Ser Gly Ser Ser Cys Leu Arg His Ser Val Leu
 50 55 60
 Gln Gly Gly Gln Asp Pro Tyr Trp Asp Pro Gly Ser Glu Val Gly Met
 65 70 75 80
 Pro Asp Phe Arg Ala Phe Glu Val Gly Gly Gly Gly Phe Gly Phe Ser
 85 90 95
 Ser Thr Ala Gly Gly Ser Glu Leu Gln Ser Arg Thr Gln Asn Leu Lys
 100 105 110
 Gln Ser Tyr Phe
 115

<210> 275
 <211> 911
 <212> DNA
 <213> Homo sapiens

<400> 275
 naaattttaa ggaacctccc ttctataacg gagagtattt attgcagctt tcctttctgt
 60
 ttattttcag gaatgaaagg aattaccag ctttctgctt ttatacctac agctgaaagt
 120
 aattcctttc agcctcaggt gaagactttg ccctctccaa ttgatgctaa acagcagttg
 180
 caacggaaaa tccagaagaa gcagcaagaa cagaaactac aatccccctt gccaggagaa
 240
 tctgcagcaa aaaagtcaga aagtgtaca agcaatggag tgactaatct tcctaattgga
 300
 aatccttcaa tcctttctcc tcaacctatt ggtatcggtg tggcagctgt ccctagtcct
 360
 attccggtcc agcggactag gcaattggta acttcaccga gtccaatgag ttcttctnga
 420

cggcaaagtt cttccccctca atgtacaggt ggtcactcag cacatgcagt ctgtgaaaca
 480
 ggcaccaaag actccccaga acgttccagc agtcctgggtg ggaatcgttc tgcccggcac
 540
 cgttaccctc agatcttacc caaaccagcg aacaccagtg cactcaccat tcgctctcca
 600
 actactgtcc tctttactag tagtcccatc aaaactgctg ttgtaccgcg ttcacacatg
 660
 agttctctaa atgtgggtgaa aatgacaaca atatccctca caccagcaa cagtaacacc
 720
 cctcttaaac attctgcctc agtcagcagt gctacaggaa caacagaaga atcaaggagt
 780
 gttccacaga tcaagaatgg ttctgtcgtg tcgcttcagt ctcttgggtc caggagcagc
 840
 agtgcggggg gaacatctgc tgtggaagtc aaagtggaac ccgaaacatc atcagatgag
 900
 catcctgtac a
 911

<210> 276

<211> 279

<212> PRT

<213> Homo sapiens

<400> 276

Met	Lys	Gly	Ile	Thr	Gln	Pro	Ser	Ala	Phe	Ile	Pro	Thr	Ala	Glu	Ser	1	5	10	15
Asn	Ser	Phe	Gln	Pro	Gln	Val	Lys	Thr	Leu	Pro	Ser	Pro	Ile	Asp	Ala	20	25	30	
Lys	Gln	Gln	Leu	Gln	Arg	Lys	Ile	Gln	Lys	Lys	Gln	Gln	Glu	Gln	Lys	35	40	45	
Leu	Gln	Ser	Pro	Leu	Pro	Gly	Glu	Ser	Ala	Ala	Lys	Lys	Ser	Glu	Ser	50	55	60	
Ala	Thr	Ser	Asn	Gly	Val	Thr	Asn	Leu	Pro	Asn	Gly	Asn	Pro	Ser	Ile	65	70	75	80
Leu	Ser	Pro	Gln	Pro	Ile	Gly	Ile	Val	Val	Ala	Ala	Val	Pro	Ser	Pro	85	90	95	
Ile	Pro	Val	Gln	Arg	Thr	Arg	Gln	Leu	Val	Thr	Ser	Pro	Ser	Pro	Met	100	105	110	
Ser	Ser	Ser	Xaa	Arg	Gln	Ser	Ser	Ser	Pro	Gln	Cys	Thr	Gly	Gly	His	115	120	125	
Ser	Ala	His	Ala	Val	Cys	Glu	Thr	Gly	Thr	Lys	Asp	Ser	Pro	Glu	Arg	130	135	140	
Ser	Ser	Ser	Pro	Gly	Gly	Asn	Arg	Ser	Ala	Arg	His	Arg	Tyr	Pro	Gln	145	150	155	160
Ile	Leu	Pro	Lys	Pro	Ala	Asn	Thr	Ser	Ala	Leu	Thr	Ile	Arg	Ser	Pro	165	170	175	
Thr	Thr	Val	Leu	Phe	Thr	Ser	Ser	Pro	Ile	Lys	Thr	Ala	Val	Val	Pro	180	185	190	
Ala	Ser	His	Met	Ser	Ser	Leu	Asn	Val	Val	Lys	Met	Thr	Thr	Ile	Ser	195	200	205	
Leu	Thr	Pro	Ser	Asn	Ser	Asn	Thr	Pro	Leu	Lys	His	Ser	Ala	Ser	Val	210	215	220	
Ser	Ser	Ala	Thr	Gly	Thr	Thr	Glu	Glu	Ser	Arg	Ser	Val	Pro	Gln	Ile				


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225          230          235          240
Lys Asn Gly Ser Val Ser Leu Gln Ser Pro Gly Ser Arg Ser Ser
          245          250          255
Ser Ala Gly Gly Thr Ser Ala Val Glu Val Lys Val Glu Pro Glu Thr
          260          265          270
Ser Ser Asp Glu His Pro Val
          275

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<210> 277
<211> 652
<212> DNA
<213> Homo sapiens

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<400> 277
nnaccggtgg ggactctcgc tgaggctcctt aatggccctt ctcgtgtccc ggacggcacc
60
atgaaccttg ttggtgggct gcgtcaggca atggccacca ctggttactc ggaggtcaaa
120
gagttccagc gcacgcagct gacgattcgc taaccgttcc accacgcaga atggtgttcc
180
ggtgagcggg tggatagcta gccttcggcc atgagtgaag tgcccgatga attggtcgtg
240
ttgctgggcg cgattgacaa catggacgcc gccctcatcc atctgcttgc cgaaagggttc
300
cggattactc gcgaggtagg ccgcctcaag gcggagtgcg gtttacctcc ggccgacccc
360
gcccgtaggg ctgagcagat cgcgcggttg cggcagttag cggtcgagtc gaacctcgac
420
cccgaattcg cgcagaaggt catcacgttc atcgtggccg aggtggtgcg tcaccacgaa
480
gctattgctg acgattctgg cgacgactct ggagtggcgg atacggggga ggcggatgtc
540
cctgggtcgg gcagctgagt tacagatcag gcgatgacgt cgccctggtg caccttcgac
600
gggattccga cgacgactgt gccggggggcg acatccttga cgaccaacgc gt
652

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<210> 278
<211> 115
<212> PRT
<213> Homo sapiens

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```

<400> 278
Met Ser Glu Val Pro Asp Glu Leu Val Val Leu Arg Gly Ala Ile Asp
1          5          10          15
Asn Met Asp Ala Ala Leu Ile His Leu Leu Ala Glu Arg Phe Arg Ile
20          25          30
Thr Arg Glu Val Gly Arg Leu Lys Ala Glu Cys Gly Leu Pro Pro Ala
35          40          45
Asp Pro Ala Arg Glu Ala Glu Gln Ile Ala Arg Leu Arg Gln Leu Ala
50          55          60
Val Glu Ser Asn Leu Asp Pro Glu Phe Ala Gln Lys Val Ile Thr Phe
65          70          75          80
Ile Val Ala Glu Val Val Arg His His Glu Ala Ile Ala Asp Asp Ser

```

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      85              90              95
Gly Asp Asp Ser Gly Val Ala Asp Thr Gly Glu Ala Asp Val Pro Gly
      100              105              110
Ser Gly Ser
      115

```

<210> 279
 <211> 348
 <212> DNA
 <213> Homo sapiens

```

<400> 279
cgggaggtca cacaagcatt caaacatag cagatggtaa atgttatgtt atgtgtatatt
60
taccacaatc cttaaaaaga aaagaaagaa aggcataatg aacccttagt tacctctcat
120
ccagcttcaa aattgtcagt gcatgggtcaa tcttgtctta tctgcccctc acccaccctt
180
ttccagaaag aagaccaga ggattccaca tctgcctgga aaccacgacc agtctcgact
240
ggaagttggt gttaatgttg catgtattca taaaacctct aggcatttct agtgtccctc
300
agaatttttc caaattcagg caaacacaga aattacttcc aaaaattt
348

```

<210> 280
 <211> 99
 <212> PRT
 <213> Homo sapiens

```

<400> 280
Met Cys Ile Leu Pro Gln Ser Leu Lys Arg Lys Glu Arg Lys Ala Tyr
  1              5              10              15
Gly Thr Pro Ser Tyr Leu Ser Ser Ser Phe Lys Ile Val Ser Ala Trp
      20              25              30
Ser Ile Leu Ser Tyr Leu Pro Leu Thr His Pro Phe Pro Glu Arg Arg
      35              40              45
Pro Arg Gly Phe His Ile Cys Leu Glu Thr Thr Thr Ser Leu Asp Trp
      50              55              60
Lys Leu Leu Leu Met Leu His Val Phe Ile Lys Pro Leu Gly Ile Ser
      65              70              75              80
Ser Val Pro Gln Asn Phe Ser Lys Phe Arg Gln Thr Gln Lys Leu Leu
      85              90              95
Pro Lys Ile

```

<210> 281
 <211> 384
 <212> DNA
 <213> Homo sapiens

```

<400> 281
agatctgctc agatcgataa tggattaaag actcttgacg ctggagtcac cgagatgaac
60

```

aacaaggtgt tgggggcaac gaaggctgtc ggtgattcca ccactaccgt caaccaggtg
120
aattctgcgt taggaantgc cgactcagcg gcagagaaga cgtcgagcgc cgttactcag
180
acgcgcgtgg gtgcccaggc gattaccggc gctgctcaaa atgtcatggc tgattcccaa
240
gctgtcaact cagccatggg tccgcttatt aataacgtga caaagaatct tcctaccttg
300
caaaaacagg ccaggaatct cgtgtcagtg aacgggtacc tgcagaaccc caacggtgat
360
tctgtcatta agattcaaca gacc
384

<210> 282

<211> 110

<212> PRT

<213> Homo sapiens

<400> 282

Met	Asn	Asn	Lys	Val	Leu	Gly	Ala	Thr	Lys	Ala	Val	Gly	Asp	Ser	Thr
1				5					10					15	
Thr	Thr	Val	Asn	Gln	Val	Asn	Ser	Ala	Leu	Gly	Xaa	Ala	Asp	Ser	Ala
		20					25						30		
Ala	Glu	Lys	Thr	Ser	Ser	Ala	Val	Thr	Gln	Thr	Arg	Val	Gly	Ala	Gln
	35					40						45			
Ala	Ile	Thr	Gly	Ala	Ala	Gln	Asn	Val	Met	Ala	Asp	Ser	Gln	Ala	Val
	50					55					60				
Asn	Ser	Ala	Met	Val	Pro	Leu	Ile	Asn	Asn	Val	Thr	Lys	Asn	Leu	Pro
65					70					75				80	
Thr	Leu	Gln	Lys	Gln	Ala	Arg	Asn	Leu	Val	Ser	Val	Asn	Gly	Thr	Leu
		85						90						95	
Gln	Asn	Pro	Asn	Gly	Asp	Ser	Val	Ile	Lys	Ile	Gln	Gln	Thr		
		100						105					110		

<210> 283

<211> 426

<212> DNA

<213> Homo sapiens

<400> 283

cgcgtagacc aatgtgagac ggccgtcacc aagggcatgc gcgacaagtc ggttggttagc
60
ggaccggata ttgtgcgtcg cgagctgcgc catgtcgtga cgagcggcac gattgtcgat
120
ggaagcgtac tggctgacga attgagcagc tactgcatga gtatcaagga gcacgtccgc
180
tctgatggcc tatecgagtt tggcatctgc accctcgacg ccgccaccgc cgagttccga
240
tacatgacat tcgtcgacga tgccgtgctg tcacaactcg agacattgct gcgttctcta
300
cgcacgaagg aagtcttgca tgaaaaaggg gtcattgtgc cttccacgct gcgcttgatc
360
cgcaacgcgg tgcccaccac ctgccaaatt accatgctca agcctgatac cgaattgtcg
420

gagaga
426

<210> 284
<211> 142
<212> PRT
<213> Homo sapiens

<400> 284
Arg Val Asp Gln Cys Glu Thr Ala Val Thr Lys Gly Met Arg Asp Lys
1 5 10 15
Ser Val Gly Ser Gly Pro Asp Ile Val Arg Arg Glu Leu Arg His Val
20 25 30
Val Thr Ser Gly Thr Ile Val Asp Gly Ser Val Leu Ala Asp Glu Leu
35 40 45
Ser Ser Tyr Cys Met Ser Ile Lys Glu His Val Arg Ser Asp Gly Leu
50 55 60
Ser Glu Phe Gly Ile Cys Thr Leu Asp Ala Ala Thr Ala Glu Phe Arg
65 70 75 80
Tyr Met Thr Phe Val Asp Asp Ala Val Leu Ser Gln Leu Glu Thr Leu
85 90 95
Leu Arg Ser Leu Arg Ile Lys Glu Val Leu His Glu Lys Gly Val Met
100 105 110
Leu Pro Ser Thr Leu Arg Leu Ile Arg Asn Ala Val Pro Thr Thr Cys
115 120 125
Gln Ile Thr Met Leu Lys Pro Asp Thr Glu Leu Ser Glu Arg
130 135 140

<210> 285
<211> 345
<212> DNA
<213> Homo sapiens

<400> 285
acgcgtgcag tcccttaccg acatgctggc agatgagctc gacggcagcc gcttcaccgg
60
cgattttctca gaaatctaca aacgtcagaa ctcgatcttc ggcgatgtaa ggaataactt
120
ttacaaaaaa ggataccgca tcatcaacgt agcgaatggg gtattgcgca agatttcact
180
ggtaagcgca ggcaatgcag acaatgtgaa aggtcaggcc ctgttcttcc gcggtgtggc
240
gcatttcgaa ctcgtcggtt tgtttgcaca accctggggg tatacttcgg acaattcaca
300
ctacggcatc ccgctccgca atgaaatcgt aattggttct attcn
345

<210> 286
<211> 107
<212> PRT
<213> Homo sapiens

<400> 286
Met Leu Ala Asp Glu Leu Asp Gly Ser Arg Phe Thr Gly Asp Phe Ser

1	5	10	15
Glu Ile Tyr Lys Arg Gln Asn Ser Ile Phe Gly Asp Val Arg Asn Asn			
	20	25	30
Phe Tyr Lys Lys Gly Tyr Arg Ile Ile Asn Val Ala Asn Gly Val Leu			
	35	40	45
Arg Lys Ile Ser Leu Val Ser Ala Gly Asn Ala Asp Asn Val Lys Gly			
	50	55	60
Gln Ala Leu Phe Phe Arg Gly Val Ala His Phe Glu Leu Val Arg Leu			
65	70	75	80
Phe Ala Gln Pro Trp Gly Tyr Thr Ser Asp Asn Ser His Tyr Gly Ile			
	85	90	95
Pro Leu Arg Asn Glu Ile Val Ile Gly Ser Ile			
	100	105	

<210> 287
 <211> 1379
 <212> DNA
 <213> Homo sapiens

<400> 287
 nnttaactgc ccctttgcag tctttattct gggacattag cactgtctgg ttatcttggc
 60
 tcagttgagg gattcgggac aatagcagtg ctgatggtaa tgttggcgat ttcctgttt
 120
 gttttgcagg tcacggccag gggctttggg ccgctgttac agtttgccta cactgccaag
 180
 ctgttactca gcagagaaaa catccgcgag gtcacccgct gtgctgagtt cctgcgcag
 240
 cacaacctgg aggactcctg cttcagcttc ctgcagaccc agctcctgaa cagtgaggat
 300
 ggccctgtttg tgtgccggaa ggatgctgag tgccagcgcc cacacgagga ctgcgagaac
 360
 tctgcaggag aggaggagga tgaagaggag gagacgatgg attcagagac ggccaagatg
 420
 gcttgcccca gggaccagat gcttccagag cccatcagct ttgaggccgc cgccatcccc
 480
 gtagcagaga aggaagaagc cctgctgccc gagcctgacg tgcccacaga caccaaggag
 540
 agctcagaaa aggacgcgtt aacgcagtac cccagataca agaaatacca gcttgcagtg
 600
 accaagaatg tctataatgc atcatcacac agtacctcag gttttgcaag cacattccgg
 660
 gaagataact ctagcaacag cctcaagccg gggcttgcca gggggcagat taaaagtgag
 720
 ccgcccagtg aagagaatga ggaagagagc atcacgctct gcctgtctgg agatgagcct
 780
 gacgccaagg acagagcggg ggatgtcgag atggaccgga aacagcccag cctgccccct
 840
 acccccacgg cccagctgg ggcgcctgc ctggagagat ccaggagcgt ggcctcgccc
 900
 tcttgcttaa ggtctctgtt cagcataacg aaaagtgtgg agctgtctgg cctgcccagt
 960
 acatctcagc agcactttgc caggagtcca gcctgcccct ttgacaaggg gatcactcag
 1020

ggtgacctta aaactgacta cacccttttc acaggggaatt atggacagcc ccacgtgggc
 1080
 cagaaggagg tgtccaactt caccatgggg tcgcccctca gggggcctgg gttggaggct
 1140
 ctctgtaaac aggaggggaga gctggaccgg aggagcgtga tcttctcttc cagcgcttgt
 1200
 gaccaagtga gcacctcggt gcattcttat tctgggggtga gcagtttgga caaagacctc
 1260
 tctgagccgg tgccaaaggg tctgtgggtg ggagccggcc agtccctccc cagctcgag
 1320
 gcctactccc acggtgggct gatggccgac cacttgccag gaaggatgag gcccaacac
 1379

<210> 288

<211> 428

<212> PRT

<213> Homo sapiens

<400> 288

Met	Val	Met	Leu	Ala	Ile	Ser	Leu	Phe	Val	Leu	Gln	Val	Thr	Ala	Arg
1				5					10					15	
Gly	Phe	Gly	Pro	Leu	Leu	Gln	Phe	Ala	Tyr	Thr	Ala	Lys	Leu	Leu	Leu
			20					25					30		
Ser	Arg	Glu	Asn	Ile	Arg	Glu	Val	Ile	Arg	Cys	Ala	Glu	Phe	Leu	Arg
		35					40					45			
Met	His	Asn	Leu	Glu	Asp	Ser	Cys	Phe	Ser	Phe	Leu	Gln	Thr	Gln	Leu
	50					55					60				
Leu	Asn	Ser	Glu	Asp	Gly	Leu	Phe	Val	Cys	Arg	Lys	Asp	Ala	Ala	Cys
65					70					75					80
Gln	Arg	Pro	His	Glu	Asp	Cys	Glu	Asn	Ser	Ala	Gly	Glu	Glu	Glu	Asp
			85					90						95	
Glu	Glu	Glu	Glu	Thr	Met	Asp	Ser	Glu	Thr	Ala	Lys	Met	Ala	Cys	Pro
			100					105					110		
Arg	Asp	Gln	Met	Leu	Pro	Glu	Pro	Ile	Ser	Phe	Glu	Ala	Ala	Ala	Ile
		115					120					125			
Pro	Val	Ala	Glu	Lys	Glu	Glu	Ala	Leu	Leu	Pro	Glu	Pro	Asp	Val	Pro
	130					135					140				
Thr	Asp	Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Ala	Leu	Thr	Gln	Tyr	Pro
145					150					155					160
Arg	Tyr	Lys	Lys	Tyr	Gln	Leu	Ala	Cys	Thr	Lys	Asn	Val	Tyr	Asn	Ala
			165						170					175	
Ser	Ser	His	Ser	Thr	Ser	Gly	Phe	Ala	Ser	Thr	Phe	Arg	Glu	Asp	Asn
		180						185					190		
Ser	Ser	Asn	Ser	Leu	Lys	Pro	Gly	Leu	Ala	Arg	Gly	Gln	Ile	Lys	Ser
	195						200					205			
Glu	Pro	Pro	Ser	Glu	Glu	Asn	Glu	Glu	Glu	Ser	Ile	Thr	Leu	Cys	Leu
	210					215					220				
Ser	Gly	Asp	Glu	Pro	Asp	Ala	Lys	Asp	Arg	Ala	Gly	Asp	Val	Glu	Met
225					230					235					240
Asp	Arg	Lys	Gln	Pro	Ser	Pro	Ala	Pro	Thr	Pro	Thr	Ala	Pro	Ala	Gly
			245						250					255	
Ala	Ala	Cys	Leu	Glu	Arg	Ser	Arg	Ser	Val	Ala	Ser	Pro	Ser	Cys	Leu
		260						265					270		
Arg	Ser	Leu	Phe	Ser	Ile	Thr	Lys	Ser	Val	Glu	Leu	Ser	Gly	Leu	Pro

275	280	285
Ser Thr Ser Gln Gln His Phe Ala Arg Ser Pro Ala Cys Pro Phe Asp		
290	295	300
Lys Gly Ile Thr Gln Gly Asp Leu Lys Thr Asp Tyr Thr Pro Phe Thr		
305	310	315
Gly Asn Tyr Gly Gln Pro His Val Gly Gln Lys Glu Val Ser Asn Phe		
325	330	335
Thr Met Gly Ser Pro Leu Arg Gly Pro Gly Leu Glu Ala Leu Cys Lys		
340	345	350
Gln Glu Gly Glu Leu Asp Arg Arg Ser Val Ile Phe Ser Ser Ser Ala		
355	360	365
Cys Asp Gln Val Ser Thr Ser Val His Ser Tyr Ser Gly Val Ser Ser		
370	375	380
Leu Asp Lys Asp Leu Ser Glu Pro Val Pro Lys Gly Leu Trp Val Gly		
385	390	395
Ala Gly Gln Ser Leu Pro Ser Ser Gln Ala Tyr Ser His Gly Gly Leu		
405	410	415
Met Ala Asp His Leu Pro Gly Arg Met Arg Pro Asn		
420	425	

<210> 289

<211> 822

<212> DNA

<213> Homo sapiens

<400> 289

```

ngcattaccg ggctgaagac ggggtgctcat gacctcaacg atataggcta ttgctagaac
60
cacgccggcc cacgccgcgc aaagcgcaga cacggcacca ggaggggtca catggctgat
120
agcaagtcca aggcgaagga cgagcgcact gccgatgaga tcaggcggga tattgcagcg
180
accctgtctt gcctggcagc cgggggtggag aacctcgtgg aggaggtgca tccggcaacc
240
ctcaagcgtg aagcatctga tcgtgcccggt gattttgtgc aggggtgagtt tgatcaggtc
300
aagagccagg tcaaagatga gaaatgggtg cgcgtgcagc ggatcgcgat ggccgcagga
360
gtgctcgctg ccggcgtcgt cagcattatt gtgctgcgcg cgatagtcgg tcgcgcaacg
420
ggcgctaccg ctcgtcgcaa gcttgagaag ctgcagcttt ctcaggcgaa gcggggttcca
480
aaagatgcca agcagcgtag taaggaagat gaaaaggcag ccaagaaaaa tgccaagctc
540
ggcaagaaga acgctaagaa gtacggcaag ctcgataccg atgactcgtc ggtaagcaac
600
cttgccgaga aaatgctcaa acaggccgcc gtgctgcgtg cacaggcggc tgccggggcg
660
tgagaacagt gccgcctagc aaacagcggg cacagcgcaa aacaggtttg gctccgaccc
720
atgggtggacc ggagccaaac tgtgttaccg catcatttga taccgccagc agccaggcct
780
gcgacaatgc gacgctggaa taccagcacc atgatgacta gt
822

```

<210> 290
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 290
 Met Ala Asp Ser Lys Ser Lys Ala Lys Asp Glu Arg Thr Ala Asp Glu
 1 5 10 15
 Ile Arg Arg Asp Ile Ala Ala Thr Arg Ala Cys Leu Ala Ala Gly Val
 20 25 30
 Glu Asn Leu Val Glu Glu Val His Pro Ala Thr Leu Lys Arg Glu Ala
 35 40 45
 Ser Asp Arg Ala Arg Asp Phe Val Gln Gly Glu Phe Asp Gln Val Lys
 50 55 60
 Ser Gln Val Lys Asp Glu Lys Trp Trp Arg Val Gln Arg Ile Ala Met
 65 70 75 80
 Ala Ala Gly Val Leu Ala Ala Gly Val Val Ser Ile Ile Val Leu Arg
 85 90 95
 Ala Ile Val Gly Arg Ala Thr Gly Ala Thr Ala Arg Arg Lys Leu Glu
 100 105 110
 Lys Leu Gln Leu Ser Gln Ala Lys Arg Val Arg Lys Asp Ala Lys Gln
 115 120 125
 Arg Ser Lys Glu Asp Glu Lys Ala Ala Lys Lys Asn Ala Lys Leu Gly
 130 135 140
 Lys Lys Asn Ala Lys Lys Tyr Gly Lys Leu Asp Thr Asp Asp Ser Ser
 145 150 155 160
 Val Ser Asn Leu Ala Glu Lys Met Leu Lys Gln Ala Ala Val Leu Arg
 165 170 175
 Ala Gln Ala Ala Ala Gly Ala
 180

<210> 291
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 291
 ctccacgccg acaagactta cgacgggCGT cgctgccggg ctgagtgccg ggccccgctcc
 60
 atcaccccc gcacgctcg ccgCGGCGTG gagaccagcg agcgcttggg ccggtatcgc
 120
 tgggtcgtcg agcgacctt cgCCTGGCTC aaccgctttc ggcgCCTCGC catccgctac
 180
 gagCGGCGTG ctgacatcca cgaagCCTTC gtgacCCTCG gctgcGCCCT catctgcctc
 240
 aaccagatca gacggttttt ttaggtgctg taaagggaga atggctgcag ctgggctatc
 300
 tgctccctcg tcaaccagaa acaggctgct catcctcact caacaacgcg t
 351

<210> 292
 <211> 87
 <212> PRT

<213> Homo sapiens

<400> 292

```

Leu His Ala Asp Lys Thr Tyr Asp Gly Arg Arg Cys Arg Ala Glu Cys
 1           5           10           15
Arg Ala Arg Ser Ile Thr Pro Arg Ile Ala Arg Arg Gly Val Glu Thr
      20           25           30
Ser Glu Arg Leu Gly Arg Tyr Arg Trp Val Val Glu Arg Thr Phe Ala
      35           40           45
Trp Leu Asn Arg Phe Arg Arg Leu Ala Ile Arg Tyr Glu Arg Arg Ala
      50           55           60
Asp Ile His Glu Ala Phe Val Ile Leu Gly Cys Ala Leu Ile Cys Leu
      65           70           75           80
Asn Gln Ile Arg Arg Phe Cys
              85

```

<210> 293

<211> 716

<212> DNA

<213> Homo sapiens

<400> 293

```

nncttcacca caccggccat caacgcacct cctcgtgata acttgacctt ctgccgaacc
60
ggttaatcag tttagtggcg aggcattgaca cgttgacgag tcagctgtgg tacatgtgcg
120
gaacactcac aatgccacgg cggcatgttg ctgtcgggtca cgacccttat ggtgatcgct
180
gtgagaaccc gaacggcaga tgcgattctg gcggcactgg atctgaacag gtttaagggt
240
gcgaagactt tcgatgttcc agtgtgcgtc atagctgggtg ccgggacagg taaaactcgt
300
gctgtcactc atcgatttgc ctacgggtgca gcgacaggca agcttgatcc gcgtcgtacc
360
ctcgcggtca cttttacgac taaggcagct ggcacgatga gaggtcgact cgccgatctg
420
gggggttgtg gtgtgcaggc tcgcactatt cattctgcgg cgttgcggca gatcaagttt
480
ttctggcctc gtgcatataa ctgtgagttg ccaccggtga gtgattctcg tttctcgatg
540
gtggcgggaga cgacccatcg cattgggtctg ggcaatgaca aggcgctgct gcgcgacttg
600
tccgccgaga tctcgtgggc gaaggtctca aatgtgccga ctgatcaata cgcattccctg
660
gctagggcgg aaggtcgggt ggtggcggga gtttcggcaa ctgacgtagg acgcgt
716

```

<210> 294

<211> 190

<212> PRT

<213> Homo sapiens

<400> 294

```

Met Leu Leu Ser Val Thr Thr Leu Met Val Ile Ala Val Arg Thr Arg

```

```

1           5           10           15
Thr Ala Asp Ala Ile Leu Ala Ala Leu Asp Leu Asn Arg Phe Lys Val
20           25           30
Ala Lys Thr Phe Asp Val Pro Val Cys Val Ile Ala Gly Ala Gly Thr
35           40           45
Gly Lys Thr Arg Ala Val Thr His Arg Ile Ala Tyr Gly Ala Ala Thr
50           55           60
Gly Lys Leu Asp Pro Arg Arg Thr Leu Ala Val Thr Phe Thr Thr Lys
65           70           75           80
Ala Ala Gly Thr Met Arg Gly Arg Leu Ala Asp Leu Gly Val Val Gly
85           90           95
Val Gln Ala Arg Thr Ile His Ser Ala Ala Leu Arg Gln Ile Lys Phe
100          105          110
Phe Trp Pro Arg Ala Tyr Asn Cys Glu Leu Pro Pro Val Ser Asp Ser
115          120          125
Arg Phe Ser Met Val Ala Glu Thr Thr His Arg Ile Gly Leu Gly Asn
130          135          140
Asp Lys Ala Leu Leu Arg Asp Leu Ser Ala Glu Ile Ser Trp Ala Lys
145          150          155          160
Val Ser Asn Val Pro Thr Asp Gln Tyr Ala Ser Leu Ala Arg Ala Glu
165          170          175
Gly Arg Val Val Ala Gly Val Ser Ala Thr Asp Val Gly Arg
180          185          190

```

<210> 295

<211> 417

<212> DNA

<213> Homo sapiens

<400> 295

```

ttcatatcag gcagtaccgc agtccatgcg atcaacaacg tcagcgtatc tttcacccat
60
tctggagtgc accttctcat gggagaaagc ggatcaggaa aaagcaccct catcaatctc
120
ctagctgggc tggatacccc agattcgggg tccgtctacg cagaaggcgt caccgtatct
180
gatcagagcg aggcgagcag agcccaattt cgattacgcc acatcgccgt catcttccag
240
gacgacaacc tcatcgctga gttgaccaat accgagaata ttgcgctacc cctgtgggagc
300
cagggcacat cgaagtccga tgccactgaa atcgcccacg aagccatgcg aaaactagga
360
atcgagtcac tgggcagacg ctaccccggc gaggtctcgg gtggccaacg gcaacgc
417

```

<210> 296

<211> 139

<212> PRT

<213> Homo sapiens

<400> 296

```

Phe Ile Ser Gly Ser Thr Arg Val His Ala Ile Asn Asn Val Ser Val
1           5           10           15
Ser Phe Thr His Ser Gly Val His Leu Leu Met Gly Glu Ser Gly Ser

```

```

          20          25          30
Gly Lys Ser Thr Leu Ile Asn Leu Leu Ala Gly Leu Asp Thr Pro Asp
      35          40          45
Ser Gly Ser Val Tyr Ala Glu Gly Val Thr Val Ser Asp Gln Ser Glu
      50          55          60
Ala Ser Arg Ala Gln Phe Arg Leu Arg His Ile Ala Val Ile Phe Gln
      65          70          75          80
Asp Asp Asn Leu Ile Ala Glu Leu Thr Asn Thr Glu Asn Ile Ala Leu
      85          90          95
Pro Leu Trp Ala Gln Gly Thr Ser Lys Ser Asp Ala Thr Glu Ile Ala
      100          105          110
His Glu Ala Met Arg Lys Leu Gly Ile Glu Ser Leu Gly Arg Arg Tyr
      115          120          125
Pro Gly Glu Val Ser Gly Gly Gln Arg Gln Arg
      130          135

```

<210> 297

<211> 378

<212> DNA

<213> Homo sapiens

<400> 297

```

tacaccatcg gtgaccagat tgtcgaagct ctgcagggtgc actcgaagat gtccgacaag
60
gacgcttgagg cgcgtgccaat cgagctgctc gacttggtgg ggattccgaa tcccagaggtg
120
cgtgccaaaag cttttccgca cgagttttcc ggtggcatga ggcaacgagt cgatcatgcc
180
atggccatcg cgaacgaccc tgacctcatc atcgccgacg agccgacgac ggccctcgac
240
gtgaccatcc aggcccagat tctcgatttg ctgcgcgtag cccagcgtga aacccatgcg
300
ggcgtcggtta tgatcaccca cgacctcggt gtggtagctg gtctggctga cagggttgcc
360
gtgatgtatg ccggacgc
378

```

<210> 298

<211> 126

<212> PRT

<213> Homo sapiens

<400> 298

```

Tyr Thr Ile Gly Asp Gln Ile Val Glu Ala Leu Gln Val His Ser Lys
  1          5          10          15
Met Ser Asp Lys Asp Ala Trp Ala Arg Ala Ile Glu Leu Leu Asp Leu
      20          25          30
Val Gly Ile Pro Asn Pro Glu Val Arg Ala Lys Ala Phe Pro His Glu
      35          40          45
Phe Ser Gly Gly Met Arg Gln Arg Val Val Ile Ala Met Ala Ile Ala
      50          55          60
Asn Asp Pro Asp Leu Ile Ala Asp Glu Pro Thr Thr Ala Leu Asp
      65          70          75          80
Val Thr Ile Gln Ala Gln Ile Leu Asp Leu Leu Arg Val Ala Gln Arg

```

```

      85          90          95
Glu Thr His Ala Gly Val Val Met Ile Thr His Asp Leu Gly Val Val
      100          105          110
Ala Gly Leu Ala Asp Arg Val Ala Val Met Tyr Ala Gly Arg
      115          120          125

```

<210> 299
 <211> 368
 <212> DNA
 <213> Homo sapiens

```

<400> 299
gtgcacgggtt tcgttggcat ggcgaatgac cgggagaact tgcgttttga tccgagactt
60
ccagcccaat ggacgtcgat caaacaccac atgctcattg gcgactctca catgctcggt
120
ttcctggaac gtgacgccat tacgttccag attctgtcgg gccatgaccg cgacgtgaca
180
gtgcgcggtg agctctacca cattgggggtt gagccggtga ggggtgccgtt gtccgatcag
240
gggccgttgc gtcttagcct gcgcgttacc catccgatct cggggttgcg tcgagctgac
300
ggttctctta tcaactgcaga agttcccggc agcattgctg agacgattgg gtcttctccg
360
atctcgac
368

```

<210> 300
 <211> 122
 <212> PRT
 <213> Homo sapiens

```

<400> 300
Val His Gly Phe Val Gly Met Arg Asn Asp Arg Glu Asn Leu Arg Phe
1      5      10      15
Asp Pro Arg Leu Pro Ala Gln Trp Thr Ser Ile Lys His His Met Leu
20     25     30
Ile Gly Asp Ser His Met Leu Val Phe Leu Glu Arg Asp Ala Ile Thr
35     40     45
Phe Gln Ile Leu Ser Gly His Asp Arg Asp Val Thr Val Arg Gly Glu
50     55     60
Leu Tyr His Ile Gly Val Glu Pro Val Arg Val Pro Leu Ser Asp Gln
65     70     75     80
Gly Pro Leu Arg Pro Ser Leu Arg Val Thr His Pro Ile Ser Gly Leu
85     90     95
Arg Arg Ala Asp Gly Ser Leu Ile Thr Ala Glu Val Pro Gly Ser Ile
100    105    110
Ala Glu Thr Ile Gly Ser Ser Pro Ile Ser
115    120

```

<210> 301
 <211> 456
 <212> DNA
 <213> Homo sapiens

```

<400> 301
ggccgggtta ttgccgccc gtttgtcggg gaaacccggc agaccttcga ggcacccggc
60
aaccggcgcg actattccgt accgccgccc gaaccgacct tgctcgacag gcttacggac
120
gcgggccgga cggtgatcgc aatcggcaag attggtgata tctacgcgca caaaggcgtg
180
tctcaggtgc gtaaggcaat ggcaatattg gccttgttcg atgaaacact cattgccatg
240
gacgacgcgc aggacggcga tctgggtcttc accaacttcg tggatttega catgctctac
300
gggcatcgca gggatgtgcc cggtatgcc gccgcgctcg aggttttcga ccggaggctg
360
ccggaagcca tggcgaaatt gcggacgggc gatcttctga tcctgacagc cgatcatggc
420
tgcgaccga ccctcaaggg aaccgaccac acgcgt
456

```

```

<210> 302
<211> 152
<212> PRT
<213> Homo sapiens

```

```

<400> 302
Gly Arg Val Ile Ala Arg Pro Phe Val Gly Glu Thr Arg Gln Thr Phe
1      5      10      15
Glu Arg Thr Gly Asn Arg Arg Asp Tyr Ser Val Pro Pro Pro Glu Pro
20     25     30
Thr Leu Leu Asp Arg Leu Thr Asp Ala Gly Arg Thr Val Ile Ala Ile
35     40     45
Gly Lys Ile Gly Asp Ile Tyr Ala His Lys Gly Val Ser Gln Val Arg
50     55     60
Lys Ala Met Ala Ile Leu Ala Leu Phe Asp Glu Thr Leu Ile Ala Met
65     70     75     80
Asp Asp Ala Gln Asp Gly Asp Leu Val Phe Thr Asn Phe Val Asp Phe
85     90     95
Asp Met Leu Tyr Gly His Arg Arg Asp Val Pro Gly Tyr Ala Ala Ala
100    105    110
Leu Glu Ala Phe Asp Arg Arg Leu Pro Glu Ala Met Ala Lys Leu Arg
115    120    125
Thr Gly Asp Leu Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro Thr
130    135    140
Leu Lys Gly Thr Asp His Thr Arg
145    150

```

```

<210> 303
<211> 402
<212> DNA
<213> Homo sapiens

```

```

<400> 303
nncgtgggca tcgaggagtt cctcgacatg aagtatcacg cgacgccgat tcatcgtcgc
60

```

tgacagcggg tttccggaac acatcagcgt tcagacagga gcgaggagac catgtacctg
 120
 ggtgctcagc tgttcagtga cagcgagtac gagcagcgcc tgagacgtgt ccgtgagctc
 180
 atggaccgtc aggggtctgtc ggcgatcatc gtcaccgatc cggccaacat cttctatctg
 240
 atcggttaca acgcctgggc gttctacacc ccgcagatgc tgttcgtgcc gatcgacgga
 300
 gagatgggcc tctacgctcg cgagatggat cgcattggcg acatcngcac gacgtcgttg
 360
 cccgccgac agatcgtcgg ttaccgggag agttatgtgc ac
 402

<210> 304

<211> 97

<212> PRT

<213> Homo sapiens

<400> 304

Met	Tyr	Leu	Gly	Ala	Gln	Leu	Phe	Ser	Asp	Ser	Glu	Tyr	Glu	Gln	Arg
1				5					10					15	
Leu	Arg	Arg	Val	Arg	Glu	Leu	Met	Asp	Arg	Gln	Gly	Leu	Ser	Ala	Ile
			20					25					30		
Ile	Val	Thr	Asp	Pro	Ala	Asn	Ile	Phe	Tyr	Leu	Ile	Gly	Tyr	Asn	Ala
		35					40					45			
Trp	Ser	Phe	Tyr	Thr	Pro	Gln	Met	Leu	Phe	Val	Pro	Ile	Asp	Gly	Glu
	50					55					60				
Met	Val	Leu	Tyr	Ala	Arg	Glu	Met	Asp	Arg	Met	Ala	His	Ile	Xaa	Thr
65					70				75					80	
Thr	Ser	Leu	Pro	Ala	Asp	Gln	Ile	Val	Gly	Tyr	Pro	Glu	Ser	Tyr	Val
				85				90						95	

His

<210> 305

<211> 375

<212> DNA

<213> Homo sapiens

<400> 305

nnacgcgtcg gttccgcac gagcgaccgg atcgcatcga cgagcacgct gcaccagtgc
 60
 gtgtcgtcct ggccaatatg ggcgatcagc cggtagcgtt cgggacgctc gctcacctcg
 120
 gccgccattt cggatgcgac acgcgcgcct gcgcgctcgg cctccagcaa ctcgtcgagc
 180
 gtcgccacca gcgcggcgcg atcttcatgc ggagtcagat cggcgcgggc gtcaggcccc
 240
 tcgccatgcg tcggaatcga catgcagcac cctcctgccg ggatcgatgg cgtaatacgt
 300
 gcgacgggtac acggcgcggtg ttgcacgaac gtgcaaatca gcgcgtgcct cgtgccatat
 360
 acgtcacatc atatg
 375

<210> 306
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 306
 Xaa Arg Val Gly Ser Ala Ser Ser Asp Arg Ile Ala Ser Thr Ser Thr
 1 5 10 15
 Leu His Gln Cys Val Ser Ser Trp Arg Ile Trp Ala Ile Ser Arg Tyr
 20 25 30
 Ser Ser Gly Ser Ser Leu Thr Ser Ala Ala Ile Ser Asp Ala Thr Arg
 35 40 45
 Ala Pro Ala Arg Ser Ala Ser Ser Asn Ser Ser Ser Val Ala Thr Ser
 50 55 60
 Ala Ala Arg Ser Ser Cys Gly Val Arg Ser Ala Arg Ala Ser Gly Pro
 65 70 75 80
 Ser Pro Cys Val Gly Ile Asp Met Gln His Pro Pro Ala Arg Ile Asp
 85 90 95
 Gly Val Ile Arg Ala Thr Val His Gly Ala Cys Cys Thr Asn Val Gln
 100 105 110
 Ile Ser Ala Cys Leu Val Pro Tyr Thr Ser His His Met
 115 120 125

<210> 307
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 307
 actagttctg gccgctcccc tggggctttg ggtaacaatt gtcagcccca cccatcctag
 60
 ggtaggaag gctattctct ttggccactc tcatacctaag acctatttgg agaacctctg
 120
 gggtttgagt ctttttttca gcagaatgag gcttgatccc gcattatagc acctcgcaca
 180
 ttgatgtct cttcttctca cccactcacc ccacctggg ggtaggggca aaaaagtggc
 240
 tcaaagctgc gggtcagagt tccttgtaaa caaggctcct ccctcactgt cctcacctg
 300
 ctccagcaga gggagcagcg gaaggaccac tctgctgcag ccatgcttgt ttctaacca
 360
 gcagaactgg acataatggg aacaggggtct gaagacaatc aatccagggc tgcagtgggt
 420
 gctgagtctg gggaagcctc cacctggagg ggcagctggg cagtggcagc tcccttgga
 480
 tggctcagcc tctggacatc accccaccca accagagccc tggctcttgc tggatgtcca
 540
 cagatgagtg cctgggattg gtctcagcca ctatgggggg gatgtgcagg gagaggtgat
 600
 gagggagtga gcaggactgt ctatgtgcct ctgtcctcat cctgaggctt gggctctgaaa
 660
 ttggtgctgc agcactggca cgcgt
 685

<210> 308
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 308
 Met Leu Val Ser Asn Pro Ala Glu Leu Asp Ile Met Gly Thr Gly Ser
 1 5 10 15
 Glu Asp Asn Gln Ser Arg Ala Ala Val Gly Ala Glu Ser Gly Glu Ala
 20 25 30
 Ser Thr Trp Arg Gly Ser Trp Ala Val Ala Ala Pro Leu Glu Trp Leu
 35 40 45
 Ser Leu Trp Thr Ser Pro His Pro Thr Arg Ala Leu Ala Leu Ala Gly
 50 55 60
 Cys Pro Gln Met Ser Ala Trp Asp Trp Ser Gln Pro Leu Trp Gly Gly
 65 70 75 80
 Cys Ala Gly Arg Gly Asp Glu Gly Val Ser Arg Thr Val Tyr Val Pro
 85 90 95
 Leu Ser Ser Ser
 100

<210> 309
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 309
 caggctcgta ctattcgat cctgtgcat atggctcgagg tcatcaataa gctggctcgc
 60
 gtccagcgtc agatgctcca ggacctaggt cgtgagccca ccccggaaga gcttgccaac
 120
 gaactcgata tgaccgcaga gaaggctcatt gaggtgcaga aatacgggtcg cgagccgatc
 180
 tcgctgcata cccactggg tgaggatggc gattctgagt tcggtgacct tattgaggat
 240
 tccgaggcca tcgtgccagc agacgccgtc aacttcaccc tgttcagga gcagctgcat
 300
 gatgtcctcg ataccttgtc cgagcgagag gccggtgtcg tgcgatgcg attcggcttg
 360
 accgacggac agcccaagac cctggatgag atcggaag tctacggtgt tactcgggag
 420
 cgcacccgag ag
 432

<210> 310
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 310
 Gln Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn
 1 5 10 15
 Lys Leu Ala Arg Val Gln Arg Gln Met Leu Gln Asp Leu Gly Arg Glu

		20					25					30							
Pro	Thr	Pro	Glu	Glu	Leu	Ala	Asn	Glu	Leu	Asp	Met	Thr	Ala	Glu	Lys				
		35					40					45							
Val	Ile	Glu	Val	Gln	Lys	Tyr	Gly	Arg	Glu	Pro	Ile	Ser	Leu	His	Thr				
		50				55					60								
Pro	Leu	Gly	Glu	Asp	Gly	Asp	Ser	Glu	Phe	Gly	Asp	Leu	Ile	Glu	Asp				
65					70					75				80					
Ser	Glu	Ala	Ile	Val	Pro	Ala	Asp	Ala	Val	Asn	Phe	Thr	Leu	Leu	Gln				
				85					90					95					
Glu	Gln	Leu	His	Asp	Val	Leu	Asp	Thr	Leu	Ser	Glu	Arg	Glu	Ala	Gly				
		100						105					110						
Val	Val	Ser	Met	Arg	Phe	Gly	Leu	Thr	Asp	Gly	Gln	Pro	Lys	Thr	Leu				
		115					120					125							
Asp	Glu	Ile	Gly	Lys	Val	Tyr	Gly	Val	Thr	Arg	Glu	Arg	Ile	Arg	Gln				
	130					135					140								

<210> 311

<211> 358

<212> DNA

<213> Homo sapiens

<400> 311

acgcgtatcg aaaatatccc tcccattatt accgctcgcc ctgaactgat ggctcatgaa
60
ctgacgccag aatctcttga tgcgagcctg gagtgggccc atgtggtggt cattggctcct
120
ggactgggac aacaagcgtg gggcaaaaaa gcgctacaaa aggtcgagaa ttgtcgtaaa
180
ccgatgctgt gggatgccga cgcgcttaac cttctggcaa tcaatcctga taaacgtcac
240
aatcgcatcc tgacgccaca ccccggcgag gccgcgcggc tgcttagctg cagcgtcgca
300
gaaattgaaa acgatcgctt acttntctgc gcacgtctgg taaaacggta acccgagt
358

<210> 312

<211> 116

<212> PRT

<213> Homo sapiens

<400> 312

Thr	Arg	Ile	Glu	Asn	Ile	Pro	Pro	Ile	Ile	Thr	Ala	Arg	Pro	Glu	Leu				
1				5				10					15						
Met	Ala	His	Glu	Leu	Thr	Pro	Glu	Ser	Leu	Asp	Ala	Ser	Leu	Glu	Trp				
		20					25				30								
Ala	Asp	Val	Val	Val	Ile	Gly	Pro	Gly	Leu	Gly	Gln	Gln	Ala	Trp	Gly				
		35				40					45								
Lys	Lys	Ala	Leu	Gln	Lys	Val	Glu	Asn	Cys	Arg	Lys	Pro	Met	Leu	Trp				
		50			55					60									
Asp	Ala	Asp	Ala	Leu	Asn	Leu	Leu	Ala	Ile	Asn	Pro	Asp	Lys	Arg	His				
65				70				75						80					
Asn	Arg	Ile	Leu	Thr	Pro	His	Pro	Gly	Glu	Ala	Ala	Arg	Leu	Leu	Ser				
			85				90						95						
Cys	Ser	Val	Ala	Glu	Ile	Glu	Asn	Asp	Arg	Leu	Leu	Xaa	Cys	Ala	Arg				

100 105 110
 Leu Val Lys Arg
 115

<210> 313
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 313
 ncaactgaaa gcattgagat gagcgacgtg ctgtccccct tccacccac caaggccaac
 60
 acccctggtg gcgaaccgcg caccatccgc acctogaacg cgcacatcat tgccgtcacc
 120
 agtggcaaag gcggcggtgg caagaccttt gtctccgcca acctggccgc cgcgctgacc
 180
 cgcctgggac tgcgcggtgct ggtactggac gccgacctgg gcttggccaa cttggacgtg
 240
 gtgctgaacc tctaccccaa ggtgacgctg cacgatgtgt tcaccggcaa ggcctcgctg
 300
 caagacgcgg tggtcacggc ccccgcgggc ttccatgtgc tgctagc
 347

<210> 314
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 314
 Xaa Thr Glu Ser Ile Glu Met Ser Asp Val Leu Ser Pro Phe His Pro
 1 5 10 15
 Thr Lys Ala Asn Thr Pro Gly Gly Glu Pro Arg Thr Ile Arg Thr Ser
 20 25 30
 Asn Ala His Ile Ile Ala Val Thr Ser Gly Lys Gly Gly Val Gly Lys
 35 40 45
 Thr Phe Val Ser Ala Asn Leu Ala Ala Leu Thr Arg Leu Gly Leu
 50 55 60
 Arg Val Leu Val Leu Asp Ala Asp Leu Gly Leu Ala Asn Leu Asp Val
 65 70 75 80
 Val Leu Asn Leu Tyr Pro Lys Val Thr Leu His Asp Val Phe Thr Gly
 85 90 95
 Lys Ala Ser Leu Gln Asp Ala Val Val Thr Ala Pro Gly Gly Phe His
 100 105 110
 Val Leu Leu
 115

<210> 315
 <211> 544
 <212> DNA
 <213> Homo sapiens

<400> 315
 nnacgcgttc gtcaacagga aaacaacaac ggcttctcgc tggagggaac catgcttgcc
 60

gaagatatct acgcgatcat gctgttttca tcgctcatcc tggtcgtccc ggggccatcc
 120
 aacaccttgc tgctcagcgc ccgtttccat ttcggctcgc tgcgggcggc gcccttcac
 180
 ctgcttgagg cgttgggcta ctcgctatcc atttcggcat ggggctgggt attggcgcg
 240
 ctgtccgaga gcaatccatg gatcatcagt ctgaccaagg cactctgcgc gctatatgtg
 300
 gcgcttctgg cggatgaagac ctggaatgcc ntcgatccgc agtgcggggc cggtaacttc
 360
 cgccatgggc ccctgcccct gttcgtggca accctgtcga accgaaggc gctgatcttc
 420
 gccagcgtga tctttcccg caaggcgttc ctcgacttct ggaacaacta cagcatctcg
 480
 ctgctggcct tcctggttgt gctggcgccc atcgggatgc tttgggtcgg gctgggggcc
 540
 ggta
 544

<210> 316
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 316
 Ile Tyr Ala Ile Met Leu Phe Ser Ser Leu Ile Leu Val Val Pro Gly
 1 5 10 15
 Pro Ser Asn Thr Leu Leu Leu Ser Ala Arg Phe His Phe Gly Ser Leu
 20 25 30
 Arg Ala Ala Pro Phe Ile Leu Leu Glu Ala Leu Gly Tyr Ser Leu Ser
 35 40 45
 Ile Ser Ala Trp Gly Trp Val Leu Ala Arg Leu Ser Glu Ser Asn Pro
 50 55 60
 Trp Ile Ile Ser Leu Thr Lys Ala Leu Cys Ala Leu Tyr Val Ala Leu
 65 70 75 80
 Leu Ala Val Lys Thr Trp Asn Ala Xaa Asp Pro Gln Cys Gly Ala Gly
 85 90 95
 Asn Phe Arg His Gly Pro Leu Pro Leu Phe Val Ala Thr Leu Ser Asn
 100 105 110
 Pro Lys Ala Leu Ile Phe Ala Ser Val Ile Phe Pro Gly Lys Ala Phe
 115 120 125
 Leu Asp Phe Trp Asn Asn Tyr Thr Ile Ser Leu Leu Ala Phe Leu Val
 130 135 140
 Val Leu Ala Pro Ile Gly Met Leu Trp Val Gly Leu Gly Ala Gly
 145 150 155

<210> 317
 <211> 343
 <212> DNA
 <213> Homo sapiens

<400> 317
 nggtcagcct ctcgccagg caattctctt aagatacatg agctgctatg agtaccaaag
 60

ccagaggttt gtccactgag agaagcacat tggaaagggg ggcgtgggcc tgggactgtg
120
tggcacttta tgcacggggg gggcctaagg gggnggtcc accaaccatg cactgngggg
180
ggggtgtggg taacatgccg tgcattttgg ggggtgtgcca tgagtggcac accatggggg
240
tggcatgtgg ggcattgtatg catgtggtgt tggcgcagca aactcagctc ttacctggct
300
ggggccagcc tctaaaactt ctcacattgg gctcccttct gac
343

<210> 318
<211> 98
<212> PRT
<213> Homo sapiens

<400> 318
Met Ser Thr Lys Ala Arg Gly Leu Ser Thr Glu Arg Ser Thr Leu Glu
1 5 10 15
Arg Gly Ala Trp Ala Trp Asp Cys Val Ala Leu Tyr Ala Arg Gly Gly
20 25 30
Pro Lys Gly Gly Gly Pro Pro Thr Met His Xaa Gly Trp Gly Val Gly
35 40 45
Asn Met Pro Cys Ile Leu Gly Val Cys His Glu Trp His Thr Met Gly
50 55 60
Val Ala Cys Gly Ala Cys Met His Val Val Leu Ala Gln Gln Thr Gln
65 70 75 80
Leu Leu Pro Gly Trp Gly Gln Pro Leu Lys Leu Leu Thr Leu Gly Ser
85 90 95
Leu Leu

<210> 319
<211> 429
<212> DNA
<213> Homo sapiens

<400> 319
gaattctcga tgtacccctt cccggcagtc ctattctcga gctgagcggg cacagtggcc
60
ccgttaacag tgtggcttgg ggtccacca gccagagcac gttgcgaaat ggacctagta
120
agggcatgat atgtacagga ggcgacgatg ctcagtgcct cgtatatgat ctgactagct
180
caactcttcg aacagcatct gctcaaggac ggcgctctcg aaacagtcca tataaacaaa
240
gccattcacc gggaatagac ggatggcgtg tcggcgcaga agtgccggtg ctcgcttata
300
cggccccgtc tatgggtcaac aatgctagct ggctcgcat gcctgcgcca tcaaaacgca
360
catcgctaca gagcaaacac cgcagccttt accgcagctt actcagttag tggactgagt
420
atacgtcen
429

<210> 320
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 320
 Met Ile Cys Thr Gly Gly Asp Asp Ala Gln Cys Leu Val Tyr Asp Leu
 1 5 10 15
 Thr Ser Ser Thr Leu Arg Thr Ala Ser Ala Gln Gly Arg Arg Ser Arg
 20 25 30
 Asn Ser Pro Tyr Lys Gln Ser His Ser Pro Gly Ile Asp Gly Trp Arg
 35 40 45
 Val Gly Ala Glu Val Pro Val Leu Ala Tyr Thr Ala Pro Ser Met Val
 50 55 60
 Asn Asn Ala Ser Trp Leu Gly Met Pro Ala Pro Ser Lys Arg Thr Ser
 65 70 75 80
 Leu Gln Ser Lys His Arg Ser Leu Tyr Arg Ser Leu Leu Ser Glu Trp
 85 90 95
 Thr Glu Tyr Thr Ser
 100

<210> 321
 <211> 530
 <212> DNA
 <213> Homo sapiens

<400> 321
 ngtgcacgac gtgctcgcca agtcctcgg gtcctctaata gcatcaacg tggttcacgc
 60
 caccgtcgat gcgttcgagc agtcgagga gcccgagag gtcgcccgtc gccgcggcaa
 120
 gtccggttgag gagatcgccc cagcagccat gctgcgtgcg cgcaaggagg ccgacgaggc
 180
 cgccgctgct gcccgcatgg aggaaaaggc ggggggtaac tgatgagcaa gctgaagatc
 240
 accagatca agtctggcat cgctaccaag ccaaatcatc gtgagaccct gcgcagcctc
 300
 ggactgaagc gtattggtga cacggctcgc aaggaggacc gcccgagatt ccgcggcatg
 360
 gtccggaccg ttcgtcacct cgtcaccatg gaagagggtg actgacatgg ctattgagct
 420
 ccatgacctc aagcccgtc ctggtgcca caaggccaag acccgcggtg gtcgtggtga
 480
 gggttccaag ggtaagaccg ctggtcgcgg taccaagggc accggtgcac
 530

<210> 322
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ser Lys Leu Lys Ile Thr Gln Ile Lys Ser Gly Ile Ala Thr Lys

```

1           5           10           15
Pro Asn His Arg Glu Thr Leu Arg Ser Leu Gly Leu Lys Arg Ile Gly
           20           25           30
Asp Thr Val Ile Lys Glu Asp Arg Pro Glu Phe Arg Gly Met Val Arg
           35           40           45
Thr Val Arg His Leu Val Thr Met Glu Glu Val Asp
           50           55           60

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<210> 323
 <211> 468
 <212> DNA
 <213> Homo sapiens

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<400> 323
ntccggaccc gctgtggcca cgtattctgc cgttcctgta ttgctaccag tctaaagaac
60
aacaagtgga cctgtcctta ttgccgggca tatcttcctt cagaaggagt tccagcaact
120
gatgtagcca aaagaatgaa atcagagtat aagaactgcg ctgagtgtga caccctgggt
180
tgccctcagt aaatgagggc acatattcgg acttgtcaga agtacataga taagtatgga
240
ccactacaag aacttgagga gacagcagca aggtgtgtat gtcccttttg tcagagggaa
300
ctgtatgaag acagcttgct ggatcattgt attactcatc acagatcgga acggaggcct
360
gtgttctgtc cactttgcca ttaataccc gatgagaatc caagcagctt cagtggcagt
420
ttaataagac atctgcaagt tagtcacact ttggtttatg atgatttc
468

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<210> 324
 <211> 156
 <212> PRT
 <213> Homo sapiens

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<400> 324
Xaa Arg Thr Arg Cys Gly His Val Phe Cys Arg Ser Cys Ile Ala Thr
1           5           10           15
Ser Leu Lys Asn Asn Lys Trp Thr Cys Pro Tyr Cys Arg Ala Tyr Leu
           20           25           30
Pro Ser Glu Gly Val Pro Ala Thr Asp Val Ala Lys Arg Met Lys Ser
           35           40           45
Glu Tyr Lys Asn Cys Ala Glu Cys Asp Thr Leu Val Cys Leu Ser Glu
           50           55           60
Met Arg Ala His Ile Arg Thr Cys Gln Lys Tyr Ile Asp Lys Tyr Gly
65           70           75           80
Pro Leu Gln Glu Leu Glu Glu Thr Ala Ala Arg Cys Val Cys Pro Phe
           85           90           95
Cys Gln Arg Glu Leu Tyr Glu Asp Ser Leu Leu Asp His Cys Ile Thr
           100          105          110
His His Arg Ser Glu Arg Arg Pro Val Phe Cys Pro Leu Cys His Leu
           115          120          125
Ile Pro Asp Glu Asn Pro Ser Ser Phe Ser Gly Ser Leu Ile Arg His

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130 135 140
 Leu Gln Val Ser His Thr Leu Val Tyr Asp Asp Phe
 145 150 155

<210> 325
 <211> 374
 <212> DNA
 <213> Homo sapiens

<400> 325
 acgcgtgaag ggaggacgag gaagtaacgg gaagcacaag gccgctgctg gggagatggc
 60
 actggagccc cctaggaagc atctcacagg ctgtggccct tggcacgggg atctggggcc
 120
 aggtcgagcg caggtctggg tatcatgcga gtgcgggctc gctggggcgg gaaagagttt
 180
 ggagctctgc tcccaggga tccccactcc cgcagatgac ttgcccagaga gagttctgct
 240
 ggtggatttt gatggaaatt ctatttgatc gcaccactt ggttcactgt gtgcttccgg
 300
 gtcccagggt tttaggtgct tcatgccctg ctgggaacga gacacgctcc tgcctcagt
 360
 gaatcttcag tcta
 374

<210> 326
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 326
 Met Lys His Leu Lys Pro Gly Asp Pro Glu Ala His Ser Glu Pro Ser
 1 5 10 15
 Gly Cys Asp Gln Ile Glu Phe Pro Ser Lys Ser Thr Ser Arg Thr Leu
 20 25 30
 Ser Gly Lys Ser Ser Ala Gly Val Gly Ile Pro Trp Glu Gln Ser Ser
 35 40 45
 Lys Leu Phe Pro Ala Pro Ala Ser Pro His Ser His Asp Thr Gln Thr
 50 55 60
 Cys Ala Arg Pro Gly Pro Arg Ser Pro Cys Gln Gly Pro Gln Pro Val
 65 70 75 80
 Arg Cys Phe Leu Gly Gly Ser Ser Ala Ile Ser Pro Ala Ala Ala Leu
 85 90 95
 Cys Phe Pro Leu Leu Pro Arg Pro Pro Phe Thr Arg
 100 105

<210> 327
 <211> 538
 <212> DNA
 <213> Homo sapiens

<400> 327
 cactataaaa tccagtttgg ggcccgtgtt ctttctatt ggtctgtcag gtgaaaaact
 60

ccggctgggg gaaaagcgtc cgggtggtttg ttggtaaaga ggggtgcgtga tgggctctgg
 120
 ggaatggagg atggcgcacc ggctgtgggt ggactgtgga aacgggggggt ggcagtgccg
 180
 gggtagttgt cctgctggtc tggttttggg atcctgggct ggagaaatgc gatccaaaag
 240
 agctcgggat gggctcagag cgaccacga aaataccagg ggccaagtaa aatgaaccca
 300
 ccctttaaca gtgcacaaag cgctggcaca cgggccacgt ctggtgacgc aggctgcccc
 360
 aagcgtcca accattttgc aaacctggga gagcaagagg ggctctgcag gtctagccgc
 420
 cgccccctgtc ccactctggc cagccggagt ttttcaccta cagaccaata ggaaagaaca
 480
 cgggccccaa actggatttt atagtctgag ctctcagcat ctaaggaatg atatgcc
 538

<210> 328

<211> 125

<212> PRT

<213> Homo sapiens

<400> 328

Met	Val	Gly	Ala	Leu	Arg	Ala	Ala	Cys	Val	Thr	Arg	Arg	Gly	Pro	Cys
1				5					10					15	
Ala	Ser	Ala	Leu	Cys	Thr	Val	Lys	Gly	Trp	Val	His	Phe	Thr	Trp	Pro
			20					25					30		
Leu	Val	Phe	Ser	Trp	Val	Ala	Leu	Ser	Pro	Ser	Arg	Ala	Leu	Leu	Asp
		35					40					45			
Arg	Ile	Ser	Pro	Ala	Gln	Asp	Pro	Lys	Thr	Arg	Pro	Ala	Gly	Gln	Leu
	50					55					60				
Pro	Arg	His	Cys	His	Pro	Pro	Phe	Pro	Gln	Ser	Thr	His	Ser	Arg	Cys
65				70					75					80	
Ala	Ile	Leu	His	Ser	Pro	Glu	Pro	Ile	Thr	His	Pro	Leu	Tyr	Gln	Gln
			85						90					95	
Thr	Thr	Gly	Arg	Phe	Ser	Pro	Ser	Arg	Ser	Phe	Ser	Pro	Asp	Arg	Pro
			100					105					110		
Ile	Gly	Lys	Asn	Thr	Gly	Pro	Lys	Leu	Asp	Phe	Ile	Val			
		115					120					125			

<210> 329

<211> 407

<212> DNA

<213> Homo sapiens

<400> 329

tccggagagt tccctcccca ggaattcctt ctaagaatcc atgtggaaat agagcctgaa
 60
 gctcttcagt ctttctgctc cactgagcag tgttttcctg atacccttgg taccctgcca
 120
 gcagcctcgt tatgactcct aactccattg cctccatgg cccctgggag ctctctctct
 180
 cttctctctcc aggtagtaga gcactgcttc tggcttcttg tgcacagaag ggtttccac
 240

agctgagagc tgggctccta ctgacatagt tatttccttt atatcctgcc ccaccttctt
 300
 ctggtagcac acagcaacct tgcatagttag ctggtatcat taccttccca atcaacaggc
 360
 cttgatttct tataggactt tttctctcag atttacattg cttcttt
 407

<210> 330
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 330
 Met Ile Pro Ala Thr Met Gln Gly Cys Cys Val Leu Pro Glu Glu Gly
 1 5 10 15
 Gly Ala Gly Tyr Lys Gly Asn Asn Tyr Val Ser Arg Ser Pro Ala Leu
 20 25 30
 Ser Cys Gly Lys Pro Phe Cys Ala Gln Glu Ala Arg Ser Ser Ala Leu
 35 40 45
 Leu Pro Gly Glu Lys Glu Arg Glu Ser Ala Gln Gly Pro Trp Arg Ala
 50 55 60
 Met Glu Leu Gly Val Ile Thr Arg Leu Leu Ala Gly Tyr Gln Gly Tyr
 65 70 75 80
 Gln Glu Asn Thr Ala Gln Trp Ser Arg Lys Thr Glu Glu Leu Gln Ala
 85 90 95
 Leu Phe Pro His Gly Phe Leu Glu Gly Ile Pro Gly Glu Gly Thr Leu
 100 105 110
 Arg

<210> 331
 <211> 523
 <212> DNA
 <213> Homo sapiens

<400> 331
 tgtaccgaac ctgctggtct cgagggcctt gctgggctcg tcgtacgcac agctgacgaa
 60
 tccaccggcc cccatcccg cgccacttct gctgaggcca tggagtcgat cggagccagc
 120
 tacgacggat cggccggggt ggccggaagt cacgtcggcg tcgatgtgcc cgtgacaagg
 180
 ttcgacgcag cggctgaact cttcgtcgaa ttgttgaaca ccacgagcct ggttgaagag
 240
 gacatcgccc gtcagatcga cgcgggcgga gcctccctgg cccagaccag ccagcgcgga
 300
 tcggccctag ccgagatggc agcagcacgt gcgctatggc cagtgggggtc acggtcgtcc
 360
 ctgcccacga tcggtaccct ctcgtcgggt gaaaagctca acgccgcagc cgcacgagaa
 420
 ttctgggccc cgcactggac gatctccgat gccgtgctgg tggttgccgg agagggagtc
 480
 gaggacctcg acttgtaaat attcaaggag tggacgacca gct
 523

<210> 332
 <211> 174
 <212> PRT
 <213> Homo sapiens

<400> 332
 Cys Thr Glu Pro Ala Gly Leu Glu Gly Leu Ala Gly Leu Val Val Arg
 1 5 10 15
 Thr Ala Asp Glu Ser Thr Gly Pro His Pro Gly Ala Thr Phe Ala Glu
 20 25 30
 Ala Met Glu Ser Ile Gly Ala Ser Tyr Asp Gly Ser Ala Gly Leu Ala
 35 40 45
 Gly Ser His Val Gly Val Asp Val Pro Val Thr Arg Phe Asp Ala Ala
 50 55 60
 Ala Glu Leu Phe Val Glu Leu Leu Asn Thr Thr Ser Leu Val Glu Glu
 65 70 75 80
 Asp Ile Ala Arg Gln Ile Asp Ala Ala Arg Ala Ser Leu Ala Gln Thr
 85 90 95
 Ser Gln Arg Gly Ser Ala Leu Ala Glu Met Ala Ala Ala Arg Ala Leu
 100 105 110
 Trp Pro Val Gly Ser Arg Ser Ser Leu Pro Thr Ile Gly Thr Leu Ser
 115 120 125
 Ser Val Glu Lys Leu Asn Ala Ala Ala Ala Arg Glu Phe Trp Ala Ala
 130 135 140
 His Trp Thr Ile Ser Asp Ala Val Leu Val Val Ala Gly Glu Gly Val
 145 150 155 160
 Glu Asp Leu Asp Leu Ser Ile Phe Lys Glu Trp Thr Thr Ser
 165 170

<210> 333
 <211> 372
 <212> DNA
 <213> Homo sapiens

<400> 333
 nntgttcgtc gtgtcgaccc ggaactcaag gcccgaggcga tgacgggtgaa ggtgcccaacc
 60
 gatccccatc accgccccggg agttccattg aagtctgcga aggaccgtat ggacatcatt
 120
 tctgcttacc gagaactcgg aagctatcgc gccgcagccg aggtgtgcgg caccacccac
 180
 aagaccgtca agcgggtggt cgatcggttt gaagccggcg atccacccac cgggtggcaag
 240
 gaacggggccc gcaactacga tgcgggtggcc cagctcgtcg cgcagcgagt cgcgcgggtca
 300
 cacggccgga tcaactgcaa acggctgcta ccggtagcgc gagcggcagg atatgagggg
 360
 tcggcgcgga at
 372

<210> 334
 <211> 88
 <212> PRT

<213> Homo sapiens

<400> 334

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Met Asp Ile Ile Ser Ala Tyr Arg Glu Leu Gly Ser Tyr Arg Ala Ala
 1           5           10           15
Ala Glu Val Cys Gly Thr Thr His Lys Thr Val Lys Arg Val Val Asp
          20           25           30
Arg Phe Glu Ala Gly Asp Pro Pro Thr Gly Gly Lys Glu Arg Ala Arg
      35           40           45
Asn Tyr Asp Ala Val Ala Gln Leu Val Ala Gln Arg Val Ala Arg Ser
      50           55           60
His Gly Arg Ile Thr Ala Lys Arg Leu Leu Pro Val Ala Arg Ala Ala
65           70           75           80
Gly Tyr Glu Gly Ser Ala Arg Asn
          85

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<210> 335

<211> 356

<212> DNA

<213> Homo sapiens

<400> 335

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gtgcacgcct tgctgggcca gggcgatgcg cctgcgcgca ccttcgtgga cggtaccttt
60
ggcaggggag ggcattcgcg gctcatcctg cagcgggttg ggccgcaagg ccgcctgggtg
120
gcgttcgaca aggacaccga agccattcaa gcagcggcgc gcatcacgga tgcgcgcttt
180
tccatcnggc accagggggt cagccatctc ggggaactgc ccgccgccag cgtgtccggt
240
gtgctgctgg acctgggcgt gagctccccg cagatcgacg acccccagcg cgggttcagt
300
tttcgtttcg atggctcgct ggacatgcgc atggacacca ctccgatgca tggatg
356

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<210> 336

<211> 118

<212> PRT

<213> Homo sapiens

<400> 336

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Val His Ala Leu Leu Gly Glu Gly Asp Ala Pro Ala Arg Thr Phe Val
 1           5           10           15
Asp Gly Thr Phe Gly Arg Gly Gly His Ser Arg Leu Ile Leu Gln Arg
      20           25           30
Leu Gly Pro Gln Gly Arg Leu Val Ala Phe Asp Lys Asp Thr Glu Ala
      35           40           45
Ile Gln Ala Ala Ala Arg Ile Thr Asp Ala Arg Phe Ser Ile Xaa His
      50           55           60
Gln Gly Phe Ser His Leu Gly Glu Leu Pro Ala Ala Ser Val Ser Gly
65           70           75           80
Val Leu Leu Asp Leu Gly Val Ser Ser Pro Gln Ile Asp Asp Pro Gln
      85           90           95
Arg Gly Phe Ser Phe Arg Phe Asp Gly Pro Leu Asp Met Arg Met Asp

```

100
Thr Thr Pro Met His Gly
115

105

110

<210> 337
<211> 447
<212> DNA
<213> Homo sapiens

<400> 337
cagcctctct ccgaccgcgc cgggtgtgaag cacgggcatg ccgggtgtgpa agtggcacca
60
cagccaaaac agcgagctca cacttcaaag tccttcaaag accccaggcc tctgtaagaa
120
ccgctcatct ctgtgcccac agctcccccg cttccatgtg acccagaaat ggaaccacgc
180
agcagaggcg gggatcacag gtgaagcagc tgtgaacatt tgcttcaggc ttctgtgcaa
240
acaggcgcca tcatgtcagc cgggtgagcag gagcaacgtg cgtgggtcag ggggtggcca
300
cacgtccaac tttataagaa atgacagatt ccctgatggc catagggatc tgcagggccca
360
gcagcaggca taggacttcc ggtggccctg cgtcttcac aacactgagt attgtcaggg
420
tttctgtact gtttttacag ccaattg
447

<210> 338
<211> 111
<212> PRT
<213> Homo sapiens

<400> 338
Met Pro Val Cys Lys Trp His His Ser Gln Asn Ser Glu Leu Thr Leu
1 5 10 15
Gln Thr Pro Ser Lys Thr Pro Gly Leu Cys Lys Asn Arg Ser Ser Leu
20 25 30
Cys Pro Gln Leu Pro Arg Phe His Val Thr Gln Lys Trp Asn His Ala
35 40 45
Ala Glu Ala Gly Ile Thr Gly Glu Ala Ala Val Asn Ile Cys Phe Arg
50 55 60
Leu Leu Cys Lys Gln Ala Pro Ser Cys Gln Pro Val Ser Arg Ser Asn
65 70 75 80
Val Arg Gly Ser Gly Gly Gly His Thr Ser Asn Phe Ile Arg Asn Asp
85 90 95
Arg Phe Pro Asp Gly His Arg Asp Leu Gln Gly Gln Gln Ala
100 105 110

<210> 339
<211> 588
<212> DNA
<213> Homo sapiens

<400> 339

tctagaatga agcgctgtat cctagcaccg gcagacgtac caagactatc aaggggcgtca
 60
 gatcgtttat cctgcagttg ccattcatca gacaaatcca gtggaaccca atggaagaca
 120
 ccgacctgca agcgctgatg gccagactcg aattgctaatt tgatcggggtc gagcaactta
 180
 agagtcaaaa cggactccta ttagctcagg aaaagacctg ggcgcganaa cgcgctcacc
 240
 tcattgaaaa aaacgaaatc gcccggcgta aggtcgaatc gatgatttcg cgctgaagg
 300
 ccctggagca agactatgag ttaagcaata gcgttacgtg cagatcctcg acaaagaata
 360
 ttcgatcatc tgcccccagg aagaacgcag cacctggtga gtgctgcccg ctacctggaa
 420
 ggccaaaagg cgtgaaatcc gcagcagcgg caaagtcatc ggtgccgacc gcatcgccgt
 480
 gatggccgcg ctgaacatca cccacgatct gctgcataag caggaacggc ctgacgttca
 540
 ggccagcggc tcaacgcgcg agcaagtgcg tgacctgctg gaacgcgt
 588

<210> 340
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 340
 Met Glu Asp Thr Asp Leu Gln Ala Leu Met Ala Arg Leu Glu Leu Leu
 1 5 10 15
 Ile Asp Arg Val Glu Gln Leu Lys Ser Gln Asn Gly Leu Leu Leu Ala
 20 25 30
 Gln Glu Lys Thr Trp Ala Arg Xaa Arg Ala His Leu Ile Glu Lys Asn
 35 40 45
 Glu Ile Ala Arg Arg Lys Val Glu Ser Met Ile Ser Arg Leu Lys Ala
 50 55 60
 Leu Glu Gln Asp Tyr Glu Leu Ser Asn Ser Val Thr Cys Arg Ser Ser
 65 70 75 80
 Thr Lys Asn Ile Arg Ser Ser Ala Pro Arg Lys Asn Ala Ala Pro Gly
 85 90 95
 Glu Cys Cys Pro Leu Pro Gly Arg Pro Lys Gly Val Lys Ser Ala Ala
 100 105 110
 Ala Ala Lys Ser Ser Val Pro Thr Ala Ser Pro
 115 120

<210> 341
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 341
 ngccgcgcgg cctacctgct gtacctggcc tatgccacct ggcgtgaccg ctcggccttt
 60
 gcaatgaacg acacgccgac agttgcgacc gcgcgcagcc tgatcctgcg tggcttcttg
 120

ctgaacattc ttaaccccaa gctgacaatt ttcttctctgg ccttctctgcc tcaattcgta
 180
 acgccaggcg gcaccgcgcc ggccttgacag atgctgggtac tgagcggcgt gttcatggcg
 240
 atgacgcttg cagtgtttgt gctgtatggc ctgttggcga atgtgtttcg tcgtgcagtg
 300
 gtcgagtcgc cacgtgtgca gaactggctg cgacgcagtt ttgccacggc ctttgccggg
 360
 ctgggggttg acctggcggt tgcgcagcgc tgaggacgcg t
 401

<210> 342
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 342
 Xaa Arg Ala Ala Tyr Leu Leu Tyr Leu Ala Tyr Ala Thr Trp Arg Asp
 1 5 10 15
 Arg Ser Ala Phe Ala Met Asn Asp Thr Pro Thr Val Ala Thr Ala Arg
 20 25 30
 Ser Leu Ile Leu Arg Gly Phe Leu Leu Asn Ile Leu Asn Pro Lys Leu
 35 40 45
 Thr Ile Phe Phe Leu Ala Phe Leu Pro Gln Phe Val Thr Pro Gly Gly
 50 55 60
 Thr Ala Pro Ala Leu Gln Met Leu Val Leu Ser Gly Val Phe Met Ala
 65 70 75 80
 Met Thr Leu Ala Val Phe Val Leu Tyr Gly Leu Leu Ala Asn Val Phe
 85 90 95
 Arg Arg Ala Val Val Glu Ser Pro Arg Val Gln Asn Trp Leu Arg Arg
 100 105 110
 Ser Phe Ala Thr Ala Phe Ala Gly Leu Gly Leu Asn Leu Ala Phe Ala
 115 120 125
 Gln Arg
 130

<210> 343
 <211> 389
 <212> DNA
 <213> Homo sapiens

<400> 343
 gtgttgcgca actacatggc gtccctgccg ttcagcgtgg tcgagtcggc gcgcatcgac
 60
 ggggtgctcca acttccagat cttctggaag ctgatcgccc cgatggcgat gccggcgatg
 120
 gcggcgttcg cgaccctgca gttcctgtgg gtgtggaacg acctgctcat cgccaagctc
 180
 ttcttcacca acgacaaccc cacgggtgatc gtcaagctcc aacagctttc cnnngggcccc
 240
 aaggcccagg gtgoggagct gctgacggcg ggcgccttca tctccatcgt gctacccatg
 300
 atcgtcttct tcgtgctcca gaacttctg gtgcgcggta tgacgtcggg tgccgtcaag
 360

gggtgaccgc tcaactgcag tggcccggg
389

<210> 344
<211> 121
<212> PRT
<213> Homo sapiens

<400> 344
Val Leu Arg Asn Tyr Met Ala Ser Leu Pro Phe Ser Val Val Glu Ser
1 5 10 15
Ala Arg Ile Asp Gly Cys Ser Asn Phe Gln Ile Phe Trp Lys Leu Ile
20 25 30
Ala Pro Met Ala Met Pro Ala Met Ala Ala Phe Ala Thr Leu Gln Phe
35 40 45
Leu Trp Val Trp Asn Asp Leu Ile Ala Lys Leu Phe Leu Thr Asn
50 55 60
Asp Asn Pro Thr Val Ile Val Lys Leu Gln Gln Leu Ser Xaa Gly Pro
65 70 75 80
Lys Ala Gln Gly Ala Glu Leu Leu Thr Ala Gly Ala Phe Ile Ser Ile
85 90 95
Val Leu Pro Met Ile Val Phe Phe Val Leu Gln Asn Phe Leu Val Arg
100 105 110
Gly Met Thr Ser Gly Ala Val Lys Gly
115 120

<210> 345
<211> 360
<212> DNA
<213> Homo sapiens

<400> 345
ctagtacttt atgctgatgg tgaacgctgt tacatccttg cccctaaagg catgggttgc
60
ggatgatgtga tccaatctgg tgaagatgca tcaattaaag taggtaactg cttaccgatg
120
cgtaatatcc cagttggtac aacagtagac gctgtagaaa tgaaacctgc taaaggtgca
180
caaattgcac gttctgctgg ttcttacagc caaattatag ctgctgatgg tgcttacggt
240
actctacggt tacgtagtgg tgaaatgcgt aaaatccctg ctgagtgtcg tgcaacaatc
300
ggatgaagttg gtaatgcaga acatatgcta cgtcaactag gtaaagctgg tgctacgcgt
360

<210> 346
<211> 120
<212> PRT
<213> Homo sapiens

<400> 346
Leu Val Leu Tyr Ala Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys
1 5 10 15
Gly Met Val Ala Gly Asp Val Ile Gln Ser Gly Glu Asp Ala Ser Ile

```

      20      25      30
Lys Val Gly Asn Cys Leu Pro Met Arg Asn Ile Pro Val Gly Thr Thr
      35      40      45
Val His Ala Val Glu Met Lys Pro Ala Lys Gly Ala Gln Ile Ala Arg
      50      55      60
Ser Ala Gly Ser Tyr Ser Gln Ile Ile Ala Arg Asp Gly Ala Tyr Val
      65      70      75      80
Thr Leu Arg Leu Arg Ser Gly Glu Met Arg Lys Ile Pro Ala Glu Cys
      85      90      95
Arg Ala Thr Ile Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Gln
      100      105      110
Leu Gly Lys Ala Gly Ala Thr Arg
      115      120

```

<210> 347
 <211> 565
 <212> DNA
 <213> Homo sapiens

```

<400> 347
accggtgatg ccaaaggtgc tgtgacaagg ggattcatcg gttcgggcaa ggtcgtcacg
60
gcagctgccg tcatcatgat ttcggtgttc gtcttcttca tccccgaggg catgaacgcc
120
atcaaggaaa tcgccctggc cctggccgctc gggatcctca cggatgcctt cttggtgagg
180
atgaccctcg tccccggcgt gatggccctg ctaggtgaca aggcattggtg gttgcccggg
240
tggctggatc gacgcctacc ccgcctcgac atcgagggag aagggatcac ccacgaggaa
300
aagctggccg cctggcccac agcggatcac accgaggccc tgcacgccga ggggatcggg
360
gtggaggggc tcttcgaagg cctcgatctg cacgtcgaac cgcgtcaggt gcaagccgtc
420
gtcggatcgc agaacagtgt ctcgccgctc ctgctggcga tcgggggacg gctgcccttg
480
gatcacggcc ggatgaggtc gggaggattg ctgctacctg agcggggcttc cagagtgcgt
540
cgggtgacgt ggttccctga cgcgt
565

```

<210> 348
 <211> 188
 <212> PRT
 <213> Homo sapiens

```

<400> 348
Thr Gly Asp Ala Lys Gly Ala Val Thr Arg Gly Phe Ile Gly Ser Gly
1      5      10      15
Lys Val Val Thr Ala Ala Ala Val Ile Met Ile Ser Val Phe Val Phe
20      25      30
Phe Ile Pro Glu Gly Met Asn Ala Ile Lys Glu Ile Ala Leu Ala Leu
35      40      45
Ala Val Gly Ile Leu Thr Asp Ala Phe Leu Val Arg Met Thr Leu Val

```



```

      50              55              60
Pro Ala Val Met Ala Leu Leu Gly Asp Lys Ala Trp Trp Leu Pro Gly
65              70              75              80
Trp Leu Asp Arg Arg Leu Pro Arg Leu Asp Ile Glu Gly Glu Gly Ile
      85              90              95
Thr His Glu Glu Lys Leu Ala Ala Trp Pro Thr Ala Asp His Thr Glu
      100              105              110
Ala Leu His Ala Glu Gly Ile Gly Val Glu Gly Leu Phe Glu Gly Leu
      115              120              125
Asp Leu His Val Glu Pro Arg Gln Val Gln Ala Val Val Gly Ser Gln
      130              135              140
Asn Ser Val Ser Ala Val Leu Leu Ala Ile Gly Gly Arg Leu Pro Leu
145              150              155              160
Asp His Gly Arg Met Arg Ser Gly Gly Leu Leu Leu Pro Glu Arg Ala
      165              170              175
Ser Arg Val Arg Arg Val Thr Trp Phe Leu Asp Ala
      180              185

```

<210> 349
 <211> 339
 <212> DNA
 <213> Homo sapiens

```

<400> 349
ntgctggcca cggataatga ccgtactctg cgtgatgtcg ttgccgctga ccctacccat
60
gagctcgggtt cggctaccgc tcatacgttt gcggacaatt tgccgttccct tcttaaactg
120
ctcgcggcag aagagccact atcgttgcag gctcatccca gtttggcgca agcacaggaa
180
gggtacgggc gggagaatcg caaaggggtg ccattagatg cccagaccg gaattaccac
240
gatcccaacc ataaaccgga gcttattgtt gggctgacgc gattccacgc actagccggc
300
ttccgtgaac cacaacgcac acttgagctt tttgacgcg
339

```

<210> 350
 <211> 113
 <212> PRT
 <213> Homo sapiens

```

<400> 350
Xaa Leu Ala Thr Asp Asn Asp Arg Thr Leu Arg Asp Val Val Ala Ala
1      5      10      15
Asp Pro Thr His Glu Leu Gly Ser Ala Thr Ala His Thr Phe Ala Asp
      20      25      30
Asn Leu Pro Phe Leu Leu Lys Leu Leu Ala Ala Glu Glu Pro Leu Ser
      35      40      45
Leu Gln Ala His Pro Ser Leu Ala Gln Ala Gln Glu Gly Tyr Gly Arg
      50      55      60
Glu Asn Arg Lys Gly Val Pro Leu Asp Ala Pro Asp Arg Asn Tyr His
65      70      75      80
Asp Pro Asn His Lys Pro Glu Leu Ile Val Gly Leu Thr Arg Phe His

```

	85		90		95										
Ala	Leu	Ala	Gly	Phe	Arg	Glu	Pro	Gln	Arg	Thr	Leu	Glu	Leu	Phe	Asp
	100						105						110		
Ala															

<210> 351
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 351
 gcgcgccccca gtgccgagac ccggggcttc aggagccggc cccgggagag aagagtgcgg
 60
 cggcgggacgg agaaaacaac tccaaagttg gcgaaaggca ccgcccctac tcccgggctg
 120
 ccgcgccttc cccgccccca gccctggcat ccagagtacg ggtcgagccc gnggccatgg
 180
 agcccccttg gggaggcggc accagggagc ctgggccccg gggctccgcc gcgaccccat
 240
 cgggtagacc acagaagctc cgggaccctt ccggcacctc tggacagccc aggatgctgt
 300
 tggccaccen ntctctctcc tctccttgg aggcgctctg gcccatccag accg
 354

<210> 352
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 352
 Ala Arg Pro Ser Ala Glu Thr Arg Gly Phe Arg Ser Arg Pro Arg Glu
 1 5 10 15
 Arg Arg Val Arg Arg Arg Thr Glu Lys Thr Thr Pro Lys Leu Ala Lys
 20 25 30
 Gly Thr Ala Pro Thr Pro Gly Leu Pro Pro Pro Pro Arg Pro Gln Pro
 35 40 45
 Trp His Pro Glu Tyr Gly Ser Ser Pro Xaa Pro Trp Ser Pro Pro Gly
 50 55 60
 Glu Ala Ala Pro Gly Ser Leu Gly Pro Gly Ala Pro Pro Arg Pro His
 65 70 75 80
 Arg Val Asp His Arg Ser Ser Gly Thr Leu Pro Ala Pro Leu Asp Ser
 85 90 95
 Pro Gly Cys Cys Trp Pro Pro Xaa Pro Pro Pro Pro Pro Trp Arg Arg
 100 105 110
 Ser Gly Pro Ser Arg Pro
 115

<210> 353
 <211> 1469
 <212> DNA
 <213> Homo sapiens

<400> 353

nntcatgaag gcttgaactt gcgtgatctt cagcctgcgg acctggcggg tgacggcggt
60
attgagccgg tggacctcgt ggtcggagat gtctctttta tctccttgac gatgatcctt
120
gaacccattt cagctgttgt cagcccacac ggcctcatgc tgttgctggg gaagcctcaa
180
tttgagggtg gttgcaaggc tttgggagcc catggcggtg tcacggaccc ggccctgcgc
240
ttgcaggcca tcgcgggtgt catggcagca gcggtagatt tgggttggcg tatgcgtgac
300
gagtgcgata gcccgttgcc cgggcaggat ggaaacgttg agcacttcgt cttgctggaa
360
cgtacgggtc ggtgacagac gtccgggcat atcatgggcc gctactgtgg tcttgtgaac
420
gacacgagcc cttcgagata cgttgctcgtc gtcacccatg ccacgcggga cgacgctttt
480
gacgcggctg ccgaattcat ctctgaaatg gcggggcgag acattggttg cgcggttccg
540
gatgatcagg tgaagccgat gtcaagcaag ctgccaggga tcgatcttga aagcttgagg
600
gagttcgccc acgaggcgga ggtggctcgtc gtctttggcg gcgacggcac gatcttgcca
660
gctgctgaat ggtcattacc tcgccacgtt cccatgattg gcgtcaacct tggccatgct
720
ggttttcttg ctgagctgga gcgctccgat atggcggatc tagtgaacaa ggtgtgttcg
780
cgcgactaca ccgttgagga tcgcctcgtg cttaaaacca ccgtcaccca gcattccgga
840
caacaccgtt ggagttcttt tgccgtcaac gagttgtctc tggaaaaggc agcccggcgg
900
cgcgtgctcg acgttctggc gtctgtcgac gagttgccgg tgcaacgctg gagttgcgac
960
gggatcctgg tctcgacccc gaccggatcg acggcctacg cgttctcagc tggcggcccc
1020
gtcatgtggc ccgatctcga cgccatgctc atggtgccgt tgagcgetca cgtctctttt
1080
gctcgaccgc tggatcatgag ccagctgct cgagtggacc ttgacatcca gccagacggt
1140
tcagaatcgg cggttctgtg gtgcgacggg cgccgatcgt gcaccgtacg accgggggaa
1200
agaatcacgg tcgtccgcca tcccgaacct ctgcgcattg ctcgtctggc cgcgcagccc
1260
ttcacatcgc gtctgggtcaa gaagtttgag ctcccgggtc gcgggtggcg tcagggtcgt
1320
gaccgtcatc acctagagga gacttcgtga tacgtagtgt gcgaattcgt ggactcggcg
1380
tcatcgatga gacggtcctc gaaccctcat ccgcgctgac ggcagtcacc ggcgagaccg
1440
gcgccgaaa gaccatggtg gtcaccggt
1469

<210> 354

<211> 318

<212> PRT

<213> Homo sapiens

<400> 354

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Met Gly Arg Tyr Cys Gly Leu Val Asn Asp Thr Ser Pro Ser Arg Tyr
 1           5           10           15
Val Val Val Val Thr His Ala Thr Arg Asp Asp Ala Phe Asp Ala Ala
 20           25           30
Ala Glu Phe Ile Ser Glu Met Ala Gly Arg Asp Ile Gly Cys Ala Val
 35           40           45
Pro Asp Asp Gln Val Lys Pro Met Ser Ser Lys Leu Pro Gly Ile Asp
 50           55           60
Leu Glu Ser Leu Gly Glu Phe Ala His Glu Ala Glu Val Val Val Val
 65           70           75           80
Phe Gly Gly Asp Gly Thr Ile Leu Arg Ala Ala Glu Trp Ser Leu Pro
 85           90           95
Arg His Val Pro Met Ile Gly Val Asn Leu Gly His Val Gly Phe Leu
100           105           110
Ala Glu Leu Glu Arg Ser Asp Met Ala Asp Leu Val Asn Lys Val Cys
115           120           125
Ser Arg Asp Tyr Thr Val Glu Asp Arg Leu Val Leu Lys Thr Thr Val
130           135           140
Thr Glu His Ser Gly Gln His Arg Trp Ser Ser Phe Ala Val Asn Glu
145           150           155           160
Leu Ser Leu Glu Lys Ala Ala Arg Arg Arg Met Leu Asp Val Leu Ala
165           170           175
Ser Val Asp Glu Leu Pro Val Gln Arg Trp Ser Cys Asp Gly Ile Leu
180           185           190
Val Ser Thr Pro Thr Gly Ser Thr Ala Tyr Ala Phe Ser Ala Gly Gly
195           200           205
Pro Val Met Trp Pro Asp Leu Asp Ala Met Leu Met Val Pro Leu Ser
210           215           220
Ala His Ala Leu Phe Ala Arg Pro Leu Val Met Ser Pro Ala Ala Arg
225           230           235           240
Val Asp Leu Asp Ile Gln Pro Asp Gly Ser Glu Ser Ala Val Leu Trp
245           250           255
Cys Asp Gly Arg Arg Ser Cys Thr Val Arg Pro Gly Glu Arg Ile Thr
260           265           270
Val Val Arg His Pro Asp Arg Leu Arg Ile Ala Arg Leu Ala Ala Gln
275           280           285
Pro Phe Thr Ser Arg Leu Val Lys Lys Phe Glu Leu Pro Val Ser Gly
290           295           300
Trp Arg Gln Gly Arg Asp Arg His His Leu Glu Glu Thr Ser
305           310           315

```

<210> 355

<211> 558

<212> DNA

<213> Homo sapiens

<400> 355

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nggatccac ctctggaat ggaaaccac ataccagttc tcttctcga tttgaatgcg
60
gatgacctca gtgccaatga gcagcttggt ggcccccatg catccggcgt gaactccatc
120

```

ctgccaagg agcatggcag ccagtttttc tacctgcca tcataaagca cagtgatgat
 180
 gaggtttcag ccacagcctc ttgggattcc tcggtgcatg attctgttca cttgaatggg
 240
 gtcacaccac agaatgaaag gatttaccta attgtgaaaa ccacagttca actcagccac
 300
 cctgctgcta tggagttagt attacgaaaa cgaattgcag ccaatattta caacaaacag
 360
 agtttcacgc agagtttgaa gaggagaata tccctgaaaa atatatttta ttctgtggt
 420
 gtaacctatg aaatagtatc caatatacca aaggcaactg aggagataga ggaccgggaa
 480
 acgctggctc tcctggcagc aaggagtga aacgaaggca catcagatgg gaagacgtac
 540
 attgagaagt acactcga
 558

<210> 356

<211> 186

<212> PRT

<213> Homo sapiens

<400> 356

Xaa	Ile	Pro	Pro	Pro	Gly	Met	Glu	Thr	His	Ile	Pro	Val	Leu	Phe	Leu
1				5					10					15	
Asp	Leu	Asn	Ala	Asp	Asp	Leu	Ser	Ala	Asn	Glu	Gln	Leu	Val	Gly	Pro
			20					25					30		
His	Ala	Ser	Gly	Val	Asn	Ser	Ile	Leu	Pro	Lys	Glu	His	Gly	Ser	Gln
		35					40					45			
Phe	Phe	Tyr	Leu	Pro	Ile	Ile	Lys	His	Ser	Asp	Asp	Glu	Val	Ser	Ala
	50					55				60					
Thr	Ala	Ser	Trp	Asp	Ser	Ser	Val	His	Asp	Ser	Val	His	Leu	Asn	Gly
65					70				75					80	
Val	Thr	Pro	Gln	Asn	Glu	Arg	Ile	Tyr	Leu	Ile	Val	Lys	Thr	Thr	Val
			85						90					95	
Gln	Leu	Ser	His	Pro	Ala	Ala	Met	Glu	Leu	Val	Leu	Arg	Lys	Arg	Ile
			100					105					110		
Ala	Ala	Asn	Ile	Tyr	Asn	Lys	Gln	Ser	Phe	Thr	Gln	Ser	Leu	Lys	Arg
		115					120				125				
Arg	Ile	Ser	Leu	Lys	Asn	Ile	Phe	Tyr	Ser	Cys	Gly	Val	Thr	Tyr	Glu
	130					135					140				
Ile	Val	Ser	Asn	Ile	Pro	Lys	Ala	Thr	Glu	Glu	Ile	Glu	Asp	Arg	Glu
145					150					155				160	
Thr	Leu	Ala	Leu	Leu	Ala	Ala	Arg	Ser	Glu	Asn	Glu	Gly	Thr	Ser	Asp
			165						170					175	
Gly	Lys	Thr	Tyr	Ile	Glu	Lys	Tyr	Thr	Arg						
			180					185							

<210> 357

<211> 323

<212> DNA

<213> Homo sapiens

<400> 357

acgcgtgcgt gtgttggtgtg agtcgggtgt gtgcatgcgt gtgggtgtgc agcaggtggg
60
gtacgatcag gctgaaggct gatcaggcac aaggctctgg gggagagccc tggttccagc
120
cctgggggtca gagcagcagg ggccagaaag acggcagggg tgagcactgc acccgctggg
180
cagggcaggg ccacagaagg cagggcatgg aggccacgtg aagggttga cagagtggat
240
ggatgtctcc ggaagcacct gcgtggccca gtcagcagga tcagactcgc atgtgtcagg
300
gtcaccatgg gtcagcgagg atn
323

<210> 358

<211> 102

<212> PRT

<213> Homo sapiens

<400> 358

Met	Val	Thr	Leu	Thr	His	Ala	Ser	Leu	Ile	Leu	Leu	Thr	Gly	Pro	Arg
1				5					10					15	
Arg	Cys	Phe	Arg	Arg	His	Pro	Ser	Thr	Leu	Ser	Ser	Pro	Ser	Arg	Gly
			20					25					30		
Leu	His	Ala	Leu	Pro	Ser	Val	Ala	Leu	Pro	Cys	Pro	Ala	Gly	Ala	Val
		35					40					45			
Leu	Thr	Pro	Ala	Val	Phe	Leu	Ala	Pro	Ala	Ala	Leu	Thr	Pro	Gly	Leu
	50					55					60				
Glu	Pro	Gly	Leu	Ser	Pro	Arg	Ala	Leu	Cys	Leu	Ile	Ser	Leu	Gln	Pro
65					70				75					80	
Asp	Arg	Thr	Pro	Pro	Ala	Ala	His	Pro	His	Ala	Cys	Thr	His	Pro	Thr
			85						90					95	
His	Thr	Thr	His	Ala	Arg										
			100												

<210> 359

<211> 265

<212> DNA

<213> Homo sapiens

<400> 359

acgcgtaccg acaagcgccc ggtgatggcc gaccttcgcg aatcggggcg aatcgagcag
60
gatgcggaca tgatcgtctt catctaccgc gacgattact acaacaagga aaattcgccg
120
gacaaggggc tggccgagat catcatcggc aagcatcggg ggggccccac cggctcgtgc
180
aagctgaagt tcttcggcga gtacaccggt ttcgacaacc tggcccacaa ctcggttggt
240
tcgttcgaat aacggatgat tccgg
265

<210> 360

<211> 83

<212> PRT

<213> Homo sapiens

<400> 360

```

Thr Arg Thr Asp Lys Arg Pro Val Met Ala Asp Leu Arg Glu Ser Gly
 1           5           10           15
Ala Ile Glu Gln Asp Ala Asp Met Ile Val Phe Ile Tyr Arg Asp Asp
          20           25           30
Tyr Tyr Asn Lys Glu Asn Ser Pro Asp Lys Gly Leu Ala Glu Ile Ile
          35           40           45
Ile Gly Lys His Arg Gly Gly Pro Thr Gly Ser Cys Lys Leu Lys Phe
          50           55           60
Phe Gly Glu Tyr Thr Arg Phe Asp Asn Leu Ala His Asn Ser Val Gly
65           70           75           80
Ser Phe Glu

```

<210> 361

<211> 453

<212> DNA

<213> Homo sapiens

<400> 361

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gctttgcagg aggaaatctc tatctctggc tgcaagatga ggctgagcta cctgagcagc
60
cggacccctg gctacaaatc tgtcctgagg atcagcctca cccacccgac catccccttc
120
aacctcatga aggtgcacct catggtagcg gtggagggcc gcctcttcag gaagtgggtc
180
gctgcagccc cagacctgtc ctattatttc atttgggaca agacagacgt ctacaaccag
240
aaggtgtttg ggctttcaga agcctttgtt tccgtggggt atgaatatga atcctgcccc
300
gatctaatacc tgtgggaaaa aagaacaaca gtgctgcagg gctatgaaat tgacgcgtcc
360
aagcttggag gatggagcct agacaaacat catgccctca acattcaaag tggcatcctg
420
cacaaagggg atggngagaa ccagtttgtg tct
453

```

<210> 362

<211> 151

<212> PRT

<213> Homo sapiens

<400> 362

```

Ala Leu Gln Glu Glu Ile Ser Ile Ser Gly Cys Lys Met Arg Leu Ser
 1           5           10           15
Tyr Leu Ser Ser Arg Thr Pro Gly Tyr Lys Ser Val Leu Arg Ile Ser
          20           25           30
Leu Thr His Pro Thr Ile Pro Phe Asn Leu Met Lys Val His Leu Met
          35           40           45
Val Ala Val Glu Gly Arg Leu Phe Arg Lys Trp Phe Ala Ala Ala Pro
          50           55           60
Asp Leu Ser Tyr Tyr Phe Ile Trp Asp Lys Thr Asp Val Tyr Asn Gln

```

```

65          70          75          80
Lys Val Phe Gly Leu Ser Glu Ala Phe Val Ser Val Gly Tyr Glu Tyr
          85          90          95
Glu Ser Cys Pro Asp Leu Ile Leu Trp Glu Lys Arg Thr Thr Val Leu
          100          105          110
Gln Gly Tyr Glu Ile Asp Ala Ser Lys Leu Gly Gly Trp Ser Leu Asp
          115          120          125
Lys His His Ala Leu Asn Ile Gln Ser Gly Ile Leu His Lys Gly Asn
          130          135          140
Gly Glu Asn Gln Phe Val Ser
145          150

```

<210> 363

<211> 502

<212> DNA

<213> Homo sapiens

<400> 363

```

ggtacaaaaa aagtttgcca cagtattcac actccagggtc tccataaacc ttccagatcc
60
gctcacacaa gctggtgttc atttgcttct tctgtaaact gttcaggacc ttcataaaag
120
cggtgatgcc tgaccggtgc tcaggggcag ctttgcaaga gtcaggctga tgtgtgatgg
180
tgtccccacc accagctact ggagggagga ggtctgaggg ctcagctggg tttgacctga
240
gacacctgct gggatctggg tcaccagctg aaagcacagc catgttctgc cttcccccta
300
gggggctctg ggcgccatgg ctttcctgat ctgaccagc actctggggc ttggacagca
360
gtagtgtgat cacttcacct tgcgtctgga ctgagcttct gtgctgcatg tctgggggct
420
tctcaggagc agcatgagcc tctgcggagg aggtatcatt tttcaacaaa aaatcatctg
480
aaaccacctc ttgagaatgc ag
502

```

<210> 364

<211> 136

<212> PRT

<213> Homo sapiens

<400> 364

```

Met Gln His Arg Ser Ser Val Gln Thr Gln Gly Glu Val Ile Thr Leu
1          5          10          15
Leu Leu Ser Lys Ala Gln Ser Ala Gly Ser Asp Gln Glu Ser His Gly
          20          25          30
Ala Gln Ser Pro Leu Gly Glu Gly Gln Asn Met Ala Val Leu Ser Ala
          35          40          45
Gly Asp Pro Asp Pro Ser Arg Cys Leu Arg Ser Asn Pro Ala Glu Ala
          50          55          60
Ser Asp Leu Leu Pro Pro Val Ala Gly Gly Gly Asp Thr Ile Thr His
65          70          75          80
Gln Pro Asp Ser Cys Lys Ala Ala Pro Glu His Arg Ser Gly Ile Thr

```


				85					90					95	
Ala	Phe	Met	Lys	Val	Leu	Asn	Ser	Leu	Gln	Lys	Lys	Gln	Met	Asn	Thr
			100						105					110	
Ser	Leu	Cys	Glu	Arg	Ile	Trp	Lys	Val	Tyr	Gly	Asp	Leu	Glu	Cys	Glu
		115					120						125		
Tyr	Cys	Gly	Lys	Leu	Phe	Trp	Tyr								
	130					135									

```
<210> 365
<211> 333
<212> DNA
<213> Homo sapiens
```

```
<400> 365
atctcaacgg atgcatccat caaggagatg atccccccag gtgctcttgt tatgctcaca
60
ccactgatcg ttgggattct atttgggggtt gagaccctct ctggagtcct tgctggtgcc
120
cttgtctctg gtgttcagat tgccatttct gcatccaaca ctggtggtgc ctgggacaac
180
gccaaagaagt acattgaggc tggagtttca gagcatgcc a ggacccttg cccaaaaggt
240
tctgaccctc acaaggcggc tgtcattggt gacaccattg gagatcctct caaggacacg
300
tctggccctt cctcaacat cctcatcaag ctt
333
```

```
<210> 366
<211> 111
<212> PRT
<213> Homo sapiens
```

```

<400> 366
Ile Ser Thr Asp Ala Ser Ile Lys Glu Met Ile Pro Pro Gly Ala Leu
 1          5          10          15
Val Met Leu Thr Pro Leu Ile Val Gly Ile Leu Phe Gly Val Glu Thr
      20          25          30
Leu Ser Gly Val Leu Ala Gly Ala Leu Val Ser Gly Val Gln Ile Ala
      35          40          45
Ile Ser Ala Ser Asn Thr Gly Gly Ala Trp Asp Asn Ala Lys Lys Tyr
      50          55          60
Ile Glu Ala Gly Val Ser Glu His Ala Arg Thr Leu Gly Pro Lys Gly
65          70          75          80
Ser Asp Pro His Lys Ala Ala Val Ile Gly Asp Thr Ile Gly Asp Pro
      85          90          95
Leu Lys Asp Thr Ser Gly Pro Ser Leu Asn Ile Leu Ile Lys Leu
      100          105          110

```

```
<210> 367
<211> 381
<212> DNA
<213> Homo sapiens
```

<400> 367

gcgttcgctcg cactacccgg cggcggcgga acccttgacg agctactcga agcatggaca
60
tggcagcagc tcggtgtaca cagcaaaccg gtgngccttg tacgactcga cnncttctgg
120
gcaccgctga ccgcgctact caaccacatg accatcgaaa gcttcattcg ccctgaggac
180
cgcgcctcgc tcgtgatcgc cgataccata catcagctga tggccgatct tgagggatgg
240
accccaccac caccgaagtg gcgctcgtga catagaacaa atgattctga ctatggctca
300
ttgacatctg cgcagcggct actagctcca ttgacttcaa atcgggcctt ggccgaggct
360
cngttcaggt ggcccgaat g
381

<210> 368

<211> 89

<212> PRT

<213> Homo sapiens

<400> 368

Ala	Phe	Val	Ala	Leu	Pro	Gly	Gly	Gly	Gly	Thr	Leu	Asp	Glu	Leu	Leu
1				5				10						15	
Glu	Ala	Trp	Thr	Trp	Gln	Gln	Leu	Gly	Val	His	Ser	Lys	Pro	Val	Xaa
			20					25					30		
Leu	Val	Arg	Leu	Asp	Xaa	Phe	Trp	Ala	Pro	Leu	Thr	Ala	Leu	Leu	Asn
		35				40					45				
His	Met	Thr	Ile	Glu	Ser	Phe	Ile	Arg	Pro	Glu	Asp	Arg	Ala	Ser	Leu
	50				55					60					
Val	Ile	Ala	Asp	Thr	Ile	His	Gln	Leu	Met	Ala	Asp	Leu	Glu	Gly	Trp
65					70					75				80	
Thr	Pro	Pro	Pro	Pro	Lys	Trp	Arg	Ser							
				85											

<210> 369

<211> 313

<212> DNA

<213> Homo sapiens

<400> 369

gatacatgat cctctcatac cgcacacaca ccgctcccct ctgccgcaat tcgcagacaa
60
acttgccgag gcttcacagc aagccgtcaa ggctgcttcc tgtgggctac cgatagtctc
120
gtacgcgagt tctcggacat caacgccaac gtcgggcaag atactgtcaa cgccatctac
180
acattctacg agcagcaagc gaccagtctc ctccgccagc tgaacgacct cccacccgaa
240
gagcttcccg acgtcatcga ggacttcttc cgccgtgtcca ctgatgtect tctttacat
300
ttccagcaag ctt
313

<210> 370

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 370
 Ser Ser His Thr Ala His Thr Pro Leu Pro Ser Ala Ala Ile Arg Arg
 1 5 10 15
 Gln Thr Cys Ala Gly Phe Thr Ala Ser Arg Gln Gly Cys Phe Leu Trp
 20 25 30
 Ala Thr Asp Ser Leu Val Arg Glu Phe Ser Asp Ile Asn Ala Asn Val
 35 40 45
 Gly Gln Asp Thr Val Asn Ala Ile Tyr Thr Phe Tyr Glu Gln Gln Ala
 50 55 60
 Thr Ser Phe Leu Arg Gln Leu Asn Asp Leu Pro Pro Glu Glu Leu Pro
 65 70 75 80
 Asp Val Ile Glu Asp Phe Phe Arg Leu Ser Thr Asp Val Leu Leu Tyr
 85 90 95
 His Phe Gln Gln Ala
 100

<210> 371
 <211> 380
 <212> DNA
 <213> Homo sapiens

<400> 371
 atgacgggtc acgtcatcct ggcgattcca caggtggtga cgatcatggat cggcctcatc
 60
 tgcacgcgcca ttggcacggg ctttatcaag ccgaacctct ccacgggtggg aggaggtctt
 120
 tacgatgacg gtgacccccg ccgcgatcag ggtttcctgt acttctacat gtcgatcagt
 180
 attggatctc tcttcgcgcc gatcgtcacc ggcctcctca aggaccatta cggctaccac
 240
 gtaggttttca ttgccgctgc tategggtatg gctctgggtc tgatcgcctt cttccacggt
 300
 cgttccaaac tgcgtgagct cgccttcgac atccccaatc cgctggcccc cggcgagggt
 360
 cgccggatgg tgetccgcgg
 380

<210> 372
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 372
 Met Thr Gly His Val Ile Leu Ala Ile Pro Gln Val Val Thr Ser Trp
 1 5 10 15
 Ile Gly Leu Ile Cys Ile Ala Ile Gly Thr Gly Phe Ile Lys Pro Asn
 20 25 30
 Leu Ser Thr Val Val Gly Gly Leu Tyr Asp Asp Gly Asp Pro Arg Arg
 35 40 45
 Asp Gln Gly Phe Leu Tyr Phe Tyr Met Ser Ile Ser Ile Gly Ser Leu

```

      50              55              60
Phe Ala Pro Ile Val Thr Gly Leu Leu Lys Asp His Tyr Gly Tyr His
65              70              75              80
Val Gly Phe Ile Ala Ala Ala Ile Gly Met Ala Leu Gly Leu Ile Ala
      85              90              95
Phe Phe His Gly Arg Ser Lys Leu Arg Glu Leu Ala Phe Asp Ile Pro
      100              105              110
Asn Pro Leu Ala Pro Gly Glu Gly Arg Arg Met Val Leu Arg
      115              120              125

```

<210> 373

<211> 475

<212> DNA

<213> Homo sapiens

<400> 373

```

acatgttggg aaaattgcct cccactctgg tgctacaggt atgaatctca gccacagtga
60
tgactgtggc agctacaggg ctgatgaaca cccaccaag aaaaggagca tcatgtgcct
120
gcttctctct ggttctctaaa tcctttggcc aaacattttc cccacaaccc tccactccag
180
ttggtgtggtc actgcctctc agaaagaagt cccagggtccc tgtcagcccc agagcgctcg
240
catggactct gccactgtc cctttccaac acggaggccc ccaattctgg ggacccctac
300
accctaccct gtaccaccac atccccatgc ctgctccaga cagcactaac ctcccatgac
360
agtgggacca aagcagttct taaagggtcca atccactcag ttcttaaagt aaaaacagtt
420
gcccatgagt cacccecaaa gacgtccgca catatgccaa acattcggtg tgcac
475

```

<210> 374

<211> 109

<212> PRT

<213> Homo sapiens

<400> 374

```

Met Gly Met Trp Trp Tyr Arg Val Gly Cys Arg Gly Pro Gln Asn Trp
1              5              10              15
Gly Pro Pro Cys Trp Lys Gly Thr Val Gly Arg Val His Ala Gly Ala
      20              25              30
Leu Gly Leu Thr Gly Thr Trp Asp Phe Phe Leu Arg Gly Ser Asp Gln
      35              40              45
Pro Thr Gly Val Glu Gly Cys Gly Glu Asn Val Trp Pro Lys Asp Leu
      50              55              60
Gly Thr Arg Glu Lys Gln Ala His Asp Ala Pro Phe Leu Gly Gly Val
65              70              75              80
Phe Ile Arg Pro Val Ala Ala Thr Val Ile Thr Val Ala Glu Ile His
      85              90              95
Thr Cys Ser Thr Arg Val Gly Gly Asn Phe Ser Asn Met
      100              105

```

<210> 375
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 375
 nnacgcgtcg cctccacctc gaaacccgcc ggcggtcggt ttttcaccat ggccgaccgc
 60
 aaggcccaag ttgcgacggt cacggacacg ctgtatttca cgccgtcgca atgggatgga
 120
 tgcattggcac ggatgcgtgg ggataagata tcagcactga agtggaatca gatgcagatg
 180
 gcggcatgct ccttcatagc ggcatgtggg gcgaagctgg gctgcccgcg gcgcactatg
 240
 ggcatggcgc agctgctgta ccagcgtttc catctatttc atgcgccgac tgagttttcg
 300
 ttacatgagg tggctttgac gtgtctcttc ac
 332

<210> 376
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 376
 Xaa Arg Val Ala Ser Thr Ser Lys Pro Ala Gly Gly Arg Phe Phe Thr
 1 5 10 15
 Met Ala Asp Arg Lys Ala Gln Val Ala Thr Val Thr Asp Thr Leu Tyr
 20 25 30
 Phe Thr Pro Ser Gln Trp Asp Gly Cys Met Ala Arg Met Arg Gly Asp
 35 40 45
 Lys Ile Ser Ala Leu Lys Trp Asn Gln Met Gln Met Ala Ala Cys Ser
 50 55 60
 Phe Ile Ala Ala Val Gly Ala Lys Leu Gly Cys Pro Gln Arg Thr Met
 65 70 75 80
 Gly Thr Ala Gln Leu Leu Tyr Gln Arg Phe His Leu Phe His Ala Pro
 85 90 95
 Thr Glu Phe Ser Leu His Glu Val Ala Leu Thr Cys Leu Phe
 100 105 110

<210> 377
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 377
 cgcggtgccag gtatgtcaac tgatctgtcg gatattttccg aggttgagta ccgtcaactg
 60
 aggctggaac gagtgggtgct gtgttcgggtg tggactcagg gaactgccgc agacgccgag
 120
 aacgctatgg cggagctgaa agcccttgct gaaacggcgg gatctcaggt actcgaagct
 180
 gtcattgcaac gtcggactac cccggatccg gcgacgtaca ttgggttcggg caagggtggct
 240

gagcttgccg aggtggtgcg ggcgactggt gccgatactg tcatttgtga cggatgaactt
 300
 gacgccgctc agttgcgcaa cctcgaggat cgggtcaagn gcaaagttgt ggaccggtcg
 360
 gtctgattc
 369

<210> 378
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 378
 Arg Val Pro Gly Met Ser Thr Asp Leu Ser Asp Ile Ser Glu Val Glu
 1 5 10 15
 Tyr Arg Gln Leu Arg Leu Glu Arg Val Val Leu Cys Ser Val Trp Thr
 20 25 30
 Gln Gly Thr Ala Ala Asp Ala Glu Asn Ala Met Ala Glu Leu Lys Ala
 35 40 45
 Leu Ala Glu Thr Ala Gly Ser Gln Val Leu Glu Ala Val Met Gln Arg
 50 55 60
 Arg Thr Thr Pro Asp Pro Ala Thr Tyr Ile Gly Ser Gly Lys Val Ala
 65 70 75 80
 Glu Leu Ala Glu Val Val Arg Ala Thr Gly Ala Asp Thr Val Ile Cys
 85 90 95
 Asp Gly Glu Leu Asp Ala Ala Gln Leu Arg Asn Leu Glu Asp Arg Val
 100 105 110
 Lys Xaa Lys Val Val Asp Arg Ser Val
 115 120

<210> 379
 <211> 408
 <212> DNA
 <213> Homo sapiens

<400> 379
 acgcgttact taaacttata tgtaaataat aaattcatta tttctagttg gtttaggtact
 60
 atgggctgtg gtttaccagg tgctatggca gctaaaattg cttatccaaa ccgtcaagca
 120
 gtagctatca caggcgacgg tgcgttccaa atggtaatgc aagactttgc tacagctggt
 180
 caatataact taccaatgac aatctttgta ttaaataaca aacaattgtc attcatataa
 240
 tatgaacaac aagctgctgg tgaattagag tatgccattg atttctctga tatggatcat
 300
 gctaaatttg ctgaagctgc tgggtggtaaa ggctatggtg tgagagatgt aagtcgtctt
 360
 gacgacatcg ttgaagaggc aatgggtcaa gatgttccaa caatcggt
 408

<210> 380
 <211> 136
 <212> PRT

<213> Homo sapiens

<400> 380

```

Thr Arg Tyr Leu Asn Leu Ser Val Asn Asn Lys Phe Ile Ile Ser Ser
 1           5           10           15
Trp Leu Gly Thr Met Gly Cys Gly Leu Pro Gly Ala Met Ala Ala Lys
      20           25           30
Ile Ala Tyr Pro Asn Arg Gln Ala Val Ala Ile Thr Gly Asp Gly Ala
      35           40           45
Phe Gln Met Val Met Gln Asp Phe Ala Thr Ala Val Gln Tyr Asn Leu
      50           55           60
Pro Met Thr Ile Phe Val Leu Asn Asn Lys Gln Leu Ser Phe Ile Lys
      65           70           75           80
Tyr Glu Gln Gln Ala Ala Gly Glu Leu Glu Tyr Ala Ile Asp Phe Ser
      85           90           95
Asp Met Asp His Ala Lys Phe Ala Glu Ala Ala Gly Gly Lys Gly Tyr
      100           105           110
Val Val Arg Asp Val Ser Arg Leu Asp Asp Ile Val Glu Glu Ala Met
      115           120           125
Ala Gln Asp Val Pro Thr Ile Val
      130           135

```

<210> 381

<211> 613

<212> DNA

<213> Homo sapiens

<400> 381

```

nacgcgtcat aggcggggccc agtggaagac caccgccaaca cagttgggttg agatccgcgt
60
tgagggcaag gtctcgcgcg tcccgcgaaa tctgggtcaag gcttaccact ctgggctgat
120
cgacgtcgag gactgaaccc tgggagcctg ggcggtccag catgactgct caggctcatt
180
accaaaacgc gtcgatcccc taggggtgtc gtcatgagca agcccgaagt gaccctgccc
240
gattccgccc ccgacgacct cgtcgttgag gacatcacca tcggcgacgg ccctgaagcg
300
tccgctggca acctcgtcga agtgcaactac gtcggcgtgg ccttaagcaa tggctcgtgag
360
ttcgattctt cctggaaccg cggggagccg ctgaccttcc aactaggggc tggccagggtg
420
atccccgagt gggatgaagg tgtccaaggt atgaaggctg gtggacgacg caaactcgtc
480
atccccacc accttgctta cgggtccgcaa ggaatctccg gtgtgatcgc tggcggtgag
540
acgctgggtc tcgtctgcga ccttgctaac atcatctgac gtgacccccg ctcaagcagt
600
cttcgcgccc ggg
613

```

<210> 382

<211> 137

<212> PRT

<213> Homo sapiens

<400> 382

```

Leu Leu Arg Leu Ile Thr Lys Thr Arg Arg Ser Arg Arg Val Val Val
 1           5           10           15
Met Ser Lys Pro Glu Val Thr Leu Pro Asp Ser Ala Pro Asp Asp Leu
      20           25           30
Val Val Glu Asp Ile Thr Ile Gly Asp Gly Pro Glu Ala Ser Ala Gly
      35           40           45
Asn Leu Val Glu Val His Tyr Val Gly Val Ala Leu Ser Asn Gly Arg
 50           55           60
Glu Phe Asp Ser Ser Trp Asn Arg Gly Glu Pro Leu Thr Phe Gln Leu
65           70           75           80
Gly Ala Gly Gln Val Ile Pro Glu Trp Asp Glu Gly Val Gln Gly Met
      85           90           95
Lys Val Gly Gly Arg Arg Lys Leu Val Ile Pro His His Leu Ala Tyr
      100          105          110
Gly Pro Gln Gly Ile Ser Gly Val Ile Ala Gly Gly Glu Thr Leu Val
      115          120          125
Phe Val Cys Asp Leu Val Asn Ile Ile
      130          135

```

<210> 383

<211> 352

<212> DNA

<213> Homo sapiens

<400> 383

```

nggagcaaca cctgggcctt gggaatgaag tgtaggagtt gcatttgctg aggttggtgt
60
ttgccaaaga gatgccagct tcttcgaact actgctgtgc aactcttcat gttcaaaacc
120
cagttttctg tttttcacac ctgaacatac acccccctgc agttgggtgg ctccccggtt
180
accagctggg ctctatctac agagagagca atggcttccc ttcccttgaa ggaagtctca
240
ccctcacaag gacacttgat ccgctgcaaa gcagaaagtg tgcggaccct ttgggaaggg
300
cgttcttttc ttgttttagaa cctaggattc tgtttttccc aaacaggatc an
352

```

<210> 384

<211> 93

<212> PRT

<213> Homo sapiens

<400> 384

```

Met Pro Ala Ser Ser Asn Tyr Cys Cys Ala Thr Leu His Val Gln Asn
 1           5           10           15
Pro Val Phe Cys Phe Ser His Leu Asn Ile His Pro Pro Ala Val Gly
      20           25           30
Trp Leu Pro Arg Tyr Gln Leu Gly Ser Ile Tyr Arg Glu Ser Asn Gly
      35           40           45
Phe Pro Ser Leu Glu Gly Ser Leu Thr Leu Thr Arg Thr Leu Asp Pro

```



```

      50              55              60
Leu Gln Ser Arg Lys Cys Ala Asp Pro Leu Gly Arg Ala Phe Phe Ser
65              70              75              80
Cys Leu Glu Pro Arg Ile Leu Phe Phe Pro Asn Arg Ile
      85              90

```

<210> 385
 <211> 342
 <212> DNA
 <213> Homo sapiens

```

<400> 385
gccggcgcca cgaaatgcaa aatgcgcctt tcaccggacg ccaggttgat cgagccgcca
60
gcacctcggg caatgtcctg ggcctgactg gcacacgcaa tcaaagcgag caacaacaca
120
caaaaacgca tcatgaggca gacgccaggg aagtgcaga agccgcagca ggcgcgcggc
180
gattggaat atcggtgagg ctaatggtca ccagcgcttg caggttgat tcggtggcca
240
attcgcgga cgacagcacc gccagttcca gctcgccgag cagcaccagg cgacgcaagc
300
tgcggcgcaa ctccgggtgc accaacaaca ccgactgtt ca
342

```

<210> 386
 <211> 109
 <212> PRT
 <213> Homo sapiens

```

<400> 386
Met Gln Asn Ala Pro Phe Thr Gly Arg Gln Val Asp Arg Ala Ala Ser
1              5              10              15
Thr Ser Gly Asn Val Leu Gly Leu Thr Gly Thr Arg Asn Gln Ser Glu
      20              25              30
Gln Gln His Thr Lys Thr His His Glu Ala Asp Ala Arg Glu Val Thr
      35              40              45
Glu Ala Ala Ala Gly Ala Arg Arg Leu Glu Ile Ser Val Arg Leu Met
      50              55              60
Val Thr Ser Ala Cys Arg Leu Tyr Ser Val Ala Asn Ser Arg Asn Asp
65              70              75              80
Ser Thr Ala Ser Ser Ser Ser Pro Arg Ser Thr Arg Arg Arg Lys Leu
      85              90              95
Arg Arg Asn Ser Gly Cys Thr Asn Asn Thr Ala Leu Phe
      100              105

```

<210> 387
 <211> 379
 <212> DNA
 <213> Homo sapiens

```

<400> 387
acgcgtgacg cgccggcatc ggaagcggtg actgcagaga agaccgcgca cgtggctgtg
60

```

ggacgtgctg gcacgtctga catggtgcgt ggacccgcct tctcttcgcc tgcgcatgcc
 120
 atgcaagagg agcttgacaa tgtgctgat ctgcgccatg cgcggcagca agcgctcgat
 180
 gctgttcggt ccgagctgct cgaagcgcag caagcatgtg cctcgtgccca gctgcagctg
 240
 cagcatgtgc cagatgatcg tgtgcgagcg cateccatat accaggcgct ccatgcggac
 300
 gttgcttaca tgcagcaaga acttgatcac gtacgagacg cattggcttc ggcagaatct
 360
 gagaatgcga gcctgcgcg
 379

<210> 388
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 388
 Met Arg Leu Val Arg Asp Gln Val Leu Ala Ala Cys Lys Gln Arg Pro
 1 5 10 15
 His Gly Ala Pro Gly Ile Trp Asp Ala Leu Ala His Asp His Leu Ala
 20 25 30
 His Ala Ala Ala Ala Ala Gly Thr Arg His Met Leu Ala Ala Leu Arg
 35 40 45
 Ala Ala Arg Asn Glu Gln His Arg Ala Leu Ala Ala Ala His Gly Arg
 50 55 60
 Asp His Ala His Cys Gln Ala Pro Leu Ala Trp His Ala Gln Ala Lys
 65 70 75 80
 Arg Arg Arg Val His Ala Pro Cys Gln Thr Cys Gln His Val Pro Gln
 85 90 95
 Pro Arg Ala Arg Ser Ser Leu Gln Ser Thr Leu Pro Met Pro Ala Arg
 100 105 110
 His Ala

<210> 389
 <211> 382
 <212> DNA
 <213> Homo sapiens

<400> 389
 ngatggccga ctgtcccact gtcagtacgc gaagctcgcc gtcgagtcgg tccacgtccg
 60
 ggccctccac gtgctccgca accctccgaa gcgatgacct ggcccggggg cggcaacgag
 120
 gtattgcgtt tggagacgct tgggggtcaat tacggccagg tgcgcgccgt cgatgccctg
 180
 acgaccaccg tagagcgcgg caccatcacc tgcctcatgg gtcgaaatgg atcaggcaag
 240
 tcgtctctga tgtgggcat ccaaggggca acaaagtcct cagggagggt actgggtcaac
 300
 cacgagggtt cttgggctga cccccgaaa gccgacgccg cgaccgctcg acgaatggtg
 360

agcttagtcc cgcagtcagc cn
382

<210> 390
<211> 127
<212> PRT
<213> Homo sapiens

<400> 390
Xaa Trp Pro Thr Val Pro Leu Ser Val Arg Glu Ala Arg Arg Arg Val
1 5 10 15
Gly Pro Arg Pro Gly Leu Pro Arg Ala Pro Gln Pro Ser Glu Ala Met
20 25 30
Thr Trp Pro Gly Gly Gly Asn Glu Val Leu Arg Leu Glu Thr Leu Gly
35 40 45
Val Asn Tyr Gly Gln Val Arg Ala Val Asp Ala Leu Thr Thr Thr Val
50 55 60
Glu Arg Gly Thr Ile Thr Cys Leu Met Gly Arg Asn Gly Ser Gly Lys
65 70 75 80
Ser Ser Leu Met Trp Ala Ile Gln Gly Ala Thr Lys Ser Ser Gly Arg
85 90 95
Val Leu Val Asn His Glu Gly Ser Trp Ala Asp Pro Arg Lys Ala Asp
100 105 110
Ala Ala Thr Ala Arg Arg Met Val Ser Leu Val Pro Gln Ser Ala
115 120 125

<210> 391
<211> 456
<212> DNA
<213> Homo sapiens

<400> 391
nnacgcgttg ccgctctgtg aggcgctat cacggtgaca ctctcgggtgc tatgagcgtg
60
tgcgacccta tcggtggcat gcacgccttg ttcagegact ctattcccca gcagatcttc
120
ctgcccgcgc cctccttctt tcgccgccga cgaggccgac gtggagacgt ggtgcagcga
180
ggccgatgaa tcctggacac ccaccgcgac gacctggccg ggatcattgt cgagcccatc
240
ttgcaaggag ccggaggcat gtggccgtgg tctccgtcct gtctgaagca cctgcgccgt
300
cgtgctgatg aacttgacct agttcttata gccgacgagg tcgctactgg atttgggagg
360
actggcaaac ttttcgcatg cgagtgggac gatatcggtc ctgacatcat ggtgggtggg
420
aaatccatga ctggcgata cctgaccag tcggcc
456

<210> 392
<211> 55
<212> PRT
<213> Homo sapiens

<400> 392

Gly Ala Tyr His Gly Asp Thr Leu Gly Ala Met Ser Val Cys Asp Pro
 1 5 10 15
 Ile Gly Gly Met His Ala Xaa Phe Ser Asp Ser Ile Pro Gln Gln Ile
 20 25 30
 Phe Leu Pro Ala Pro Ser Phe Phe Arg Arg Arg Arg Gly Arg Arg Gly
 35 40 45
 Asp Val Val Gln Arg Gly Arg
 50 55

<210> 393

<211> 371

<212> DNA

<213> Homo sapiens

<400> 393

nacgcgttgc tcgtcattgg tggctactcg gcctacgaag gtatctacac catgatgact
 60
 gagcgggacc ggtacccggc tttccgtatt cgcacgggtgt gcatcccggc ttctatcgac
 120
 aacaacctcc ccggttcgga actgtccatc ggcaccgaca ccgctctcaa cgtcatcgtc
 180
 gaggcgatgg acaagattaa ggagtcgggt atcgcgcca gacgctgctt cgtcgctgag
 240
 acgatggggtc gtgactgcgg atacctcgcg ttgatgtcgg gtatcgcagc tggcgctgag
 300
 cggatctata ccaacgagga cggtatctcc ctggacgac tagccaacga cgtccattgg
 360
 ttgcgggagt c
 371

<210> 394

<211> 123

<212> PRT

<213> Homo sapiens

<400> 394

Xaa Ala Leu Leu Val Ile Gly Gly Tyr Ser Ala Tyr Glu Gly Ile Tyr
 1 5 10 15
 Thr Met Met Thr Glu Arg Asp Arg Tyr Pro Ala Phe Arg Ile Pro Thr
 20 25 30
 Val Cys Ile Pro Ala Ser Ile Asp Asn Asn Leu Pro Gly Ser Glu Leu
 35 40 45
 Ser Ile Gly Thr Asp Thr Ala Leu Asn Val Ile Val Glu Ala Met Asp
 50 55 60
 Lys Ile Lys Glu Ser Gly Ile Ala Ser Arg Arg Cys Phe Val Val Glu
 65 70 75 80
 Thr Met Gly Arg Asp Cys Gly Tyr Leu Ala Leu Met Ser Gly Ile Ala
 85 90 95
 Ala Gly Ala Glu Arg Ile Tyr Thr Asn Glu Asp Gly Ile Ser Leu Asp
 100 105 110
 Asp Leu Ala Asn Asp Val His Trp Leu Arg Glu
 115 120

<210> 395
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 395
 gaattctagt tgggagattc attgaccaga cttttggaat aaacactagt catcatgcta
 60
 ggcacaggtg gtcttgtgca tggtagaaag gcagtccaag cctatgtctc tgaaacctgc
 120
 tctcatttct gttttctact ttacgattta tgttatctca tactcccat gttgectgtt
 180
 ctccagtttt tttacttgtg ttatttccat tcttctattc ctgctcaatt tctgcctcag
 240
 ggcagaattg tgtccaacag ctcttaaatg cagcgcagaa actgtgatgt taaaaacatc
 300
 ttgttatccg gccccaaaac atgttgctct tggtaactct tactggtttg t
 351

<210> 396
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 396
 Met Val Glu Arg Gln Ser Lys Pro Met Ser Leu Lys Pro Ala Leu Ile
 1 5 10 15
 Ser Val Phe Tyr Phe Thr Ile Tyr Val Ile Ser Tyr Ser Pro Cys Cys
 20 25 30
 Leu Phe Ser Ser Phe Phe Thr Cys Val Ile Ser Ile Leu Leu Phe Leu
 35 40 45
 Leu Asn Phe Cys Leu Arg Ala Glu Leu Cys Pro Thr Ala Leu Lys Cys
 50 55 60
 Ser Ala Glu Thr Val Met Leu Lys Thr Ser Cys Tyr Pro Ala Pro Lys
 65 70 75 80
 His Val Val Leu Gly Asn Ser Tyr Trp Phe
 85 90

<210> 397
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 397
 gccgtcatta aagagatcac ccctctctc caacctggtg atgtcctcgt cgacggtggt
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 aatgcttatt ttggtgatac ccgccgccgt gaggaggaaa tacgtccac cggcattcac
 120
 tatgttggtg ctggcatctc cgggtggggga gtcggggccc tgagggtccc atcaattatg
 180
 cctggcgggg ttaaggaatc ttacgaaatc atcggaccgg tcttagaaaa aatctccgcc
 240
 cagctcgacg gtgaaccctg ctgcgcatgg atgggtactg acggcgccgg acacttcgtc
 300

aagatgggtcc ataatggcat cgagtagccc gatatgcagt tcattggcga ggcgcccttc
 360
 ctttttgcgn tgcccgcggg tttagaccaat gctgaggccg ccgatgcctt cgagtcgtgg
 420
 aaccatggcg acctcaattc ctacctcgtc gaaatcactt ctcgggtact gcgtgccaaag
 480
 gat
 483

<210> 398
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 398
 Ala Val Ile Lys Glu Ile Thr Pro Leu Leu Gln Pro Gly Asp Val Leu
 1 5 10 15
 Val Asp Gly Gly Asn Ala Tyr Phe Gly Asp Thr Arg Arg Arg Glu Glu
 20 25 30
 Glu Ile Arg Pro Thr Gly Ile His Tyr Val Gly Thr Gly Ile Ser Gly
 35 40 45
 Gly Gly Val Gly Ala Leu Arg Val Pro Ser Ile Met Pro Gly Gly Val
 50 55 60
 Lys Glu Ser Tyr Glu Ile Ile Gly Pro Val Leu Glu Lys Ile Ser Ala
 65 70 75 80
 His Val Asp Gly Glu Pro Cys Cys Ala Trp Met Gly Thr Asp Gly Ala
 85 90 95
 Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp Met
 100 105 110
 Gln Phe Ile Gly Glu Ala Pro Phe Leu Phe Ala Xaa Pro Ala Gly Leu
 115 120 125
 Thr Asn Ala Glu Ala Ala Asp Ala Phe Glu Ser Trp Asn His Gly Asp
 130 135 140
 Leu Asn Ser Tyr Leu Val Glu Ile Thr Ser Arg Val Leu Arg Ala Lys
 145 150 155 160
 Asp

<210> 399
 <211> 314
 <212> DNA
 <213> Homo sapiens

<400> 399
 nngggaatga agaccaccca gcccttcctt tcctcaaate ttctccagge ttctgtgcat
 60
 ggctcatcca cccatccact cattcaccca tctatccatc cactcatcca cccatccagt
 120
 cattcactca tttgtccatc cactcatgta cccatccact cattcgccca tttatccatc
 180
 cactcaacca tccactcatc caccatcca nctcatcatc cgtccagtca cccatctatc
 240
 caccatgta tccatccact catccaccca tccactcatc tgtccatcca cttatccacc
 300

catctactca ccca

314

<210> 400

<211> 104

<212> PRT

<213> Homo sapiens

<400> 400

Xaa	Gly	Met	Lys	Thr	Thr	Gln	Pro	Phe	Leu	Ser	Ser	Asn	Leu	Leu	Gln
1				5					10				15		
Ala	Ser	Val	His	Gly	Ser	Ser	Thr	His	Pro	Leu	Ile	His	Pro	Ser	Ile
		20					25					30			
His	Pro	Leu	Ile	His	Pro	Ser	Ser	His	Ser	Leu	Ile	Cys	Pro	Ser	Thr
	35					40					45				
His	Val	Pro	Ile	His	Ser	Phe	Ala	His	Leu	Ser	Ile	His	Ser	Thr	Ile
	50					55					60				
His	Ser	Ser	Thr	His	Pro	Xaa	His	His	Pro	Ser	Ser	His	Pro	Ser	Ile
65					70					75				80	
His	Pro	Cys	Ile	His	Pro	Leu	Ile	His	Pro	Ser	Thr	His	Leu	Ser	Ile
			85						90					95	
His	Leu	Ser	Thr	His	Leu	Leu	Thr								

<210> 401

<211> 2165

<212> DNA

<213> Homo sapiens

<400> 401

gagaaaaatgg aactacctgt atataaatta ggtgagcaaa cagtgatata ggtagtttta
60
agaagcaaat atatacagtc aatttaacag tgtttacttc tctggattgt ttaatgggtgt
120
caaaatgaaa gatctattga agtttactta tacattgcat tgattgaacc ttggagagtt
180
ttatgaaaaa gaggggcatc ccttgccatc tgtttgccag tcttccttgc cccttccttt
240
gaaatgcctg cctctttttt gccagatttg tttcctgacc atccgaactc agatgggggc
300
ctctaagttc ttcctggata ttcacaaatc ccttcacaag gccacagtgc gaagtgaatg
360
atctggaggt gcctgggcat ctgtgttgga agggagtcaa gactcaccag ccagtcagtt
420
tgtgggctac agttgtccca caaaaatcag gcatgttcac ctcccctctg ggcccctaca
480
gctgggactg atcatagcct cagattagaa gaaataactga cttctaactc tataagccag
540
cactcctggg taaggagtga agctctgttg gccatgccgc tttggactgc tgggcagagc
600
tgagcctaca gttttgtact ggggtgcacg gatgacagct gggaagatgg aaaggcagct
660
tgaggattta tagcagctaa agggtaaatg ctgttatgca aaaggtcccc atatgaactt
720

cctacaggtg tagccgcagc caagtgtctg tacagctgct gagaatttgt cggatgatgta
780
aaaattcctc tttgcatcac aagcgagtgg aaagccaggg gctgcatgag tggagaaagc
840
acagtctggt ttttcaagta ctgcagagaa tgagaatacc cagccgggag cctggagttg
900
aggcccgagt tacacaggct cccggaatac agacctggga agatagggga ggagagggga
960
agcttggtgc cttttgatcc gccccggaa tgcccaccgt gcgctgcttt gctgccttca
1020
tctcctgctc agaggccttc tccttcccag agacctcctt ggatgggtct aaggagagaca
1080
ctgcccgggc ctttttccct gcaatcacia ggtccaaatc ctccaggctg cgcttgatcg
1140
gccgcgccgc cccaatgttc tacgggctca ttttccggtg caggattggg tggaccatgc
1200
cttccatctt cctgaaatc tccagtctca catggtgagg ttttctgat cttgaaagcg
1260
attcagggtg ttttttaggg cctgacatgg tcatgggtga taccgacag gctttggggt
1320
gacagtctcg actctggctg cctaagacct ggaactggga gatgcctttg ctctcctggg
1380
gcctgtggt ggaatgagcc agggccagga ccttgccggt aggtttgtgc gggttcttgg
1440
gaaggctcag atctgtaggc tgatcatccg taggggcttc tgctgccgcc gactttttgt
1500
cttgacggtg cagggacgtg agataattta catggagctt ttcttgggtg ctgtgggaag
1560
gaaaagaact gttttccgat tcctgtaca tgccttgga agggatattg gatgtctgtt
1620
cattatgaag atgggtgctg gtgtgtctgt agaggctatg gagatgaggg gacgagtaga
1680
agtcagccag gaagctaggc atgtgggaat gggggagggc ctttttctt aagagtttat
1740
ccttgccctc ctgaatttct tgcttcagga cgtaggagtc agcaaggggg ttaaggtgat
1800
gcttgagaa gctgcagcgg tggggatctg atcgactcag tttctcatgc ttaaagatgt
1860
cattgatggt ctttctctct tccgagggtg tgcttctgaa actctggacg tgctgaatca
1920
ctgatggccg gctgaccgcc atatggtcag tgctttggcc atgggtgggtc tgggacaaac
1980
tggaacacaa gtcaccceta gcaatcagtt tctttttgct gatcaaaggg ggtggggagc
2040
cataagggtg gctgctggag aggctggccc cactcacttg ggacaaaagc tttttcttgg
2100
ccagtgggga catcatgcct ggggtgcccc tagagtagag caggggctg taattaagtc
2160
catgg
2165

<210> 402

<211> 87

<212> PRT

<213> Homo sapiens

<400> 402

```

Glu Tyr Pro Ala Gly Ser Leu Glu Leu Arg Pro Glu Leu His Arg Leu
 1             5             10             15
Pro Glu Tyr Arg Pro Gly Lys Ile Gly Glu Glu Arg Gly Ser Leu Trp
          20             25             30
Pro Phe Asp Pro Pro Pro Glu Cys Pro Pro Cys Ala Ala Leu Leu Pro
          35             40             45
Ser Ser Pro Ala Gln Arg Pro Ser Pro Ser Gln Arg Pro Pro Trp Met
          50             55             60
Gly Leu Arg Glu Thr Leu Pro Gly Pro Phe Ser Leu Gln Ser Gln Gly
65             70             75             80
Pro Asn Pro Pro Gly Cys Ala
          85

```

<210> 403

<211> 369

<212> DNA

<213> Homo sapiens

<400> 403

```

cccatggggtg tgtcccagga cggcgctcatg aagcgtcagg taaatgacaa ggaaacggtc
60
gcgcacttgt tcgaatacac gacgcaagtg tctgtcgact cgacgccgca actcgtccag
120
ccttcgcccc cgtcgcacga caacctcgtg cctgtccaga tgatcttttg cttcaagcag
180
cgcaacgcga aaaagatcaa tagccaccgc tgggtatttc atgcactggg ccgcatgcta
240
cagcccgaca tggtcgtctt ggtggacgtc ggcacgaagc ccggccacct cgcctatac
300
catctatggc aggcattcta tcaccgacct accttggggcg gtgcttgcg cgaaattcat
360
gctatgatc
369

```

<210> 404

<211> 123

<212> PRT

<213> Homo sapiens

<400> 404

```

Pro Met Gly Val Ser Gln Asp Gly Val Met Lys Arg Gln Val Asn Asp
 1             5             10             15
Lys Glu Thr Val Ala His Leu Phe Glu Tyr Thr Thr Gln Val Ser Val
          20             25             30
Asp Ser Thr Pro Gln Leu Val Gln Pro Ser Pro Thr Ser His Asp Asn
          35             40             45
Leu Val Pro Val Gln Met Ile Phe Cys Phe Lys Gln Arg Asn Ala Lys
          50             55             60
Lys Ile Asn Ser His Arg Trp Val Phe His Ala Leu Gly Arg Met Leu
65             70             75             80
Gln Pro Asp Met Val Val Leu Val Asp Val Gly Thr Lys Pro Gly His

```

				85						90					95				
Leu	Ala	Leu	Tyr	His	Leu	Trp	Gln	Ala	Phe	Tyr	His	Arg	Pro	Thr	Leu				
			100					105							110				
Gly	Gly	Ala	Cys	Gly	Glu	Ile	His	Ala	Met	Ile									
		115					120												

<210> 405
 <211> 840
 <212> DNA
 <213> Homo sapiens

<400> 405
 gaattcccgc gcaccagctc gaagctggag cactttgtgt ctatcctgct gaagtgcttc
 60
 gactcgccct ggaccacgag ggccctgtcg gagacagtgg tggaggagag cgaccccaag
 120
 ccggccttca gcaagatgaa tgggtccatg gacaaaaagt catcgaccgt cagtgaggac
 180
 gtggaggcca ccgtgcccat gctgcagcgg accaagtcac ggatcgagca gggatatcgtg
 240
 gaccgctcag agacgggctg gctggacaag aaggaggggg agcaagccaa ggcgctgttt
 300
 gagaaggtga agaagttccg gacccatgtg gaggaggggg acattgtgta ccgcctctac
 360
 atgcggcaga ccatcatcaa ggtgatcaag ttcatactca tcattctgta caccgtctac
 420
 tacgtgcaca acatcaagtt cgacgtggac tgcaccgtgg acattgagag cctgacgggc
 480
 taccgcacct accgctgtgc ccacccctg gccacactct tcaagatcct ggcgtccttc
 540
 tacatcagcc tagtcatctt ctacggctc atctgcatgt atacactgtg gtggatgcta
 600
 cggcgctccc tcaagaagta ctggttgag tcgatccgtg aggagagcag ctacagcgac
 660
 atccccgacg tcaagaacga ctctgccttc atgctgcacc tcattgacca atacgacccg
 720
 ctctactcca agcgtctcgc cgtcttctg tcggaggtga gtgagaacaa gctgcggcag
 780
 ctgaacctca acaacgagtg gacgctggac aagctccggt acggagagaa gacaacgcgt
 840

<210> 406
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 406
 Leu Ile Cys Met Tyr Thr Leu Trp Trp Met Leu Arg Arg Ser Leu Lys
 1 5 10 15
 Lys Tyr Ser Phe Glu Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile
 20 25 30
 Pro Asp Val Lys Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln
 35 40 45
 Tyr Asp Pro Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val

```

      50              55              60
Ser Glu Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu
65              70              75              80
Asp Lys Leu Arg Tyr Gly Glu Lys Thr Thr Arg
      85              90

```

<210> 407
 <211> 535
 <212> DNA
 <213> Homo sapiens

```

<400> 407
gcctattgta ccagctctcc agggctgggg acttgctaga gcagggttcc cagtgcctcc
60
aggctctact ttgctctgcc tggctctcagg gtgtagggga tggagagctg gacttccagc
120
ctgtctcttg gctgtctagg ggccaggggc tcgggacaca gagctcctgg aggccgagca
180
caagccttgg gcagaggtga ggcagagctc tgactgtttc attcgactac gttgcccaagg
240
agatgctcgc tcggagtggg tgctctggct ctgggattcc aaaccaagct gccttctctg
300
atgtggcctt agtgcctctg gcggatgtac cttggctctg cctggaccct ctctctcttc
360
caggcctctg tcccaccagg atgatgcta tccagagctc attgtcctct cccacttctt
420
ccccgagctt cccattccgt gtctctctgg agggcccatc atcatcctgg tggaggtggt
480
gcactgagga ccacagcagc cctcgcattc ccacgggcaa aggggtatgt gtagg
535

```

<210> 408
 <211> 97
 <212> PRT
 <213> Homo sapiens

```

<400> 408
Met Leu Ala Arg Ser Gly Cys Ser Gly Ser Gly Ile Pro Asn Gln Ala
1              5              10              15
Ala Phe Ser Asp Val Ala Leu Val Leu Trp Ala Asp Val Pro Trp Leu
      20              25              30
Cys Leu Asp Pro Leu Ser Leu Pro Gly Leu Cys Pro Thr Arg Met Met
      35              40              45
Pro Ile Gln Ser Ser Leu Ser Ser Pro Thr Ser Ser Pro Ser Phe Pro
      50              55              60
Phe Arg Val Ser Leu Glu Gly Pro Ser Ser Ser Trp Trp Arg Cys Cys
65              70              75              80
Thr Glu Asp His Ser Ser Pro Arg Ile Pro Thr Gly Lys Gly Val Cys
      85              90              95
Val

```

<210> 409
 <211> 375

<212> DNA

<213> Homo sapiens

<400> 409

ngtgtcatgg gtgtctatac cagcgatgag gccaaagactg ccaagacttt tggatttggg
 60
 ggacttccga ttacgactaa tatttctctt gccacaact tcaatatgga tgaaatttct
 120
 gatattgtct tccgtgtcaa tgataccagt ttgacaccaa ctgtgggacc agaattagct
 180
 agaaaattga ccgaaattgc tggctctcag caaggggagt atcaggtgtc agatgcgact
 240
 gcagccttcc aagaagtgca acaattgttc ggctttataa ctacgattat tagtgccatt
 300
 gcaggaattt ccctttttgt tggagggact ggtgttatga acatcatgct ggtttcgggtg
 360
 acggagcgta cgcg
 375

<210> 410

<211> 125

<212> PRT

<213> Homo sapiens

<400> 410

Xaa	Val	Met	Gly	Val	Tyr	Thr	Ser	Asp	Glu	Ala	Lys	Thr	Ala	Lys	Thr
1			5						10				15		
Phe	Gly	Ile	Gly	Leu	Pro	Ile	Thr	Thr	Asn	Ile	Ser	Leu	Ala	Asn	
			20					25				30			
Asn	Phe	Asn	Met	Asp	Glu	Ile	Ser	Asp	Ile	Val	Phe	Arg	Val	Asn	Asp
			35				40					45			
Thr	Ser	Leu	Thr	Pro	Thr	Val	Gly	Pro	Glu	Leu	Ala	Arg	Lys	Leu	Thr
			50			55					60				
Glu	Ile	Ala	Gly	Leu	Gln	Gln	Gly	Glu	Tyr	Gln	Val	Ser	Asp	Ala	Thr
65				70					75					80	
Ala	Ala	Phe	Gln	Glu	Val	Gln	Gln	Leu	Phe	Gly	Phe	Ile	Thr	Thr	Ile
			85					90					95		
Ile	Ser	Ala	Ile	Ala	Gly	Ile	Ser	Leu	Phe	Val	Gly	Gly	Thr	Gly	Val
			100				105						110		
Met	Asn	Ile	Met	Leu	Val	Ser	Val	Thr	Glu	Arg	Thr	Arg			
			115				120					125			

<210> 411

<211> 409

<212> DNA

<213> Homo sapiens

<400> 411

ccacatactt caccctcctc accccctcca cctactccac cacctggcag tcgccatcga
 60
 ggatgggacg caactccacg tccacatgct ccggaccacg cggcgtgtgg tggatgtgca
 120
 gcacgcggtc ggggccctt gagctcgaag gcgcggcgca tcgggcagtg ctcgccggcc
 180

tggtcgcagg gcacgtcgta ctggtgcgag acgcggaagc acttgaggcc gatgtaggcg
 240
 cgatcggctg tcccgaactg gcgctgatag gccgtgtaca caacacaaac tgttgctactc
 300
 ccggtccacc acgatcatgg gctggggactc gtgttcagg tggggggcca gggcttgggc
 360
 ctgcggtgag cgcgtggggg ggatggggca tagcgtcggt gaggaggtg
 409

<210> 412
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 412
 Met Pro His Pro Pro His Ala Leu Thr Ala Gly Pro Ser Pro Gly Pro
 1 5 10 15
 Pro Pro Gly Thr Arg Val Pro Ala His Asp Arg Gly Gly Pro Gly Val
 20 25 30
 Gln Gln Phe Val Leu Cys Thr Arg Pro Ile Ser Ala Ser Ser Gly Gln
 35 40 45
 Pro Ile Ala Pro Thr Ser Ala Thr Ser Ala Ser Ala Ser Arg Thr Ser
 50 55 60
 Thr Thr Cys Pro Ala Thr Arg Pro Ala Ser Thr Ala Arg Cys Ala Ala
 65 70 75 80
 Pro Ser Ser Ser Arg Gly Pro Asp Arg Val Leu His Ile His His Thr
 85 90 95
 Pro Arg Gly Pro Glu His Val Asp Val Glu Leu Arg Pro Ile Leu Asp
 100 105 110
 Gly Asp Cys Gln Val Val Glu
 115

<210> 413
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 413
 ccgggcatcc caccaccggg tgtcatgaac caagtagtgg cccctatggt agggactcca
 60
 gcaccgggtg gaagtccata tggacaacag gtgggagttt tggggcctcc agggcagcag
 120
 gcaccacctc catatcccg gcccacatcca gctggacccc ctgtcataca gcagccaaca
 180
 acacccatgt ttgtagctcc cccccaaaag acccagcggc ttcttcactc agaggcctac
 240
 ctgaaataca ttgaaggact cagtgcggag tccaacagca ttagcaagtg ggatcagaca
 300
 ctggcagctc ggagacgca cgtccatttg tcgaaagaac aggagagccg cctaccc
 357

<210> 414
 <211> 119
 <212> PRT

<213> Homo sapiens

<400> 414

```

Pro Gly Ile Pro Pro Pro Gly Val Met Asn Gln Val Val Ala Pro Met
 1             5             10             15
Val Gly Thr Pro Ala Pro Gly Gly Ser Pro Tyr Gly Gln Gln Val Gly
      20             25             30
Val Leu Gly Pro Pro Gly Gln Gln Ala Pro Pro Pro Tyr Pro Gly Pro
      35             40             45
His Pro Ala Gly Pro Pro Val Ile Gln Gln Pro Thr Thr Pro Met Phe
      50             55             60
Val Ala Pro Pro Pro Lys Thr Gln Arg Leu Leu His Ser Glu Ala Tyr
65             70             75             80
Leu Lys Tyr Ile Glu Gly Leu Ser Ala Glu Ser Asn Ser Ile Ser Lys
      85             90             95
Trp Asp Gln Thr Leu Ala Ala Arg Arg Asp Val His Leu Ser Lys
      100            105            110
Glu Gln Glu Ser Arg Leu Pro
      115

```

<210> 415

<211> 332

<212> DNA

<213> Homo sapiens

<400> 415

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tctagagcca acttggttat cgtaatgaat agagagacta catctatattc aattattacg
60
ctctatagta atcatgaagc ttgggttata tgtatgacaa aaattgcaga aaaatcgaaa
120
caagaatatg gcgacttact aaaagaaaaa gaccattttac aagatatgga acagcttgag
180
atgactatcg tctcgatcca tacgccgtat ccgtccattg tcagaattca aggaaaaatc
240
aacacattac agccagagct ttggcaagct cccaatttag caattcgggtt aattgtgagc
300
aatccgccag agggacaacc catctcacgc gt
332

```

<210> 416

<211> 102

<212> PRT

<213> Homo sapiens

<400> 416

```

Met Asn Arg Glu Thr Thr Ser Ile Ser Ile Ile Thr Leu Tyr Ser Asn
 1             5             10             15
His Glu Ala Trp Val Ile Cys Met Thr Lys Ile Ala Glu Lys Ser Lys
      20             25             30
Gln Glu Tyr Gly Asp Leu Leu Lys Glu Lys Asp His Leu Gln Asp Met
      35             40             45
Glu Gln Leu Glu Met Thr Ile Val Ser Ile His Thr Pro Tyr Pro Ser
      50             55             60
Ile Val Arg Ile Gln Gly Lys Ile Asn Thr Leu Gln Pro Glu Leu Trp

```

65		70		75		80									
Gln	Ala	Pro	Asn	Leu	Ala	Ile	Arg	Leu	Ile	Val	Ser	Asn	Pro	Pro	Glu
			85						90					95	
Gly	Gln	Pro	Ile	Ser	Arg										
			100												

<210> 417
 <211> 483
 <212> DNA
 <213> Homo sapiens

<400> 417
 gaattcctcg ccgtctctga ggtgggagag gacacctttg tgcgctccac cgagggagac
 60
 tacgcggcca acgtcgaggc cgtggtgacc ccagcaccgg cggagaaaga tattgagggc
 120
 cagccagaag cacaggaaca tgacaccccg ggtacagaga ccattgagaa gctggtcgaa
 180
 tgggcccagg gcgcaggcat tactgtaaac cccgcggttg tttgttatta taccctcaag
 240
 tgcgatgatga tcaagctcca ccacccggcc gcggagagcg aagagcgcgga gtccgagttg
 300
 gcggcgggttc tcatccctgg cgatcgagag ctggatgaaa agcgccttga ggccgcactc
 360
 gagccggttg agtttgagtt ggcaggggat aaggactttg cagacaatga cttcctagtc
 420
 aagggttatg ttggcccgcg cgctttgaac gccaatgga tcaaggtctt ggccgatcca
 480
 cgc
 483

<210> 418
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 418
 Glu Phe Leu Ala Val Ser Glu Val Gly Glu Asp Thr Phe Val Arg Ser
 1 5 10 15
 Thr Glu Gly Asp Tyr Ala Ala Asn Val Glu Ala Val Val Thr Pro Ala
 20 25 30
 Pro Ala Glu Lys Asp Ile Glu Gly Gln Pro Glu Ala Gln Glu His Asp
 35 40 45
 Thr Pro Gly Thr Glu Thr Ile Glu Lys Leu Val Glu Trp Ala Gln Gly
 50 55 60
 Ala Gly Ile Thr Val Asn Pro Arg Val Val Cys Tyr Tyr Thr Leu Lys
 65 70 75 80
 Cys Met Met Ile Lys Leu His His Pro Ala Ala Glu Ser Glu Glu Arg
 85 90 95
 Glu Ser Glu Leu Ala Ala Val Leu Ile Pro Gly Asp Arg Glu Leu Asp
 100 105 110
 Glu Lys Arg Leu Glu Ala Ala Leu Glu Pro Val Glu Phe Glu Leu Ala
 115 120 125
 Gly Asp Lys Asp Phe Ala Asp Asn Asp Phe Leu Val Lys Gly Tyr Val

130		135		140											
Gly	Pro	Arg	Ala	Leu	Asn	Ala	Asn	Gly	Ile	Lys	Val	Leu	Ala	Asp	Pro
145				150						155					160
Arg															

<210> 419
 <211> 797
 <212> DNA
 <213> Homo sapiens

<400> 419
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 cggatccata agtaccggcc gccaggggtg ctggaatttg ggctcccccc ggtgaaaata
 120
 tccatgcagc cgcgttgtct taggtagaaa agggagactg ggggtggggtg ggctgagctc
 180
 aagcccctgc ctacatactt tagtagtaac gactcccgat ctgcatccaa cacatttacc
 240
 gaatttctag taagcgcccc ccgctgcaag cgaaagcact ccctgccaa gaaacagatc
 300
 ttttccactt aaaattccca aactcagacc ttccactttt tactgaacaa aaagcgtgta
 360
 catgatctga agggttgaca tgacattttc taaattgggc gaatcaggaa gaggttgatg
 420
 aaaatccttg acgttttctg gggataggac atttgtgtgt gataacgttc ttaagtcgaa
 480
 tttcagtgtg gcagtgcacg cagattcttc attgggtgta gtgtatttcc atacggtatg
 540
 tattagtaca agaaatagtg ttccctttga cactcgaacc caaggagtgg tccgaggctt
 600
 tttgaggcaa cgtaggatca atgtctctga agcagatttg gtgaaggatg caggtctcat
 660
 aatttacaga gcaatcacag ccttctttga aacggagaaa ttagattcta tgaaattttg
 720
 tcagtgcaga tagatatgat gtggagaaac ggggaaaatt gagtacaaaa agatgaggct
 780
 tgaatgatgg ctggcca
 797

<210> 420
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 420
 Met Arg Pro Ala Ser Phe Thr Lys Ser Ala Ser Glu Thr Leu Ile Leu
 1 5 10 15
 Arg Cys Leu Lys Lys Pro Arg Thr Thr Pro Trp Val Arg Val Ser Lys
 20 25 30
 Gly Thr Leu Phe Leu Val Leu Ile His Thr Val Trp Lys Tyr Thr Asn
 35 40 45
 Thr Asn Glu Glu Ser Ala Cys Thr Ala Thr Leu Lys Phe Asp Leu Arg

50		55		60											
Thr	Leu	Ser	His	Thr	Asn	Val	Leu	Ser	Pro	Glu	Asn	Val	Lys	Asp	Phe
65					70					75					80
His	Gln	Pro	Leu	Pro	Asp	Ser	Pro	Asn	Leu	Glu	Asn	Val	Met	Ser	Thr
			85						90					95	
Leu	Gln	Ile	Met	Tyr	Thr	Leu	Phe	Val	Gln						
			100						105						

<210> 421

<211> 406

<212> DNA

<213> Homo sapiens

<400> 421

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ggatccacca tgatggagcc caccaccca tcctcagtc acctgctgca gcttctccat
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aaccaaacac aggtcaatct tgtctcccta aacacaccat gtgctctcat gctgccatgg
120
tttgccctggg gccctctcta cctcctctgc tttctggaga acccttgac tcctcccaag
180
cettcaagtt ggaaagtga cagtcagcat atgtctctag ctcagccctt actgcggtgga
240
ttcatgaaga ttggttcact gtcagccctt gaccagaacg tgtgttttag gaaagcagga
300
accaagtctt accaatgtct gtagtcccag cctccaccct ggcatacagt aggtgctcat
360
tgaatgtggg agggaaagag gagacacatg gaagggaatg tcattc
406

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<210> 422

<211> 104

<212> PRT

<213> Homo sapiens

<400> 422

Met	Met	Glu	Pro	Thr	His	Pro	Ser	Ser	Val	His	Leu	Leu	Gln	Leu	Leu
1				5					10				15		
His	Asn	Pro	Thr	Gln	Val	Asn	Leu	Val	Ser	Leu	Asn	Thr	Pro	Cys	Ala
			20					25					30		
Leu	Met	Leu	Pro	Trp	Phe	Ala	Trp	Gly	Pro	Leu	Tyr	Leu	Leu	Cys	Phe
	35						40					45			
Leu	Glu	Asn	Pro	Cys	Thr	Pro	Pro	Lys	Pro	Ser	Ser	Trp	Lys	Val	Asn
	50					55					60				
Ser	Gln	His	Met	Ser	Leu	Ala	Gln	Pro	Leu	Leu	Arg	Gly	Phe	Met	Lys
65					70					75					80
Ile	Gly	Ser	Leu	Ser	Ala	Pro	Asp	Gln	Asn	Val	Cys	Phe	Arg	Lys	Ala
			85					90						95	
Gly	Thr	Lys	Ser	Tyr	Gln	Cys	Leu								
							100								

<210> 423

<211> 628

<212> DNA

<213> Homo sapiens

<400> 423
 ngccacccta cgcctcgcct gcaatggcaa cttcagatcc ccggtggcac cgtagtctta
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 gagccaccgg ttctgagcgg ggaggacgac ggggttgggg cggaggaagg agagggagaa
 120
 ggagatgggg atttgctgac gcagacccaa gcccaaacgc cgactccagc acccgcttgg
 180
 ccggcgcccc cagccacacc gcgcttctctg gccctcgcaa atggctccct gttggtgccc
 240
 ctcttgagtg ccaaggaggc gggcgtctac acttgccgtg cacacaatga gctgggcgcc
 300
 aactctacgt caatacgcgt ggcggtggca gcaaccgggc ccccaaaaca cgcgcctggc
 360
 gccgggggag aaccgacgg acaggccccg acctctgagc gcaagtccac agccaagggc
 420
 cggggcaaca gcgtcttgcc ttccaaaccc gagggcaaaa tcaaaggcca aggctggcc
 480
 aaggtcagca ttctcgggga gaccgagacg gagccggagg aggacacaag tgagggagag
 540
 gaggccgaag accagatcct cgcggacccg gcggaggagc agcgctgtgg caacggggac
 600
 ccctctcggg acgtttctaa ccacgcgt
 628

<210> 424
 <211> 209
 <212> PRT
 <213> Homo sapiens

<400> 424
 Xaa His Pro Thr Pro Arg Leu Gln Trp Gln Leu Gln Ile Pro Gly Gly
 1 5 10 15
 Thr Val Val Leu Glu Pro Pro Val Leu Ser Gly Glu Asp Asp Gly Val
 20 25 30
 Gly Ala Glu Glu Gly Glu Gly Glu Gly Asp Gly Asp Leu Leu Thr Gln
 35 40 45
 Thr Gln Ala Gln Thr Pro Thr Pro Ala Pro Ala Trp Pro Ala Pro Pro
 50 55 60
 Ala Thr Pro Arg Phe Leu Ala Leu Ala Asn Gly Ser Leu Leu Val Pro
 65 70 75 80
 Leu Leu Ser Ala Lys Glu Ala Gly Val Tyr Thr Cys Arg Ala His Asn
 85 90 95
 Glu Leu Gly Ala Asn Ser Thr Ser Ile Arg Val Ala Val Ala Ala Thr
 100 105 110
 Gly Pro Pro Lys His Ala Pro Gly Ala Gly Gly Glu Pro Asp Gly Gln
 115 120 125
 Ala Pro Thr Ser Glu Arg Lys Ser Thr Ala Lys Gly Arg Gly Asn Ser
 130 135 140
 Val Leu Pro Ser Lys Pro Glu Gly Lys Ile Lys Gly Gln Gly Leu Ala
 145 150 155 160
 Lys Val Ser Ile Leu Gly Glu Thr Glu Thr Glu Pro Glu Glu Asp Thr
 165 170 175
 Ser Glu Gly Glu Glu Ala Glu Asp Gln Ile Leu Ala Asp Pro Ala Glu

	180		185		190										
Glu	Gln	Arg	Cys	Gly	Asn	Gly	Asp	Pro	Ser	Arg	Tyr	Val	Ser	Asn	His
	195					200						205			
Ala															

<210> 425
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 425
 ccggccgctcg aagactttga ggacgatgta gctcgcagcg cagcgttacg agccctggag
 60
 tacgtggatt tgaccccagg cactnaagtg cgcgtcatcg ccattgacac cgtgttccta
 120
 ggatcgtgca cgaatggccg tgaggactta cggctggctg ctgagggtcc caaaggacga
 180
 catatcgcag cgggcacccg gatgctcgtc gccctggat ctgctcgtgt ccgtctgcag
 240
 gctatggagg aaggcctcga cgagatcggg tcccggtttg ctgacatctt tcgcaataac
 300
 tctgcgaaca atggcttggt actggctcag gttgaccccg aggtcgtcga agagttgtgg
 360
 gactttgccg agcagcatcc tgggtgagcag ctcaccgtct ccctcgagaa tcggacgatc
 420
 aaccttcggt gtcgcacgac ctacccgttc catattgatg acgtcacggt t
 471

<210> 426
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 426
 Pro Ala Val Glu Asp Phe Glu Asp Asp Val Ala Arg Ser Ala Ala Leu
 1 5 10 15
 Arg Ala Leu Glu Tyr Val Asp Leu Thr Pro Gly Thr Xaa Val Arg Val
 20 25 30
 Ile Ala Ile Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Gly Arg Glu
 35 40 45
 Asp Leu Arg Leu Ala Ala Glu Val Pro Lys Gly Arg His Ile Ala Ala
 50 55 60
 Gly Thr Arg Met Leu Val Ala Pro Gly Ser Ala Arg Val Arg Leu Gln
 65 70 75 80
 Ala Met Glu Glu Gly Leu Asp Glu Ile Gly Ser Arg Phe Ala Asp Ile
 85 90 95
 Phe Arg Asn Asn Ser Ala Asn Asn Gly Leu Leu Leu Ala Gln Val Asp
 100 105 110
 Pro Glu Val Val Glu Glu Leu Trp Asp Phe Ala Glu Gln His Pro Gly
 115 120 125
 Glu Gln Leu Thr Val Ser Leu Glu Asn Arg Thr Ile Asn Leu Pro Gly
 130 135 140
 Arg Thr Thr Tyr Pro Phe His Ile Asp Asp Val Thr Arg

145

150

155

<210> 427

<211> 546

<212> DNA

<213> Homo sapiens

<400> 427

ctagcggtag tagaagggtat gcagtttgat cgcggtact tgtctccgta tttcatcaac
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aatcaagaaa caatgaatgc agagctagaa aaccatttta ttcttcttgt tgataagaaa
120
atttctaata tccgtgactt gctaccaatt ttggaagggt ttgctaaagc atcgcgccca
180
ttgttgatca ttgcggaaga cgttgaaggc gaagcggttg caaccttggg tgtaaacact
240
atgcgcggca tcgtaaaagt agcggcagcg aaagcgccag gttttggtga tcgccgtaaa
300
gcaatgcttc aagacattgc tgtgctaacg ggttcaactg ttatttcaga agaaattggc
360
attaagcttg aagaagcgac aattgaacag ttgggtacag cgaagcgcggt tacattgaca
420
aaagaaagta caacgattgt tgatggtgcg ggtggttcag ctaatattac tggctgtggt
480
gagcaaattc gtgcagaaat tgctaactct tcttctggct acgataaaga gaaattgcaa
540
gaacgc
546

<210> 428

<211> 182

<212> PRT

<213> Homo sapiens

<400> 428

Leu Ala Val Val Glu Gly Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro
1 5 10 15
Tyr Phe Ile Asn Asn Gln Glu Thr Met Asn Ala Glu Leu Glu Asn Pro
20 25 30
Phe Ile Leu Leu Val Asp Lys Lys Ile Ser Asn Ile Arg Asp Leu Leu
35 40 45
Pro Ile Leu Glu Gly Val Ala Lys Ala Ser Arg Pro Leu Leu Ile Ile
50 55 60
Ala Glu Asp Val Glu Gly Glu Ala Leu Ala Thr Leu Val Val Asn Thr
65 70 75 80
Met Arg Gly Ile Val Lys Val Ala Ala Ala Lys Ala Pro Gly Phe Gly
85 90 95
Asp Arg Arg Lys Ala Met Leu Gln Asp Ile Ala Val Leu Thr Gly Ser
100 105 110
Thr Val Ile Ser Glu Glu Ile Gly Ile Lys Leu Glu Glu Ala Thr Ile
115 120 125
Glu Gln Leu Gly Thr Ala Lys Arg Val Thr Leu Thr Lys Glu Ser Thr
130 135 140
Thr Ile Val Asp Gly Ala Gly Val Ala Ala Asn Ile Thr Gly Arg Val

145 150 155 160
 Glu Gln Ile Arg Ala Glu Ile Ala Asn Ser Ser Ser Gly Tyr Asp Lys
 165 170 175
 Glu Lys Leu Gln Glu Arg
 180

<210> 429
 <211> 425
 <212> DNA
 <213> Homo sapiens

<400> 429
 gctagcagcc cttacaggag acgggctaata aataatgcag cagtggctcc gacaacttgc
 60
 ccgttgcagc cggtcacgga tccatttgct tttagtagac aggcgctcca aagtacacca
 120
 ctgggcagtt cgtccaaaag cagtccacct gtcttgcaag gccagcccc cgcagggttt
 180
 tctcaacacc ccggtttgct tgtgccttac acacaatgca aaaaatagct ctcagggacc
 240
 ctgtgagccc ctgcctggac ctctgacaca gccagagca catgccagtc cgttttctgg
 300
 tgcattgaca ccttcagcac ctctggggcc tgagatgaac aggagtgcag aggtcgggtcc
 360
 cagttcagag cctgaagttc agactctgcc atatcttct cactacattc caggagtgga
 420
 tcctg
 425

<210> 430
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 430
 Met Gln Gln Trp Leu Arg Gln Leu Ala Arg Cys Ser Arg Ser Arg Ile
 1 5 10 15
 His Leu Leu Leu Val Asp Arg Arg Ser Lys Val His His Trp Ala Val
 20 25 30
 Arg Pro Lys Ala Val His Leu Ser Cys Lys Ala Gln Pro Pro Gln Gly
 35 40 45
 Phe Leu Asn Thr Pro Val Cys Leu Cys Leu Thr His Asn Ala Lys Asn
 50 55 60
 Ser Ser Gln Gly Pro Cys Glu Pro Leu Pro Gly Pro Leu Thr Gln Pro
 65 70 75 80
 Arg Ala His Ala Ser Pro Phe Ser Gly Ala Leu Thr Pro Ser Ala Pro
 85 90 95
 Pro Gly Pro Glu Met Asn Arg Ser Ala Glu Val Gly Pro Ser Ser Glu
 100 105 110
 Pro Glu Val Gln Thr Leu Pro Tyr Leu Pro His Tyr Ile Pro Gly Val
 115 120 125
 Asp Pro
 130

<210> 431
 <211> 192
 <212> DNA
 <213> Homo sapiens

<400> 431
 ctagccatcc accagcgtac acacacggga gagaggccct acactggcct cgggtgcaac
 60
 cgccgcttcc gccagcgcac ggccctcgtc atccaccagc gcatccacac gggcgagaag
 120
 cctnaccctg gcccggaactg cgagcggcgc ttctcctcct cctctcgcct ggtcagtcac
 180
 cggcgtgtgc ac
 192

<210> 432
 <211> 64
 <212> PRT
 <213> Homo sapiens

<400> 432
 Leu Ala Ile His Gln Arg Thr His Thr Gly Glu Arg Pro Tyr Thr Gly
 1 5 10 15
 Leu Gly Cys Asn Arg Arg Phe Arg Gln Arg Thr Ala Leu Val Ile His
 20 25 30
 Gln Arg Ile His Thr Gly Glu Lys Pro Xaa Pro Cys Pro Asp Cys Glu
 35 40 45
 Arg Arg Phe Ser Ser Ser Ser Arg Leu Val Ser His Arg Arg Val His
 50 55 60

<210> 433
 <211> 635
 <212> DNA
 <213> Homo sapiens

<400> 433
 nngccggcgg ctgcgttggg atacgacgtc gctgcgattg ggcgtagta tctttggtac
 60
 ctcattggagg agcgtggcgc gtatgcggag gccgccgcgc tcatgccgct gctgctccgg
 120
 accgaccgag gcgcgtggga cacgtttgtg tgctgctacc tcgagcggca ccaaagggat
 180
 gcgatactcc cgcacattcc gacgcaggac cccagctga gtgagatggt gtacgatctc
 240
 gtgctggtgc atctgctgca gcacgatccc acgcagctgt tggcgacgct ccgcgcatgg
 300
 ccgagtcaca tctactcgaa gcaggcgggtg gctgcggcga tcggcgatca cgcacgaacc
 360
 agccgcacgc tgctcgagtg cctcgcacag ctgtacatgg ccgcacatca gcccggaag
 420
 gctctgacat actacatgcg cctgcgtgat ccatgcgtgt ttgatctcat tcgcgagtac
 480
 gatctgctga tcgatgtgca gcaccacatc ggcacgctcg tcgagctcga tcaggaatgc
 540

gccggctcca ctgagccgcg ctccagcgcg cttatgccgc tgctcgtgcc atataccac
 600
 tcgattccca tccagcgcgc catggcgcag ctcca
 635

<210> 434
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 434
 Xaa Pro Ala Ala Leu Gly Tyr Asp Val Ala Ala Ile Gly Arg Glu
 1 5 10 15
 Tyr Leu Trp Tyr Leu Met Glu Glu Arg Gly Ala Tyr Ala Glu Ala Ala
 20 25 30
 Ala Leu Met Pro Leu Leu Leu Arg Thr Asp Arg Gly Ala Trp Asp Thr
 35 40 45
 Phe Val Cys Cys Tyr Leu Glu Arg His Gln Arg Asp Ala Ile Leu Pro
 50 55 60
 His Ile Pro Thr Gln Asp Pro Gln Leu Ser Glu Met Val Tyr Asp Leu
 65 70 75 80
 Val Leu Val His Leu Leu Gln His Asp Pro Thr Gln Leu Leu Ala Thr
 85 90 95
 Leu Arg Ala Trp Pro Ser His Ile Tyr Ser Lys Gln Ala Val Ala Ala
 100 105 110
 Ala Ile Gly Asp His Ala Arg Thr Ser Arg Thr Leu Leu Glu Cys Leu
 115 120 125
 Ala Gln Leu Tyr Met Ala Ala His Gln Pro Gly Lys Ala Leu Thr Tyr
 130 135 140
 Tyr Met Arg Leu Arg Asp Pro Cys Val Phe Asp Leu Ile Arg Glu Tyr
 145 150 155 160
 Asp Leu Leu Ile Asp Val Gln His His Ile Gly Thr Leu Val Glu Leu
 165 170 175
 Asp Gln Glu Cys Ala Gly Ser Thr Glu Pro Arg Ser Ser Ala Leu Met
 180 185 190
 Pro Leu Leu Val Pro Tyr Thr His Ser Ile Pro Ile Gln Arg Ala Met
 195 200 205
 Ala Gln Leu
 210

<210> 435
 <211> 493
 <212> DNA
 <213> Homo sapiens

<400> 435
 nncgtacgtt cgcgtatattt ccgcgcccgga gaagctatcg ataataaagt tcaaccgctg
 60
 atccagcgtt agcaatggcg ggcacaggaa gggacttag gcatgcagaa agaaaagctt
 120
 tccgctctga tggatgggga atcgttcgac agcgagctgt tgagttctct gtcgcaagat
 180
 cgaacgcttc aacaaagctg gcagggctat cacctgatac gtgacacact gcgaggtgat
 240

gtcgggcaag tgatgcatct cgacatcgcc gatcgcgtag ccgctgcact tgagaaagaa
 300
 cccgcccggc tgggtgccttc cgccgttcag gaatctcagc cgcagcctca cacctggcag
 360
 aaaatgccgt tctgggacaa agtgcgtccc tgggagagcc agattacgca aatcggtatg
 420
 gcggcctgcg tgtcgctggc ggtgatcgtc ggcgtgcagc agtacaacca gccttctgcg
 480
 ccatcgaacg cgt
 493

<210> 436

<211> 130

<212> PRT

<213> Homo sapiens

<400> 436

Met	Gln	Lys	Glu	Lys	Leu	Ser	Ala	Leu	Met	Asp	Gly	Glu	Ser	Phe	Asp
1				5					10					15	
Ser	Glu	Leu	Leu	Ser	Ser	Leu	Ser	Gln	Asp	Arg	Thr	Leu	Gln	Gln	Ser
			20					25					30		
Trp	Gln	Gly	Tyr	His	Leu	Ile	Arg	Asp	Thr	Leu	Arg	Gly	Asp	Val	Gly
		35					40					45			
Gln	Val	Met	His	Leu	Asp	Ile	Ala	Asp	Arg	Val	Ala	Ala	Ala	Leu	Glu
	50					55				60					
Lys	Glu	Pro	Ala	Arg	Leu	Val	Pro	Ser	Ala	Val	Gln	Glu	Ser	Gln	Pro
65					70					75				80	
Gln	Pro	His	Thr	Trp	Gln	Lys	Met	Pro	Phe	Trp	Asp	Lys	Val	Arg	Pro
				85					90					95	
Trp	Ala	Ser	Gln	Ile	Thr	Gln	Ile	Gly	Met	Ala	Ala	Cys	Val	Ser	Leu
			100					105					110		
Ala	Val	Ile	Val	Gly	Val	Gln	Gln	Tyr	Asn	Gln	Pro	Ser	Ala	Pro	Ser
		115				120							125		
Asn	Ala														
	130														

<210> 437

<211> 447

<212> DNA

<213> Homo sapiens

<400> 437

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 cgtaattatg taacacgcat ctgtttggag tctgttaatg gaattaagga caacttttac
 120
 attaatacat tctcatataa aacaatcggt tataaagggtc agttaaccac tgaacaagt
 180
 ccacaatatt tcttagattt acaaaatcca agtatggtaa cggcatttag gcttgtttat
 240
 tcacgtttct caacaaatac atttcctcgt tggcgtttag cacaaccatt ccgttacatc
 300
 gtcataatg gcgaaatcaa tacggttcgc ggtaatatca attggatgaa agcacgtgaa
 360

gcgttacttg aagctgaatt tttcactcgc tcagaattag atatgttaat gccaatctgt
 420
 acggatggta tgtctgactc ggcaagg
 447

<210> 438
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 438
 Xaa Val Thr Gly Val Pro Asp Met Asp Pro Ala Val Leu Glu Arg Lys
 1 5 10 15
 Leu Phe Ile Leu Arg Asn Tyr Val Thr Arg Ile Cys Leu Glu Ser Val
 20 25 30
 Asn Gly Ile Lys Asp Asn Phe Tyr Ile Asn Thr Phe Ser Tyr Lys Thr
 35 40 45
 Ile Val Tyr Lys Gly Gln Leu Thr Thr Glu Gln Val Pro Gln Tyr Phe
 50 55 60
 Leu Asp Leu Gln Asn Pro Ser Met Val Thr Ala Leu Ala Leu Val His
 65 70 75 80
 Ser Arg Phe Ser Thr Asn Thr Phe Pro Arg Trp Arg Leu Ala Gln Pro
 85 90 95
 Phe Arg Tyr Ile Ala His Asn Gly Glu Ile Asn Thr Val Arg Gly Asn
 100 105 110
 Ile Asn Trp Met Lys Ala Arg Glu Ala Leu Leu Glu Ala Glu Phe Phe
 115 120 125
 Thr Arg Ser Glu Leu Asp Met Leu Met Pro Ile Cys Thr Asp Gly Met
 130 135 140
 Ser Asp Ser Ala Arg
 145

<210> 439
 <211> 395
 <212> DNA
 <213> Homo sapiens

<400> 439
 nacgcgtgaa gggagagtgg ggccgagccc caggaggctg tcctgcagca gctgcaccag
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 cttcccagggg gccggctgga cctggccacg caaagcctga cggtggagac ctgcagggcc
 120
 ctgggcaagc tgctgccgag ggagacgctg tgcacggagc tggtcctgag tgactgcatg
 180
 ctacgcgagg aagggggccac actgctgctc cgaggcctgt gtgccaacac cgtgctgcgc
 240
 tttctggact taaagggcaa caaccttcgg gctgcagggg ccgaggctct gggaaaactc
 300
 ctccaacaga acaagtccat tcagagcctc acgctggagt ggaacagcct gggcacgtgg
 360
 gacgatgcct tcgccacctt ctgcgggggc ctggc
 395

<210> 440

<211> 128
 <212> PRT
 <213> Homo sapiens

<400> 440
 Arg Glu Ser Gly Ala Glu Pro Gln Glu Ala Val Leu Gln Gln Leu His
 1 5 10 15
 Gln Leu Pro Arg Gly Arg Leu Asp Leu Ala Thr Gln Ser Leu Thr Val
 20 25 30
 Glu Thr Cys Arg Ala Leu Gly Lys Leu Leu Pro Arg Glu Thr Leu Cys
 35 40 45
 Thr Glu Leu Val Leu Ser Asp Cys Met Leu Ser Glu Glu Gly Ala Thr
 50 55 60
 Leu Leu Leu Arg Gly Leu Cys Ala Asn Thr Val Leu Arg Phe Leu Asp
 65 70 75 80
 Leu Lys Gly Asn Asn Leu Arg Ala Ala Gly Ala Glu Ala Leu Gly Lys
 85 90 95
 Leu Leu Gln Gln Asn Lys Ser Ile Gln Ser Leu Thr Leu Glu Trp Asn
 100 105 110
 Ser Leu Gly Thr Trp Asp Asp Ala Phe Ala Thr Phe Cys Gly Gly Leu
 115 120 125

<210> 441
 <211> 364
 <212> DNA
 <213> Homo sapiens

<400> 441
 gccagctact acgtgaacat gttcgatgcc gagcagggct tcttcgacag gcgcagcccg
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 ggcggcgagt tccaagccgg cttggatccg gaatcctggg gcggtctgtt cactgagacc
 120
 gacggttgga acttcgcctt ccacgctcca caggacggcc gggggctggc cgcgctctac
 180
 ggcgggtccga aaggcttgga gaacaagctc gatgcctttt tcgcgacgcc ggaaaacgcg
 240
 gacaagccgg cgtacggcgg aatccacgaa atggctcgagg ccagagcggg ccggatgggg
 300
 caattgggca tgtccaacga gccctcgac catattccct acatctacaa ctatgccggc
 360
 gcgc
 364

<210> 442
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 442
 Ala Gln Tyr Tyr Val Asn Met Phe Asp Ala Glu Gln Gly Phe Phe Asp
 1 5 10 15
 Arg Arg Ser Pro Gly Gly Glu Phe Gln Ala Gly Leu Asp Pro Glu Ser
 20 25 30
 Trp Gly Gly Leu Phe Thr Glu Thr Asp Gly Trp Asn Phe Ala Phe His

```

      35              40              45
Ala Pro Gln Asp Gly Arg Gly Leu Ala Ala Leu Tyr Gly Gly Pro Lys
      50              55              60
Gly Leu Glu Asn Lys Leu Asp Ala Phe Phe Ala Thr Pro Glu Asn Ala
      65              70              75              80
Asp Lys Pro Ala Tyr Gly Gly Ile His Glu Met Val Glu Ala Arg Ala
      85              90              95
Val Arg Met Gly Gln Leu Gly Met Ser Asn Glu Pro Ser His His Ile
      100              105              110
Pro Tyr Ile Tyr Asn Tyr Ala Gly Ala
      115              120

```

<210> 443
 <211> 430
 <212> DNA
 <213> Homo sapiens

```

<400> 443
accggttacg gctcagtgca acaagagatg ttcgccaaca acctcgtgcg gatgccgctg
60
ctcatgggtgc tggcaatccc ctctcgccaag atcctctcga cgaccctgtc catcggatcg
120
ggcgggtccgg cggcgtcttc cggccctggc atgggtcatcg gcggagccac tggcgcggca
180
ctgtggcgcc tcctcgaggg gctgccaggt atcccatcct caccgatgag ttctgtcatt
240
gtcggcatga tcgcctgctt cggtgcggtt gcccatgccc cactcggcgt gctgctcatg
300
gttggcgaga tgaccggaaa cctgtcgctg ctcgctcctg gcatgatcgc cgtcgccgtc
360
gctggccgag ttgtcgggga cacttcgatc tacacctctc agctcaagga tcgcctggag
420
ggcgacgcgt
430

```

<210> 444
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 444
Thr Gly Tyr Gly Ser Val Gln Gln Glu Met Phe Ala Asn Asn Leu Val
1      5      10      15
Arg Met Pro Leu Leu Met Val Leu Ala Ile Pro Phe Ala Lys Ile Leu
20     25     30
Ser Thr Thr Leu Ser Ile Gly Ser Gly Gly Pro Ala Ala Ser Ser Gly
35     40     45
Pro Gly Met Val Ile Gly Gly Ala Thr Gly Ala Ala Leu Trp Arg Leu
50     55     60
Leu Glu Gly Leu Pro Gly Ile Pro Ser Ser Pro Met Ser Phe Val Ile
65     70     75     80
Val Gly Met Ile Ala Cys Phe Gly Ala Val Ala His Ala Pro Leu Gly
85     90     95
Val Leu Leu Met Val Gly Glu Met Thr Gly Asn Leu Ser Leu Leu Ala

```

```

          100          105          110
Pro Gly Met Ile Ala Val Ala Val Ala Gly Arg Val Val Gly Asp Thr
          115          120          125
Ser Ile Tyr Thr Ser Gln Leu Lys Asp Arg Leu Glu Gly Asp Ala
          130          135          140

```

<210> 445
 <211> 360
 <212> DNA
 <213> Homo sapiens

```

<400> 445
ccatggggct gcctagcctc tggggaggcc cctcagctgg tgacaccagc agggcagatt
60
tcttgcttta ttgctcacc tgtccagggt tccctctggt tgtgaggag ctgctgccac
120
cttgggtcca ggaagcatga agctccgcag gtcagcctcc tgggtgggagg acttttcctt
180
agttttcttt gctcttctgc tctgagtcca gccctggetg gacctttgat cccttctctc
240
tttatcagga aattttctga ctttcttctt ttgccttttc aagatctgtg atgccatctc
300
caagtgggaa caagccatga aggagctgca ccccgaaag tctgagggtg ggacacgcgt
360

```

<210> 446
 <211> 101
 <212> PRT
 <213> Homo sapiens

```

<400> 446
Met Ala Cys Ser His Leu Glu Met Ala Ser Gln Ile Leu Lys Arg Gln
1      5      10      15
Lys Lys Lys Val Arg Lys Phe Pro Asp Lys Glu Arg Arg Asp Gln Arg
20     25     30
Ser Ser Gln Gly Trp Thr Gln Ser Arg Arg Ala Lys Lys Thr Lys Glu
35     40     45
Lys Ser Ser His Gln Glu Ala Asp Leu Arg Ser Phe Met Leu Pro Gly
50     55     60
Pro Lys Val Ala Ala Ala Pro Ser Gln Thr Glu Gly Thr Leu Asp Arg
65     70     75     80
Val Ser Asn Lys Ala Arg Asn Leu Pro Cys Trp Cys His Gln Leu Arg
85     90     95
Gly Leu Pro Arg Gly
100

```

<210> 447
 <211> 487
 <212> DNA
 <213> Homo sapiens

```

<400> 447
acgcgtgaag ggggaaattg ctctgtgccac ctgaggatta atcattaccc tggaaccctt
60

```

cccaaggcca tcaaggaaca cgcacccctt accagacctt ccagctgctg ggggctctcc
 120
 gagtgaggct gaggtcatgg agaaggggaat gggggggcccc catggccagc tggacctgat
 180
 cactgcctcc ccactcagcc acagccctca gggccctgtg ccagtccaga agccccattca
 240
 gggacacctt tggccaatgt tctgtttcat ctgcgaggca accttccccca gtgccccaac
 300
 catagcgttt tcccccaaac accctcagga aggaggggacc actacctgtg caggggggggc
 360
 caggagcctc ctgagagcct catatgggga ggaagtggta ccatctcacc cccattgcct
 420
 ttctctccta cttccacctg gccagcttcc ctcagtgcc ctcctgcctc agtgccccctt
 480
 cacgcgt
 487

<210> 448

<211> 117

<212> PRT

<213> Homo sapiens

<400> 448

Met	Glu	Lys	Gly	Met	Gly	Gly	Pro	His	Gly	Gln	Leu	Asp	Leu	Ile	Thr
1				5					10					15	
Ala	Ser	Pro	Leu	Ser	His	Ser	Pro	Gln	Gly	Pro	Val	Pro	Val	Gln	Lys
			20					25					30		
Pro	Ile	Gln	Gly	His	Leu	Trp	Pro	Met	Phe	Cys	Phe	Ile	Cys	Glu	Ala
		35					40					45			
Thr	Phe	Pro	Ser	Ala	Pro	Thr	Ile	Ala	Phe	Ser	Pro	Lys	His	Pro	Gln
	50					55					60				
Glu	Gly	Gly	Thr	Thr	Thr	Cys	Ala	Gly	Gly	Ala	Arg	Ser	Leu	Leu	Arg
65					70				75					80	
Ala	Ser	Tyr	Gly	Glu	Glu	Val	Val	Pro	Ser	His	Pro	His	Cys	Leu	Ser
			85					90					95		
Leu	Leu	Leu	Pro	Pro	Gly	Gln	Leu	Pro	Ser	Val	Pro	Leu	Leu	Pro	Gln
			100				105					110			
Cys	Pro	Phe	Thr	Arg											
			115												

<210> 449

<211> 353

<212> DNA

<213> Homo sapiens

<400> 449

gagctcagcc agttggagtt tgagaagcgg cagctgcaca gggacttgga gcaggccaag
 60
 gagaaggggg agcgggcaga gaagctggag agggagctac agcgactcca ggaggagaac
 120
 gggaggctgg ccaggaaggt gacctccctg gagacagcca ccgagaaagt cgaggccctg
 180
 gagcatgaga gccagggcct gcagctggag aaccggactc tgaggaagtc tctggacacc
 240

ttgcagaacg tgtccctgca gcttgagggc ctggagcgtg acaacaagca gctggacgca
 300
 gagaacctgg agctgcgcag gctggtggag accatgcgga gacgacaacg cgt
 353

<210> 450
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 450
 Glu Leu Ser Gln Leu Glu Phe Glu Lys Arg Gln Leu His' Arg Asp Leu
 1 5 10 15
 Glu Gln Ala Lys Glu Lys Gly Glu Arg Ala Glu Lys Leu Glu Arg Glu
 20 25 30
 Leu Gln Arg Leu Gln Glu Glu Asn Gly Arg Leu Ala Arg Lys Val Thr
 35 40 45
 Ser Leu Glu Thr Ala Thr Glu Lys Val Glu Ala Leu Glu His Glu Ser
 50 55 60
 Gln Gly Leu Gln Leu Glu Asn Arg Thr Leu Arg Lys Ser Leu Asp Thr
 65 70 75 80
 Leu Gln Asn Val Ser Leu Gln Leu Glu Gly Leu Glu Arg Asp Asn Lys
 85 90 95
 Gln Leu Asp Ala Glu Asn Leu Glu Leu Arg Arg Leu Val Glu Thr Met
 100 105 110
 Arg Arg Arg Gln Arg
 115

<210> 451
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 451
 gtgatgcggc tgactaagcc tactttattc accaatatcc cagtaacatg tgaagagaaa
 60
 gacttacctg gagatctctt taaccagctg atgagagatg atccttcaac cgттаатггт
 120
 gcagaagttt таатгттггг агaaатгctg actttaccac agaattttgg gaatatattt
 180
 ttgggagaga cctttttccag ttatatcagc gttcataatg atagcaatca agttgtaaaa
 240
 gacatattag taaaagctga tcttcagaca agttctcagc gtttaaатct ttcagcctcc
 300
 аатгctgcag тггctgaact тааaccggat тгттгтattg atgatgtcat acatcatgaa
 360
 gtcaaagaaa ttggaacaca catcttggtg tgtgctgtga gttatacaac tcaggctgga
 420
 gaaaaaatgt atttcagaaa attt
 444

<210> 452
 <211> 148
 <212> PRT

<213> Homo sapiens

<400> 452

```

Val Met Arg Leu Thr Lys Pro Thr Leu Phe Thr Asn Ile Pro Val Thr
 1           5           10           15
Cys Glu Glu Lys Asp Leu Pro Gly Asp Leu Phe Asn Gln Leu Met Arg
      20           25           30
Asp Asp Pro Ser Thr Val Asn Gly Ala Glu Val Leu Met Leu Gly Glu
      35           40           45
Met Leu Thr Leu Pro Gln Asn Phe Gly Asn Ile Phe Leu Gly Glu Thr
      50           55           60
Phe Ser Ser Tyr Ile Ser Val His Asn Asp Ser Asn Gln Val Val Lys
65           70           75           80
Asp Ile Leu Val Lys Ala Asp Leu Gln Thr Ser Ser Gln Arg Leu Asn
      85           90           95
Leu Ser Ala Ser Asn Ala Ala Val Ala Glu Leu Lys Pro Asp Cys Cys
      100          105          110
Ile Asp Asp Val Ile His His Glu Val Lys Glu Ile Gly Thr His Ile
      115          120          125
Leu Val Cys Ala Val Ser Tyr Thr Thr Gln Ala Gly Glu Lys Met Tyr
      130          135          140
Phe Arg Lys Phe
145

```

<210> 453

<211> 373

<212> DNA

<213> Homo sapiens

<400> 453

```

gctagctctg accccacctt tgccaagtgg cactaggggtg gccaatgggg actaggggtg
60
tataattgga aaatacagtc tcccctgttg tccaagaaag gcccagatg acctgggggt
120
tgaaaggcac tcccgtggg tgcttcctgg gaggaggtgg ggggcagcgg ggcggcgggg
180
cctgtctgtg ctgagcatcc ccagctccag ggcaggtgct gggctctgag cccactggt
240
gcgttttggg atgggctggc ctgcgcggct gtcgtttcag agcacacaga agagaccctg
300
ccacaggagg agtgggagga gaagctgttg atgttcctgc gagacaccct ggccatcatt
360
tctgacaacg cgt
373

```

<210> 454

<211> 108

<212> PRT

<213> Homo sapiens

<400> 454

```

Met Met Ala Arg Val Ser Arg Arg Asn Ile Asn Ser Phe Ser Ser His
 1           5           10           15
Ser Ser Cys Gly Arg Val Ser Ser Val Cys Ser Glu Thr Thr Ala Ala

```

```

      20      25      30
Gln Ala Ser Pro Ser Gln Asn Ala Pro Val Gly Leu Arg Ala Gln His
      35      40      45
Leu Pro Trp Ser Trp Gly Cys Ser Ala Gln Thr Gly Pro Ala Ala Pro
      50      55      60
Leu Pro Pro Thr Cys Ser Gln Glu Ala Pro Ser Gly Ser Ala Phe Gln
      65      70      75      80
Ala Pro Gly His Leu Gly Pro Phe Leu Asp Asn Arg Gly Asp Cys Ile
      85      90      95
Phe Gln Leu Tyr Asn Pro Ser Pro His Trp Pro Pro
      100      105

```

<210> 455
 <211> 602
 <212> DNA
 <213> Homo sapiens

```

<400> 455
cctaggcaaa gcatgcccac cctacctccc cttaccctta cccttcattt tcccctaagc
60
acccatcacc accgatgtta ctgtatgtgt ttgcttacgc tgacagccca ccacccacac
120
tggaatgtcc gcacgacaaa ggcaggactc ttggctgcct tagccacagc tggatcccca
180
gagctttgta ggggtgttggg cacagagtgg agtgggtact taataagtat ctgtggaatg
240
aacatgtaca gagtgaagcc ctgtgcccag aacaggctca aaataagctc aattcctttc
300
cttgccactt actaagtcct ttttctctcg cccctctca ctgacctggt tttgatgcca
360
gacagcacag atgggctagg gaggcagggtg gggaagcaga gatctgcgtc tcttgagct
420
ggagctggtg ggtggggctc cttcctggtg ctgcggaggc tcattggggga ggtggcagcg
480
acccctcag gagcctctgt cgctgcact cagatctgtg cctttccaca gcgcccggag
540
gaagacttgc tcaggagata aattcaaaga caacaggaag ctggacgtgg tggctcacgc
600
gt
602

```

<210> 456
 <211> 100
 <212> PRT
 <213> Homo sapiens

```

<400> 456
Met Pro Thr Leu Pro Pro Leu Thr Leu Thr Leu His Phe Pro Leu Ser
1      5      10      15
Thr His His His Arg Cys Tyr Cys Met Cys Leu Leu Thr Leu Thr Ala
20      25      30
His His Pro His Trp Asn Val Arg Thr Thr Lys Ala Gly Leu Leu Ala
35      40      45
Ala Leu Ala Thr Ala Gly Ser Pro Glu Leu Cys Arg Val Leu Gly Thr

```



```

      50              55              60
Glu Trp Ser Gly Tyr Leu Ile Ser Ile Cys Gly Met Asn Met Tyr Arg
65              70              75              80
Val Lys Pro Cys Ala Gln Asn Arg Leu Lys Ile Ser Ser Ile Pro Phe
      85              90              95
Leu Ala Thr Tyr
      100

```

<210> 457
 <211> 324
 <212> DNA
 <213> Homo sapiens

```

<400> 457
acgcgtcatg tggatattcc tgggaggttc ccaggaacgt ttctggacgg gccccgacc
60
agagggtcagg gaacttttct tattattctg cacgtgccca gggatagtca aaccaggtct
120
tcccccttctg ctggccgcaa cagccagcc gccgccacga ccgcacgctg aattcatgac
180
ccgacacgcg acgtggcagc gagcacaccc accgctagga gaaagagcgc tcatcgaaga
240
tcgttttctg tccactggcc agcgccacta tgatcaggtg gggatatccgc cggcgggcgg
300
gagcacccggg acgccggggc gccg
324

```

<210> 458
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 458
Met Trp Ile Phe Leu Gly Gly Ser Gln Glu Arg Phe Trp Thr Gly Pro
1              5              10              15
Arg Pro Glu Val Arg Glu Leu Phe Leu Leu Phe Cys Thr Cys Pro Gly
      20              25              30
Ile Val Lys Pro Gly Leu Pro Leu Leu Leu Ala Ala Thr Arg Gln Pro
      35              40              45
Pro Pro Arg Pro His Ala Glu Phe Met Thr Arg His Ala Thr Trp Gln
      50              55              60
Arg Ala His Pro Pro Leu Gly Glu Arg Ala Leu Ile Glu Asp Arg Phe
65              70              75              80
Leu Ser Thr Gly Gln Arg His Tyr Asp Gln Val Gly Tyr Pro Pro Gly
      85              90              95
Gly Gly Ser Thr Gly Thr Pro Gly Arg
      100              105

```

<210> 459
 <211> 415
 <212> DNA
 <213> Homo sapiens

<400> 459

acgcgttcat tcggcatctg cttccatgga tttcctgcgg ggaggcgcgg ccgagagtgc
60
gggtgtcgaa cacgacactt cagtgatcgt ttcaaccacc ggccgagatg ggtcctgacg
120
ctgggcttca agccgcttgc gctcgcgctc ctgatctcgg gcagcgcgat tccggtggtt
180
tatgctgccg gcagacgact gcgcacgccc ctcacgaggt atctgcacat gcttaaaggg
240
agaggcctca cccgacagct gggcatcgga ttacgaagc ccacgacgaa tcttcctcgc
300
ctcctcaaag ccgatcatcg gcatgccagg tttgtggttg aatgcttcga tcaacacact
360
aggatcggtg ggggtccacca catacaccga gcggcaatcg agcggatacg acctc
415

<210> 460
<211> 105
<212> PRT
<213> Homo sapiens

<400> 460
Met Pro Met Ile Gly Phe Glu Glu Ala Arg Lys Ile Arg Arg Gly Leu
1 5 10 15
Arg Lys Ser Asp Ala Gln Leu Ser Gly Glu Ala Ser Pro Phe Lys His
20 25 30
Val Gln Ile Pro Arg Glu Gly Arg Ala Gln Ser Ser Ala Gly Ser Ile
35 40 45
Asn His Arg Asn Arg Ala Ala Arg Asp Gln Glu Arg Glu Arg Lys Arg
50 55 60
Leu Glu Ala Gln Arg Gln Asp Pro Ser Arg Pro Val Val Glu Thr Ile
65 70 75 80
Thr Glu Val Ser Cys Ser Thr Pro Ala Leu Ser Ala Ala Pro Pro Arg
85 90 95
Arg Lys Ser Met Glu Ala Asp Ala Glu
100 105

<210> 461
<211> 357
<212> DNA
<213> Homo sapiens

<400> 461
acgcgttcga ggtcggctaa atttatcatg cgcacgacaa agagagtagt gggtcacaac
60
cgggtcacat gcatgatgac aaaaactggc agaataagagt tgatgtcatc ccgtctacca
120
gtccttagaa ccagctcaga gagtcccggg gtcgggtaccg tcgagactca gtacacaact
180
gtcgcgatac cggacgaccc tcttcatctg gttgcagatg ggcgtctcaa tcacgtcact
240
gtcgtttacg aaacctacgg gaagctcaat acgtccagcg acaatgcggg ctatacctgt
300
catgcgctta ctggtgatgc ccatgcagcc ggatttcacc ccggtgtagt ccgtccg
357

<210> 462
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 462
 Thr Arg Ser Arg Ser Ala Lys Phe Ile Met Arg Thr Thr Lys Arg Val
 1 5 10 15
 Val Ala His Asn Arg Val Thr Cys Met Met Thr Lys Thr Gly Arg Ile
 20 25 30
 Glu Leu Met Ser Ser Arg Leu Pro Ala Pro Arg Thr Ser Ser Glu Ser
 35 40 45
 Pro Gly Val Gly Thr Val Glu Thr Gln Tyr Thr Thr Val Ala Ile Pro
 50 55 60
 Asp Asp Pro Leu His Leu Val Ala Asp Gly Arg Leu Asn His Val Thr
 65 70 75 80
 Val Ala Tyr Glu Thr Tyr Gly Lys Leu Asn Thr Ser Ser Asp Asn Ala
 85 90 95
 Val Tyr Thr Cys His Ala Leu Thr Gly Asp Ala His Ala Ala Gly Phe
 100 105 110
 His Pro Gly Val Val Arg Pro
 115

<210> 463
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 463
 gtgcacgggg tatgcgaggg atgcggcatt gccaccaatg ccgctgacct gcgcagatac
 60
 gaggcagctg gtgacgatga agtggtgcca tgcgaggaat gcgatcgtat cctggtgcgt
 120
 accggagagt ccatctgagc ccttcttggtg gcggtgatgc cgggatatcc gtagaattag
 180
 cggtcggacg agccatccgg gtgatcgagg cagcgggtgag ttgtcgagga aagtccgggc
 240
 tccatagagc aggggtggtgg gtaacgcccc cccgggggtga cccgcgggaa agtgccacag
 300
 agaacagact gccggtttcg agccgggtgag ggtgaaacgg tggagtaagt gcccaccgag
 360
 tcatcggtga cggtgacggc atggcaaacc ccacctggag caaggccaag aagaccgtga
 420
 ggtcgaggac gcgt
 434

<210> 464
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 464
 Met Pro Ser Pro Ser Pro Met Thr Arg Trp Ala Leu Thr Pro Pro Phe

```

      1             5             10             15
His Pro His Arg Leu Glu Thr Gly Ser Leu Phe Ser Val Ala Leu Ser
      20             25             30
Arg Gly Ser Pro Arg Val Gly Val Thr His His Pro Ala Leu Trp Ser
      35             40             45
Pro Asp Phe Pro Arg Gln Leu Thr Ala Ala Ala Ile Thr Arg Met Ala
      50             55             60
Arg Pro Thr Ala Asn Ser Thr Asp Ile Pro Ala Ser Pro Pro Gln Glu
      65             70             75             80
Gly Leu Arg Trp Thr Leu Arg Tyr Ala Pro Gly Tyr Asp Arg Ile Pro
      85             90             95
Arg Ile Ala Pro Leu His Arg His Gln Leu Pro Arg Ile Cys Ala Gly
      100             105             110
Gln Arg His Trp Trp Gln Cys Arg Ile Pro Arg Ile Pro Arg Ala
      115             120             125

```

<210> 465
 <211> 438
 <212> DNA
 <213> Homo sapiens

```

<400> 465
gatcatttag aatttatgga agaagctgat gtgaaagcta tgggtcaaatac tggcactgtg
60
gctgtattgc taccaggagc attttacacc ttgaaagaaa ctcaacttcc accgatgaat
120
ttgttacgtc agtacggagt agacattgct atttcgacgg atgctaatacc agggacgtcg
180
ccagcggttat cattacgggtt aatgatgaat atggcatgta ccttggtttgg tatgacacct
240
gaaaccgccc ttgcaggggtt aacaattcat gcggcaaaaag cggtggggat tagcgattct
300
catggcactt tagaagttgg caaggtagct gattttgtct gctgggatgt ggaaagcccc
360
ggtgaacttt gttattggtt aggagagcag ttagtaaagc aacgtattca gcacggagta
420
tcccatgaat aatctaga
438

```

<210> 466
 <211> 143
 <212> PRT
 <213> Homo sapiens

```

<400> 466
Asp His Leu Glu Phe Met Glu Glu Ala Asp Val Lys Ala Met Val Lys
1             5             10             15
Ser Gly Thr Val Ala Val Leu Leu Pro Gly Ala Phe Tyr Thr Leu Lys
      20             25             30
Glu Thr Gln Leu Pro Pro Met Asn Leu Leu Arg Gln Tyr Gly Val Asp
      35             40             45
Ile Ala Ile Ser Thr Asp Ala Asn Pro Gly Thr Ser Pro Ala Leu Ser
      50             55             60
Leu Arg Leu Met Met Asn Met Ala Cys Thr Leu Phe Gly Met Thr Pro

```

65		70		75		80
Glu Thr Ala Leu	Ala Gly Val Thr Ile His	Ala Ala Lys Ala Leu Gly				
	85	90		95		
Ile Ser Asp Ser	His Gly Thr Leu Glu Val Gly Lys Val Ala Asp Phe					
	100	105		110		
Val Cys Trp Asp	Val Glu Ser Pro Gly Glu Leu Cys Tyr Trp Leu Gly					
	115	120		125		
Glu Gln Leu Val	Lys Gln Arg Ile Gln His Gly Val Ser His Glu					
	130	135		140		

<210> 467
 <211> 460
 <212> DNA
 <213> Homo sapiens

<400> 467
 ntctccctgg ctattggcca tgtgggacac aacgttccgc ctaccccaga gcgggtaagc
 60
 tgcacccctg caccttcttc tcccaccgct tcaaagccac agtgaggaac ttcggagctt
 120
 ctgcagtgga agatggcggt ggaggaatgg atgccctggc tagaagaggg ggaatatctg
 180
 ttgattgtgt ggaccgacca caaaaacctg gagtatctcc acacaaccaa gtgcctcaac
 240
 tccaggcaag caagaagggc ccagctgttt acctgggtcc acttttccct ctccctaccg
 300
 ccgggggtcca agaacatcag gctggatgcc ctttcttgcc actttatggg catgggcccc
 360
 ttccctccagg cttgcctgtc acccggggtc ccgtcaaacc ctggccttcg tgcgacaaca
 420
 ctcttggtgc cttctatggt tctgtatggt gccgcaattg
 460

<210> 468
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 468
 Gly Thr Ser Glu Leu Leu Ala Val Lys Met Ala Leu Glu Glu Trp Met
 1 5 10 15
 Pro Trp Leu Glu Ala Glu Tyr Leu Leu Ile Val Trp Thr Asp His
 20 25 30
 Lys Asn Leu Glu Tyr Leu His Thr Thr Lys Cys Leu Asn Ser Arg Gln
 35 40 45
 Ala Arg Arg Ala Gln Leu Phe Thr Trp Phe His Phe Ser Leu Ser Tyr
 50 55 60
 Arg Pro Gly Ser Lys Asn Ile Arg Leu Asp Ala Leu Ser Cys His Phe
 65 70 75 80
 Met Gly Met Gly Pro Phe Leu Gln Ala Cys Leu Ser Pro Gly Leu Pro
 85 90 95
 Ser Asn Pro Gly Leu Arg Ala Thr Thr Leu Leu Val Pro Ser Met Val
 100 105 110
 Leu Tyr Val Ala Ala Ile

115

<210> 469
 <211> 381
 <212> DNA
 <213> Homo sapiens

<400> 469
 cttgtgcaca cgttatTTTT ccaatacaaaa tagtttaaaaa agtaaaactcc aaatacctat
 60
 aagccccctc aaagcacctt ccaaatatga accttggttaa tgcccaaggt ccagaggggt
 120
 cccccagaaa ggcccaggag cctggggcat gggaaagctg tcgggggtccc catgctgact
 180
 ccctggactc caagcgatat tccataaagc cagggcctcc tggctgcggg agggaggcct
 240
 tgacccaaaa tccattcggc cctggatact ggagaggcag aggcctctgc tgatgagaag
 300
 ccctgagttc ctggctagct gtgggtaacc acaaaaaatg cgggggggtga tgattttcga
 360
 agtccatcgg caaagaaaga c
 381

<210> 470
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Phe Glu Asn His His Pro Pro His Phe Leu Trp Leu Thr Thr
 1 5 10 15
 Ala Ser Gln Glu Leu Arg Ala Ser His Gln Gln Arg Pro Leu Pro Leu
 20 25 30
 Gln Tyr Pro Gly Pro Asn Gly Phe Trp Val Lys Ala Ser Leu Pro Gln
 35 40 45
 Pro Gly Gly Pro Gly Phe Met Glu Tyr Arg Leu Glu Ser Arg Glu Ser
 50 55 60
 Ala Trp Gly Pro Arg Gln Leu Ser His Ala Pro Gly Ser Trp Ala Phe
 65 70 75 80
 Leu Gly Asp Pro Ser Gly Pro Trp Ala Leu Thr Arg Phe Ile Phe Gly
 85 90 95
 Arg Cys Phe Glu Gly Ala Tyr Arg Tyr Leu Glu Phe Thr Phe
 100 105 110

<210> 471
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 471
 accggtgact acctgcagca ctggattgac atgggtaaaa agggcggcga ccgcatgccca
 60
 gaggtcttcc tgggtaactg gttccgccgc ggcgacgatg gccgcttcct gtggccgngg
 120

cttggcgaaa acttcccggg cctanagtgg atcatcgacc gcattgaagg caacgtagag
 180
 gccgaggaca cgggtggtcgg acgcaccgcc cgcgccgagg acatcgactt gcaaggcctt
 240
 gacttcgatg tcgacgacgt tcgcgccgca ctgcgcgttg acccgaagga atgggaaggc
 300
 gatatgcaag acaacgccga gtacctgaac ttcttgggct cccgcgtgcc cgaggaagtg
 360
 tggaaccagt tccgcgcc
 378

<210> 472

<211> 126

<212> PRT

<213> Homo sapiens

<400> 472

Thr	Gly	Asp	Tyr	Leu	Gln	His	Trp	Ile	Asp	Met	Gly	Lys	Lys	Gly	Gly
1				5				10						15	
Asp	Arg	Met	Pro	Glu	Val	Phe	Leu	Val	Asn	Trp	Phe	Arg	Arg	Gly	Asp
			20					25					30		
Asp	Gly	Arg	Phe	Leu	Trp	Pro	Xaa	Leu	Gly	Glu	Asn	Phe	Pro	Val	Leu
			35				40					45			
Xaa	Trp	Ile	Ile	Asp	Arg	Ile	Glu	Gly	Asn	Val	Glu	Ala	Glu	Asp	Thr
	50					55				60					
Val	Val	Gly	Arg	Thr	Ala	Arg	Ala	Glu	Asp	Ile	Asp	Leu	Gln	Gly	Leu
65					70					75				80	
Asp	Phe	Asp	Val	Asp	Asp	Val	Arg	Ala	Ala	Leu	Ala	Val	Asp	Pro	Lys
				85				90					95		
Glu	Trp	Glu	Gly	Asp	Met	Gln	Asp	Asn	Ala	Glu	Tyr	Leu	Asn	Phe	Leu
			100					105					110		
Gly	Ser	Arg	Val	Pro	Glu	Glu	Val	Trp	Asn	Gln	Phe	Arg	Ala		
			115				120						125		

<210> 473

<211> 339

<212> DNA

<213> Homo sapiens

<400> 473

accggttggt gggggaagg acccatccca tgccacctgt cctagaaaat gtttcccctt
 60
 gttgagcagc tgctggatct agggctgctg ggtctaagtc caaaaaggga aaaaggaaaa
 120
 aggaccaag taaaagaagg gggaagctgc caaaaccccc cctgccaaaa ctctcccacc
 180
 ctgcttccat ttccctctcc agggaaacagg tgtacctccc ctctctccctg tctcctcag
 240
 atgccccagg ggctctctac ttcatctctg ccgaccctgc caggagtggc ctcaggggta
 300
 gaggctccta gttggagaat ttgcttgag gaaggtgaa
 339

<210> 474

<211> 97
 <212> PRT
 <213> Homo sapiens

<400> 474
 Met Phe Pro Leu Val Glu Gln Leu Leu Asp Leu Gly Leu Leu Gly Leu
 1 5 10 15
 Ser Pro Lys Arg Glu Lys Gly Lys Arg His Gln Val Lys Glu Gly Gly
 20 25 30
 Ser Cys Gln Asn Pro Pro Cys Gln Asn Ser Pro Thr Leu Leu Pro Phe
 35 40 45
 Pro Ser Pro Gly Asn Arg Cys Thr Ser Pro Pro Pro Cys Pro Pro Gln
 50 55 60
 Met Pro Gln Gly Leu Ser Thr Ser Phe Leu Pro Thr Leu Pro Gly Val
 65 70 75 80
 Ala Ser Gly Val Glu Ala Pro Ser Trp Arg Ile Cys Leu Gln Glu Gly
 85 90 95
 Glu

<210> 475
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 475
 acgcgtgaag ggtccctcc aaactctgag cctccttcca agccttgctg ggagctcccc
 60
 agcgctgcc ggagaggcct ctctccagg cgggcttccc gcgccgatgt gaaggagagg
 120
 ctgccccaga ggggtctgga tcgtaatcca gaaagggaca gtccacacgc cataatcccc
 180
 aatgctggga ctcttcagta aaggaagaga tggctttttc gttcatctgc ctttctgaaa
 240
 ggtaaaatat ctccagatcc gggctctctg ggcgactgcg tatgtggggg tccctgaagc
 300
 ctttgatgga tcttgtaga agtgggttgt tcatcttggg gtttt
 345

<210> 476
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 476
 Met Asn Asn Pro Leu Leu Thr Arg Ser Ile Lys Gly Phe Arg Asp Pro
 1 5 10 15
 His Ile Arg Ser Arg Pro Glu Ser Pro Asp Leu Glu Ile Phe Tyr Leu
 20 25 30
 Ser Glu Arg Gln Met Asn Glu Lys Ala Ile Ser Ser Phe Thr Glu Glu
 35 40 45
 Ser Gln His Ser Gly Leu Trp Leu Trp Asp Cys Pro Phe Leu Asp Tyr
 50 55 60
 Asp Pro Asp Pro Ser Gly Ala Ala Ser Pro Ser His Arg Arg Gly Lys

65					70					75				80	
Pro	Ala	Trp	Arg	Arg	Gly	Leu	Ser	Gly	Arg	Arg	Trp	Gly	Ala	Pro	Ser
				85					90					95	
Lys	Ala	Trp	Lys	Glu	Ala	Gln	Ser	Leu	Glu	Gly	Thr	Leu	His	Ala	
			100					105					110		

<210> 477
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 477
 acgcgtggcc gagccagcgt gctcaaggaa atgggtcaacg gcactcttat taacggctgg
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 gactctcccg aggtggaacg ggcactggac ctgtgcatgg cgtgcaaagg gtgcgcccga
 120
 gattgccccca ccggaatcga catggccagc taccgcagca cggttcttga cgaaaaatac
 180
 cgtcaccgtc tccgccctcg ctcccacctg acgatggggc tgctgcccac gtgggaacgt
 240
 ttgctcaatc ggaccccagg agcgccgtcg ctggctaacg cagtgccttc gatgccggtc
 300
 ttgcacgtc ttgctagatg gacagccggg gtggatcagc gtcgtccctt ccccgattc
 360
 cagccctcgg ccagattggc cagtccgcag gccgccccgg ttaaggagat tgtggcggat
 420
 cc
 422

<210> 478
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 478
 Thr Arg Gly Arg Ala Ser Val Leu Lys Glu Met Val Asn Gly Thr Leu
 1 5 10 15
 Ile Asn Gly Trp Asp Ser Pro Glu Val Glu Arg Ala Leu Asp Leu Cys
 20 25 30
 Met Ala Cys Lys Gly Cys Ala Arg Asp Cys Pro Thr Gly Ile Asp Met
 35 40 45
 Ala Ser Tyr Arg Ser Thr Val Leu Asp Glu Lys Tyr Arg His Arg Leu
 50 55 60
 Arg Pro Arg Ser His Leu Thr Met Gly Leu Leu Pro Met Trp Glu Arg
 65 70 75 80
 Leu Leu Asn Arg Thr Pro Gly Ala Pro Ser Leu Ala Asn Ala Val Leu
 85 90 95
 Ser Met Pro Val Phe Ala Arg Leu Ala Arg Trp Thr Ala Gly Val Asp
 100 105 110
 Gln Arg Arg Pro Leu Pro Arg Phe Gln Pro Ser Ala Arg Leu Ala Ser
 115 120 125
 Pro Gln Ala Ala Pro Val Lys Glu Ile Val Ala Asp
 130 135 140

<210> 479
 <211> 348
 <212> DNA
 <213> Homo sapiens

<400> 479
 cgcggtggcca ttggccgggc gctggtgctg caccgcgac tgggtgattgc cgatgagccg
 60
 atctcggcgt tggacatgac catccagaag cagattcttg agctgttcga gcgcctgcag
 120
 gcgcagtacg gctttgcctg cctgttcac tcccacgacc tggcagcggg ggaacgcac
 180
 gcccaccggg tggcggatgat gagcgagggc aggggtggtg aaatgggtgc ccgcgacgag
 240
 atcttcgacc gcccgcagca cccctacacc cgcaagctgc tggccgccgc cagccccttg
 300
 gagaaacttg aaaacgggtg ctaccgcac cgccagggcc ccgtaccg
 348

<210> 480
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 480
 Arg Val Ala Ile Gly Arg Ala Leu Val Arg His Pro Arg Leu Val Ile
 1 5 10 15
 Ala Asp Glu Pro Ile Ser Ala Leu Asp Met Thr Ile Gln Lys Gln Ile
 20 25 30
 Leu Glu Leu Phe Glu Arg Leu Gln Ala Gln Tyr Gly Phe Ala Cys Leu
 35 40 45
 Phe Ile Ser His Asp Leu Ala Ala Val Glu Arg Ile Ala His Arg Val
 50 55 60
 Ala Val Met Ser Glu Gly Arg Val Val Glu Met Gly Ala Arg Asp Glu
 65 70 75 80
 Ile Phe Asp Arg Pro Gln His Pro Tyr Thr Arg Lys Leu Leu Ala Ala
 85 90 95
 Ala Ser Pro Leu Glu Lys Leu Glu Asn Gly Gly Tyr Arg Ile Arg Gln
 100 105 110
 Gly Pro Val Pro
 115

<210> 481
 <211> 441
 <212> DNA
 <213> Homo sapiens

<400> 481
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 gcaaaatcct gcttatgctt tgggactagc tcaaagacca ctcccttgga tgggtgccttc
 120
 cctgccctgc cggttgctgc tggcttctc agtgtttaga ttaccatcac attgcatcat
 180

gagagcagaa gaccatctcc atgtgactgc tgcccctgct cccagcaggg cccacaanca
 240
 cccagtcacag gacctggctc acgctgggtg gcggatgccc aggaatgggg ctctggatct
 300
 gcctcttctc ctgcaggacc aggaaaccgc tgccctgtcc ctgccccagg aaaccctcag
 360
 taaatcccca gtcatttgag tttcccctca gcgccagaga ccaataacac atctccacca
 420
 acctgaaaaa ccttcacgcg t
 441

<210> 482

<211> 120

<212> PRT

<213> Homo sapiens

<400> 482

Lys	Leu	Leu	Thr	Val	Ala	Phe	Ser	Leu	Leu	Asn	Met	Ser	Ser	Ile	Ser
1				5				10						15	
Pro	Thr	Tyr	Trp	Ala	Lys	Ser	Cys	Leu	Cys	Phe	Gly	Thr	Ser	Ser	Lys
			20					25					30		
Thr	Thr	Pro	Leu	Asp	Gly	Ala	Phe	Pro	Ala	Leu	Pro	Ala	Cys	Ala	Gly
		35				40						45			
Phe	Leu	Ser	Val	Arg	Ile	Thr	Ile	Thr	Leu	His	His	Glu	Ser	Arg	Arg
	50				55					60					
Pro	Ser	Pro	Cys	Asp	Cys	Cys	Pro	Cys	Ser	Gln	Gln	Gly	Pro	Gln	Xaa
65				70						75				80	
Pro	Ser	Pro	Gly	Pro	Gly	Ser	Arg	Trp	Val	Ala	Asp	Ala	Gln	Glu	Trp
			85					90					95		
Gly	Ser	Gly	Ser	Ala	Ser	Ser	Pro	Ala	Gly	Pro	Gly	Asn	Arg	Cys	Pro
			100					105					110		
Val	Pro	Ala	Pro	Gly	Asn	Pro	Gln								
		115					120								

<210> 483

<211> 330

<212> DNA

<213> Homo sapiens

<400> 483

acgcgttcat tccctgatgg ccacgcacga gctaacggag ggatggggcg aaggggaaggc
 60
 caagggtgcc tcgaagacca aggagtgtgc agggcaggac ctcgttttaa aggaatatcc
 120
 tctcaccaga gacacgcggc ggccaggcag ggccggagcg gggcctgtgc ccagggtccg
 180
 agcgtctgcc cagcccagca tccctgtccc cagccaggaa tatgtcttcg tggcatagag
 240
 ggagctcttg gagccacacc tgcgtgtgca catgtgtcac cccactgctg ggaggggctc
 300
 tcccgggacc ctgcagcgtg ggctggggccc
 330

<210> 484

<211> 96
 <212> PRT
 <213> Homo sapiens

<400> 484

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Met Gly Arg Arg Glu Gly Gln Gly Cys Leu Glu Asp Gln Gly Val Cys
 1           5           10          15
Arg Ala Gly Pro Arg Phe Lys Gly Ile Ser Ser His Gln Arg His Ala
      20           25          30
Ala Ala Arg Gln Gly Arg Ser Gly Ala Cys Ala Gln Ala Pro Ser Val
      35           40          45
Cys Pro Ala Gln His Pro Cys Pro Gln Pro Gly Ile Cys Leu Arg Gly
      50           55          60
Ile Glu Gly Ala Leu Gly Ala Thr Pro Ala Cys Ala His Val Ser Pro
65           70          75          80
His Cys Trp Glu Gly Leu Ser Arg Asp Pro Ala Ala Trp Ala Gly Pro
      85           90          95

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<210> 485
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 485

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acgcgtgctc ggcgggacga agtcggcgct gatcgcccag tcatgcgccc tgcccgtgcc
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gcccagttcg gcgatcgccg cattcggccg gccggaatcg agaaggaatg cgtggacgta
120
cggggggatac caaaggaatc ttgtcgaggg cttcgcggcc ctcgacgtgg atcacctgta
180
cccgaaggac gtggggaagc cgtcccgcga gctcacggga ctccgcgaca tcgatgtgcg
240
atacgatttg caccgtcgtc ggctgcgctg gcgacacatg ctccgcgata gcctcagcgg
300
tggtttccga cgtcagcagg aacgtggcga cgggtggcat ggcggtcgcc gttatgtcgg
360
cattcccatt cctcggg
377

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<210> 486
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 486

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Met Arg Pro Ala Arg Ala Ala Gln Phe Gly Asp Arg Arg Ile Arg Pro
 1           5           10          15
Ala Gly Ile Glu Lys Glu Cys Val Asp Val Arg Gly Ile Pro Lys Glu
      20           25          30
Ser Cys Arg Gly Leu Arg Gly Pro Arg Arg Gly Ser Pro Val Pro Asp
      35           40          45
Gly Arg Gly Glu Ala Val Pro Gln Ala His Gly Thr Pro Arg His Arg
      50           55          60
Cys Ala Ile Arg Phe Ala Pro Ser Ser Ala Ala Cys Ala Thr His Ala

```

65					70						75				80
Pro	Arg	Ser	Pro	Gln	Arg	Trp	Phe	Pro	Thr	Ser	Ala	Gly	Thr	Trp	Arg
				85					90					95	
Arg	Val	Ala	Trp	Arg	Ser	Pro	Leu	Cys	Arg	His	Ser	His	Ser	Ser	
			100					105					110		

<210> 487
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 487
 nnacgcgtaa gatcgattgt ggatcagcac cgatgctggg ccccccgcgc ttgttgttgg
 60
 cggtgttgt tgtaaggagt gtgtgtgatg cgtgttggg ttctactga ggttaagaat
 120
 agtgagtttc gtgtggtgt gacgccggcg ggtgttcacg cgttggttgg tcgtgggtcat
 180
 gaggtgttgg ttcaggctgg tgctggtgtg ggttcgggta ttccggattc ggattttgtg
 240
 ggtgctggtg cgcggttgt ggggtgatgt gagtcggtgt ggggtgatgc tgatttggtg
 300
 ttgaagggtga aggagcctgt tgcggaggag tatgggcggt tgcattgaggg tttggttctt
 360
 ttacgtatc ttcatttggc tgctgatgag gcgttgactc gtgagctttt ggggcgtggg
 420
 gtgacgtcga ttgcgtatga gacggtggag ttggccgat
 459

<210> 488
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 488
 Met Arg Val Gly Val Pro Thr Glu Val Lys Asn Ser Glu Phe Arg Val
 1 5 10 15
 Ala Val Thr Pro Ala Gly Val His Ala Leu Val Gly Arg Gly His Glu
 20 25 30
 Val Leu Val Gln Ala Gly Ala Gly Val Gly Ser Gly Ile Pro Asp Ser
 35 40 45
 Asp Phe Val Gly Ala Gly Ala Arg Val Val Gly Asp Val Glu Ser Val
 50 55 60
 Trp Gly Asp Ala Asp Leu Val Leu Lys Val Lys Glu Pro Val Ala Glu
 65 70 75 80
 Glu Tyr Gly Arg Leu His Glu Gly Leu Val Leu Phe Thr Tyr Leu His
 85 90 95
 Leu Ala Ala Asp Glu Ala Leu Thr Arg Glu Leu Leu Gly Arg Gly Val
 100 105 110
 Thr Ser Ile Ala Tyr Glu Thr Val Glu Leu Ala Asp
 115 120

<210> 489
 <211> 542

<212> DNA

<213> Homo sapiens

<400> 489

nacgcgtttg gcgctactgag tgcggtggtg gatggcgacg acagtggcaa gccgctgctc
 60
 aaccagcacg gttgctacaa agtgcgcttt ccattttaccc gcgatcaaaa gccagcact
 120
 cgggggttcgg catggctgcg caggggtgctg ttgtctgccg gttccagcca tggcatgcac
 180
 ttccgctgc tcaaaggcag tgaagtgttg gtgtcatttc tggggggcga ccccgaccgg
 240
 ccgattatcg ttggctgctg accaaactcg gaaacccccga gcatggctcg tgagcgtaac
 300
 gccacccaga gcggcttctc caccggccgga gggcacttcc tggcgatgga agaccacccc
 360
 ggggctgccc atctgaagct ggggtgcgctt ggcggcaaca gcgtcttcac actgggcaat
 420
 ggcaaagtcg ccggcgcgca actgcgccacc aacgccccac atgcaattga catcgtcttc
 480
 gctcaaacac gaagtgcctg gcgtgtactc attgtcgatg ggcaccgggg acccgggcggc
 540
 cg
 542

<210> 490

<211> 180

<212> PRT

<213> Homo sapiens

<400> 490

Xaa	Ala	Phe	Gly	Val	Leu	Ser	Ala	Val	Val	Asp	Gly	Asp	Asp	Ser	Gly
1				5					10					15	
Lys	Pro	Leu	Leu	Asn	Gln	His	Gly	Cys	Tyr	Lys	Val	Arg	Phe	Pro	Phe
		20						25					30		
Thr	Arg	Asp	Gln	Lys	Pro	Ser	Thr	Arg	Gly	Ser	Ala	Trp	Leu	Arg	Arg
		35					40					45			
Val	Ser	Leu	Ser	Ala	Gly	Ser	Ser	His	Gly	Met	His	Phe	Pro	Leu	Leu
	50					55					60				
Lys	Gly	Ser	Glu	Val	Leu	Val	Ser	Phe	Leu	Gly	Gly	Asp	Pro	Asp	Arg
65				70					75					80	
Pro	Ile	Ile	Val	Gly	Cys	Val	Pro	Asn	Ser	Glu	Thr	Pro	Ser	Met	Val
			85					90						95	
Val	Glu	Arg	Asn	Ala	Thr	Gln	Ser	Gly	Phe	Ser	Thr	Ala	Gly	Gly	His
			100					105					110		
Phe	Leu	Ala	Met	Glu	Asp	His	Pro	Gly	Ala	Ala	His	Leu	Lys	Leu	Gly
	115						120				125				
Ala	Pro	Gly	Gly	Asn	Ser	Val	Phe	Thr	Leu	Gly	Asn	Gly	Lys	Val	Ala
	130					135					140				
Gly	Ala	Gln	Leu	Arg	Thr	Asn	Ala	Pro	His	Ala	Ile	Asp	Ile	Val	Phe
145					150				155					160	
Ala	Gln	Thr	Arg	Ser	Ala	Arg	Arg	Val	Leu	Ile	Val	Asp	Gly	His	Arg
			165					170						175	
Gly	Pro	Gly	Gly												

180

<210> 491
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 491
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 gcacgcgtgc cggattccgg actgccttaa ccacagcctt ggaacgcacc gatgaatggg
 120
 tgggcggccc tgacagcaag cccctcaacg aagtcgagac actgcgccgg tgcgccgatg
 180
 aactcatcgg cgggcccgtc ggcgcggttg ccgcgatgca cggagggtca atcgaattgg
 240
 tcgacgtgtc ggtcgggtgac gaagagcgca gagtcgacgt caccatgaag ggagcatgcc
 300
 gaggttgccc ggcagccatc agaccctaca tcagcgcctg gaacatcaac tgagtctgcy
 360
 nattgcgcga gccggtcacc gtgcgggaaa tctgacacct actccgacag ctccacctcg
 420
 acgagcacct ccacgacgag gccaagccac tcgtagacgc attcctcttc ggcatccaat
 480
 tcctccccggg ccgcccgagc gacttcgtcg gcagtaacct ggtcgatgat ccctagcctg
 540
 gcggccatca tgccacgcag cgcattgaca gtacgaagcc aacgttgcyt catcacaggg
 600
 ttcattggaga tacagccggt tcggtgcaac gtctccacat cagcacttaa ggactgagcy
 660
 tcttcccagc gcgccgcgac atcctcggcg tcatgggtga catggaattg cgcgtcagct
 720
 gagtcgtcgt cacgataggc gctgggcagg atcaatcgac gcacctcgtc gtcctcctgg
 780
 agtccagaaa actggctctc ccaaaaagcg aacgggtccc cctcc
 825

<210> 492
 <211> 58
 <212> PRT
 <213> Homo sapiens

<400> 492
 Met Asn Gly Trp Ala Ala Leu Thr Ala Ser Pro Ser Thr Lys Ser Arg
 1 5 10 15
 His Cys Ala Gly Ala Pro Met Asn Ser Ser Ala Gly Pro Ser Ala Arg
 20 25 30
 Leu Pro Arg Cys Thr Glu Gly Gln Ser Asn Trp Ser Thr Cys Arg Ser
 35 40 45
 Val Thr Lys Ser Ala Glu Ser Thr Ser Pro
 50 55

<210> 493
 <211> 863

<212> DNA

<213> Homo sapiens

<400> 493

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 60
 cctcgcggcg atcggatgtg ttctgagaa tatagctccc ttcgatcccc accagggtgga
 120
 tgtgtccatc aatgacattc agatctgtaa ggccgggggt atcggggagg accgcaacct
 180
 cgtcgatatg aggccacgag aggttcacat cgatattgag ctgcatgcgg gtgatgccga
 240
 agctgcggta tggactaatg atctgaccca ccaatacgtc gaagagaata gcgcgtatac
 300
 atcatgaccc ttgctcttga catccccctc aacgactccc agttctcggc tcagcggaaa
 360
 tctgaggtcc tggtagaagc gctgccttgg atcaggcggt ttcagggccg cactgtcgtc
 420
 gtgaaatatg gcggcaacgc gatggttgat cccgggtctgc agcaggcctt cgccgacgac
 480
 attgtgttta tggcctctgt ggggattcgc cctattgtcg tccacgggtg tggccctcag
 540
 atcaatgccca tgcttgctga atccgctacc ccggtggagt tccgtaatgg tttgcgggtg
 600
 acatctccgg aggtcatgga ggttgtccgg atggtgctcg tcgggcaggt gggccgtcag
 660
 ctcgttaacc gaatcaacgc ctatgcgccg ctagcagctg gcatgtcagg cgaggacttt
 720
 ggcctttttt cggcccggaa gtcgcgggta attgttgatg gcgagcaaata agacatgggt
 780
 ttagtgggag acatcgttga cgtcaacatc gatctcgta tctctatgct tgatcgcggc
 840
 cagattccgg tcattgcacc ggt
 863

<210> 494

<211> 186

<212> PRT

<213> Homo sapiens

<400> 494

Met Thr Leu Ala Leu Asp Ile Pro Leu Asn Asp Ser Gln Phe Ser Ala
 1 5 10 15
 Gln Arg Lys Ser Glu Val Leu Val Glu Ala Leu Pro Trp Ile Arg Arg
 20 25 30
 Phe Gln Gly Arg Thr Val Val Val Lys Tyr Gly Gly Asn Ala Met Val
 35 40 45
 Asp Pro Gly Leu Gln Gln Ala Phe Ala Asp Asp Ile Val Phe Met Ala
 50 55 60
 Ser Val Gly Ile Arg Pro Ile Val Val His Gly Gly Gly Pro Gln Ile
 65 70 75 80
 Asn Ala Met Leu Ala Glu Ser Ala Thr Pro Val Glu Phe Arg Asn Gly
 85 90 95
 Leu Arg Val Thr Ser Pro Glu Val Met Glu Val Val Arg Met Val Leu

	100		105		110
Val Gly Gln Val Gly Arg Gln Leu Val Asn Arg Ile Asn Ala Tyr Ala					
115			120		125
Pro Leu Ala Ala Gly Met Ser Gly Glu Asp Phe Gly Leu Phe Ser Ala					
130			135		140
Arg Lys Ser Arg Val Ile Val Asp Gly Glu Gln Ile Asp Met Gly Leu					
145			150		155
Val Gly Asp Ile Val Asp Val Asn Ile Asp Leu Val Ile Ser Met Leu					
	165		170		175
Asp Arg Gly Gln Ile Pro Val Ile Ala Pro					
180			185		

<210> 495

<211> 514

<212> DNA

<213> Homo sapiens

<400> 495

gcgcgcgaca ccggtgcccc gattagcgtg ccagtgggtg acgtcactaa gggtcacgtc
60
tggaatgtga caggtgacgt tcttaacgcc ngatccctcc acaatcgagg tgacnntgag
120
cgttggccga tccaccggga tcccccgcc ttcgatgacc ttgagccga gaccgagatg
180
ctggagaccg gtattaaggt ccttgacttg ctgactcctt acgtcaaggg cggcaagatt
240
ggcctctttg gcggcgctgg tgtgggtaag acggtgctca ttcaggagat gatttaccgt
300
atcgcccaca acttcggcgg tacttcggtt ttcgccggtg tcggtgagcg taccgcgag
360
ggtaacgacc tcatcaacga gatggacgag gccggtgtgc tcaaagacac cgccctggta
420
ttcggccaga tggacgagcc cccgggcacg cggtacgagc tgtcgcgctg gcagccctgc
480
ggcccatgcc tggccaactg ctgtgggacc ttgg
514

<210> 496

<211> 171

<212> PRT

<213> Homo sapiens

<400> 496

Ala Arg Asp Thr Gly Ala Pro Ile Ser Val Pro Val Gly Asp Val Thr															
1				5				10					15		
Lys Gly His Val Trp Asn Val Thr Gly Asp Val Leu Asn Ala Xaa Ser															
			20					25				30			
Leu His Asn Arg Gly Asp Xaa Glu Arg Trp Pro Ile His Arg Asp Pro															
		35					40				45				
Pro Ala Phe Asp Asp Leu Glu Pro Glu Thr Glu Met Leu Glu Thr Gly															
	50					55				60					
Ile Lys Val Leu Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile															
65					70				75					80	
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu															

Met	Ile	Tyr	Arg	Ile	Ala	His	Asn	Phe	Gly	Gly	Thr	Ser	Val	Phe	Ala
			100					105					110		
Gly	Val	Gly	Glu	Arg	Thr	Arg	Glu	Gly	Asn	Asp	Leu	Ile	Asn	Glu	Met
		115					120					125			
Asp	Glu	Ala	Gly	Val	Leu	Lys	Asp	Thr	Ala	Leu	Val	Phe	Gly	Gln	Met
	130					135					140				
Asp	Glu	Pro	Pro	Gly	Thr	Arg	Tyr	Glu	Leu	Ser	Arg	Trp	Gln	Pro	Cys
145					150					155					160
Gly	Pro	Cys	Leu	Val	Asn	Cys	Cys	Gly	Thr	Leu					
			165						170						

```
<210> 497
<211> 662
<212> DNA
<213> Homo sapiens
```

```

<400> 497
acgcgtcctg ggatctcaac cccagcagtc tggtctgttt ctcatccca caatttcctg
60
ggttccacca agcagcgaaa actgccagga tgaatgagga aaaaaccag cccacaaaac
120
gagacacacg ctggcgggga gagacgcagc agagctcctt cctgtctgtg gactcggagc
180
aaagacgtgg ggccccatct tttgtgtttt cctcaagcgg ggaaagaatg gactgtttgc
240
atgcttcgtg ccacacgccc gcggtgatcc cagccagggc cccgagcgca gaggcggagc
300
tgtgtcagc acaggcctgg gacctcccc ggccaggcacc tgtgggggggt gcagcccccg
360
ggaaggaggc aactgcctca cttaacatcc tccgctgcaa ggtggtggcg cccgagaggcg
420
tgtctgtgaa gacaggtagc aggatggcag gacccgcacg cctcttccca cacctgtcag
480
cttcggaagc atctctcgag gactctggtc ccaggatgtc tcccaggaca agccagtctg
540
cctcttcctc ctacttctgc tgtagcctgg gaccagacct ggccaaggtc agccagcggg
600
gagggccgag gtctgagctc tcgtcctgcc gtggcccccg cgatggcttg gggtgcaagc
660
tt
662

```

```
<210> 498
<211> 191
<212> PRT
<213> Homo sapiens
```

```

<400> 498
Met Asn Glu Glu Lys Thr Gln Pro His Lys Arg Asp Thr Arg Trp Arg
 1          5          10          15
Gly Glu Thr Gln Gln Ser Ser Phe Leu Ser Val Asp Ser Glu Gln Arg
      20          25          30
Arg Gly Ala Pro Ser Phe Val Phe Ser Ser Ser Gly Glu Arg Met Asp

```

```

      35      40      45
Cys Leu His Ala Ser Cys His Thr Pro Ala Val Ile Pro Ala Arg Ala
  50      55      60
Pro Ser Ala Glu Ala Glu Leu Cys Ser Ala Gln Ala Trp Asp Leu Pro
  65      70      75      80
Arg Gln Ala Pro Val Gly Gly Ala Ala Pro Gly Lys Glu Ala Thr Ala
      85      90      95
Ser Leu Asn Ile Leu Arg Cys Lys Val Val Ala Pro Arg Gly Val Ser
      100      105      110
Val Lys Thr Gly Thr Arg Met Ala Gly Pro Ala Arg Leu Phe Pro His
      115      120      125
Leu Ser Ala Ser Glu Ala Ser Leu Glu Asp Ser Gly Pro Arg Met Ser
      130      135      140
Pro Arg Thr Ser Gln Ser Ala Ser Ser Ser Tyr Phe Cys Cys Ser Leu
      145      150      155      160
Gly Pro Asp Leu Ala Lys Val Ser Gln Arg Gly Gly Pro Arg Ser Glu
      165      170      175
Leu Ser Ser Cys Arg Gly Pro Arg Asp Gly Leu Gly Cys Lys Leu
      180      185      190

```

<210> 499
 <211> 444
 <212> DNA
 <213> Homo sapiens

```

<400> 499
acgcgtgaag ggtgggcagt gttgagctga gtgagccctc ctccctgcaa tgctggagcc
  60
ctgccttctg cctgaccctc tggcttecta agcagtctat acgtgagaag ccctttcttc
  120
aagtgaaagc ttctgagctc actacgagag cactggagct ggaacctctc tgggttcaaa
  180
tcctcaactg gggggttgga ggaggttact tcacttctca aaacctcaat ttccttatct
  240
gcaaaatggg gtaataggag cccctcttca tcaatgcttg gagggaatgc ctggcacagt
  300
agggcagtta ccgtcatgga gaacagaaag gccccgagct atcctggatg tggtgagaat
  360
gggtcctgga tcctgctgc tcggcctttt cattctcttc ttcacctaca ggctcccaca
  420
aagggcctct gaaaacacag ggtg
  444

```

<210> 500
 <211> 105
 <212> PRT
 <213> Homo sapiens

```

<400> 500
Met Thr Val Thr Ala Leu Leu Cys Gln Ala Phe Pro Pro Ser Ile Asp
  1      5      10      15
Glu Glu Gly Leu Leu Leu Pro His Phe Ala Asp Lys Glu Ile Glu Val
      20      25      30
Leu Arg Ser Glu Val Thr Ser Ser Asn Pro Pro Val Glu Asp Leu Asn

```

```

      35              40              45
Pro Glu Arg Phe Gln Leu Gln Cys Ser Arg Ser Glu Leu Arg Ser Phe
  50              55              60
His Leu Lys Lys Gly Leu Leu Thr Tyr Arg Leu Leu Arg Lys Pro Glu
  65              70              75              80
Gly Gln Ala Glu Gly Arg Ala Pro Ala Leu Gln Gly Gly Gly Leu Thr
      85              90              95
Gln Leu Asn Thr Ala His Pro Ser Arg
      100              105

```

<210> 501
 <211> 800
 <212> DNA
 <213> Homo sapiens

```

<400> 501
agatctgac cgagaagtgg ctgctcaggg aaatgactac tccatggctt tcttaactca
60
ggtagctcctt attcaatgag aggcctgagg tgagaccgcg catgcggcgc gtggatcgca
120
tgggtgtagt gcacactagc aaggggctta ggtctccagc tgaggtcaga tgcacacttg
180
gaccttgtagc tggggagtaa cacacatctc tgtgttcagc gaaccatcca ggagctgttt
240
gaagtttatt ctcccatgga tgatgctggc ttcccgggtca aagctgagga gtttgtggtg
300
ctttctcagg aaccttctgt cacggaaacc attgcaccca aaattgcaag acctttcata
360
gaggccctca agagtattga gtatctggag gaggatgccc agaagtccgc acaggagggg
420
gtgctgggac cacacactga tgctctgtca tcagactctg agaacatgcc gtgtgatgaa
480
gaaccatccc aattagagga gctagctgac ttcattggagc agcttacacc aattgaaaaa
540
tatgctttaa attacctgga atcttgaggc agggcctgag agagcacgct gcgccgtact
600
tccagcagct gcggcagacc acggctccac gcctgctgca gttccctgag ctgaggctgg
660
tgcagttcga ctcaggtatg cggcagttgg gggcgtggcc cgtgcgggag ctgcactggc
720
cctggatgat gaggcgctct tgatgtgatt cgtttcccag ggaagttgga agctttagct
780
atcttgcttc agaaactgaa
800

```

<210> 502
 <211> 103
 <212> PRT
 <213> Homo sapiens

```

<400> 502
Met Asp Asp Ala Gly Phe Pro Val Lys Ala Glu Glu Phe Val Val Leu
  1              5              10              15
Ser Gln Glu Pro Ser Val Thr Glu Thr Ile Ala Pro Lys Ile Ala Arg

```

```

      20      25      30
Pro Phe Ile Glu Ala Leu Lys Ser Ile Glu Tyr Leu Glu Glu Asp Ala
      35      40      45
Gln Lys Ser Ala Gln Glu Gly Val Leu Gly Pro His Thr Asp Ala Leu
      50      55      60
Ser Ser Asp Ser Glu Asn Met Pro Cys Asp Glu Glu Pro Ser Gln Leu
65      70      75      80
Glu Glu Leu Ala Asp Phe Met Glu Gln Leu Thr Pro Ile Glu Lys Tyr
      85      90      95
Ala Leu Asn Tyr Leu Glu Ser
      100

```

<210> 503

<211> 538

<212> DNA

<213> Homo sapiens

<400> 503

```

nnacgcggttg tcgtctctcc gatcattgat tttgttgtat tctgcaatga tgtaaaggaa
60
gatgatgaca cggagaagtt taaagaagcc attgtgaaat ttcataggct gtttgggatg
120
ccagaggaag agaaactcgt caactattac tcttgcagct attggaaggg gaagggtccc
180
cgtcagggtt ggatgtacct cagcattaac cacctttgct tttattcttt tcttatggga
240
agggaaagcga aactgggtcat ccggtgggta gacatcactc agcttgagaa gaatgcccc
300
ctgcttctgc ctgatgtgat caaagtgagc acacgggtcca gtgagcattt cttctctgta
360
ttcctcaaca tcaacgagac cttcaagtta atggagcagc ttgccaacat agccatgagg
420
caactcttag acaatgaggg atttgaacaa gatcgatccc tgcccaaact caaaaggaaa
480
tctcctaaaa aagtgtctgc tctaaaacgt gatcttgatg cctggggccct tcacgcgt
538

```

<210> 504

<211> 179

<212> PRT

<213> Homo sapiens

<400> 504

```

Xaa Arg Val Val Val Ser Pro Ile Ile Asp Phe Val Val Phe Cys Asn
1      5      10      15
Asp Val Lys Glu Asp Asp Asp Thr Glu Lys Phe Lys Glu Ala Ile Val
      20      25      30
Lys Phe His Arg Leu Phe Gly Met Pro Glu Glu Glu Lys Leu Val Asn
      35      40      45
Tyr Tyr Ser Cys Ser Tyr Trp Lys Gly Lys Val Pro Arg Gln Gly Trp
      50      55      60
Met Tyr Leu Ser Ile Asn His Leu Cys Phe Tyr Ser Phe Leu Met Gly
65      70      75      80
Arg Glu Ala Lys Leu Val Ile Arg Trp Val Asp Ile Thr Gln Leu Glu

```

<400> 506															
Val	His	Asp	Thr	Glu	Arg	Tyr	Glu	Arg	Ile	Ser	Gln	Ala	Arg	Arg	Glu
1				5					10					15	
Glu	Gln	Gln	Ala	Met	Leu	Gly	Tyr	Asp	Xaa	Ser	Arg	Thr	Cys	Arg	Met
			20					25					30		
Thr	Leu	Leu	Thr	Gly	Gln	Leu	Asp	Asp	Pro	Ser	Thr	Thr	Pro	Cys	Gly
		35					40					45			
Arg	Cys	Asp	Val	Cys	Ala	Gly	Pro	Trp	Tyr	Ser	Val	Glu	Val	Asp	Gln
	50					55					60				
Ser	Ala	Ala	Val	Arg	Ala	Val	Gln	Ser	Leu	Asn	Arg	Val	Gly	Val	Pro
65					70					75					80
Val	Glu	Pro	Arg	Ala	Ala	Trp	Pro	Ala	Gly	Met	Asp	Ala	Leu	Gln	Val
				85					90					95	
Ala	Leu	Lys	Gly	Arg	Ile	Ser	Ala	Glu	Glu	Ile	Ala	Ala	Glu	Gly	Arg

	100		105		110									
Val	Ile	Ala	Arg	Leu	Ser	Asp	Leu	Gly	Trp	Gly	Gly	Ala	Leu	Arg
	115			120								125		

<210> 507
 <211> 499
 <212> DNA
 <213> Homo sapiens

<400> 507
 gccggcggtg tcaacctcat ggtgtggggc ttcattaccg acgtcatcga tgcccaggag
 60
 gtcattgtccg gggagcgtga agacggtgtc atctatggcg tgaactcctt cgcccgcaaa
 120
 cttgcccagg ccattgccgg tggaatcggc ggagccatgc tgacgatgat cggctaccag
 180
 tcctcctccc aaggtggtgc cgttcagtcg gagtccgtcg tcaatcacct gtacacgctc
 240
 gccaccgcca tcccgacgat ctgctgcctc ggcgctgccc tgctcatgct gggctaccg
 300
 ctcacccgcg acaaggtggt cgccaacgcc gacgagttgg ctcgtcgcca cgcagtacag
 360
 gccgagcaaa actcctgacc cataacggag gcacatcatg gacacgctca tgcggatcac
 420
 cgaccacttg acaacctcgc cgggtatcca attgaaaatt gacaagcgat ggggtgcctc
 480
 cgtcacattt gtgacgcgt
 499

<210> 508
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 508
 Ala Gly Val Phe Asn Leu Met Val Trp Ala Phe Ile Thr Asp Val Ile
 1 5 10 15
 Asp Ala Gln Glu Val Met Ser Gly Glu Arg Glu Asp Gly Val Ile Tyr
 20 25 30
 Gly Val Asn Ser Phe Ala Arg Lys Leu Ala Gln Ala Ile Ala Gly Gly
 35 40 45
 Ile Gly Gly Ala Met Leu Thr Met Ile Gly Tyr Gln Ser Ser Ser Gln
 50 55 60
 Gly Gly Ala Val Gln Ser Glu Ser Val Val Asn His Leu Tyr Thr Leu
 65 70 75 80
 Ala Thr Ala Ile Pro Thr Ile Cys Cys Leu Gly Ala Ala Leu Leu Met
 85 90 95
 Leu Gly Tyr Pro Leu Thr Arg Asp Lys Val Val Ala Asn Ala Asp Glu
 100 105 110
 Leu Ala Arg Arg His Ala Val Gln Ala Glu Gln Asn Ser
 115 120 125

<210> 509
 <211> 360

<212> DNA

<213> Homo sapiens

<400> 509

```

ttggccatgg atttggtcgc caagttcagt cccaaagatg tcacgctcta tctaattggac
60
ttcggggacca atggtgtggc accactaggc caattaccac aggtggccga caccttgctt
120
ttggatcata cggagaagat tgccaagttt gtacgcatca tggagcggga gctcaaccgg
180
cgtaagaagc tcttgtccga ctacgggtgtt ggtacactag agctctaccg tcaggctagc
240
ggtcagcaag agccggccat cgtcatcctg ctggacagtt atgagtccat gaaggaagag
300
gcctatgaag cggagctctt cacgctcttg gtgcggatct cccgggaagg tctcagcatc
360

```

<210> 510

<211> 120

<212> PRT

<213> Homo sapiens

<400> 510

```

Leu Ala Met Asp Leu Ala Arg Lys Phe Ser Pro Lys Asp Val Thr Leu
1      5      10      15
Tyr Leu Met Asp Phe Gly Thr Asn Gly Val Ala Pro Leu Gly Gln Leu
20     25     30
Pro Gln Val Ala Asp Thr Leu Leu Asp His Thr Glu Lys Ile Ala
35     40     45
Lys Phe Val Arg Ile Met Glu Arg Glu Leu Asn Arg Arg Lys Lys Leu
50     55     60
Leu Ser Asp Tyr Gly Val Gly Thr Leu Glu Leu Tyr Arg Gln Ala Ser
65     70     75     80
Gly Gln Gln Glu Pro Ala Ile Val Ile Leu Leu Asp Ser Tyr Glu Ser
85     90     95
Met Lys Glu Glu Ala Tyr Glu Ala Glu Leu Phe Thr Leu Leu Val Arg
100    105    110
Ile Ser Arg Glu Gly Leu Ser Ile
115    120

```

<210> 511

<211> 361

<212> DNA

<213> Homo sapiens

<400> 511

```

ntcgcgaacc gcggctatgc ggtgctccag cccaatttcc gcggatcggg cggttatggc
60
actgcgttcg gcgatgccgg catcggccag atcgggcgca agatgcagga cgatctcgac
120
gacgggatgg actggctggt caaggagggc atcgtcgaca agggccgggt gtgcatcgtc
180
ggggcctcct atggcgggcta tgccgcgatg tggggcgcca tccgcaatcc cgaacgctat
240

```


cgctgcgcgg cgagcctggc ggggggttgcc gattaaggcc atgctcaaataaaccggcg
 300
 ctatctcgac aaggaggcgg gcaagcgcgtg gccgccccgn tcaaccggcg aaccgaatt
 360
 c
 361

<210> 512
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 512
 Xaa Ala Asn Arg Gly Tyr Ala Val Leu Gln Pro Asn Phe Arg Gly Ser
 1 5 10 15
 Gly Gly Tyr Gly Thr Ala Phe Gly Asp Ala Gly Ile Gly Gln Ile Gly
 20 25 30
 Arg Lys Met Gln Asp Asp Leu Asp Asp Gly Met Asp Trp Leu Val Lys
 35 40 45
 Glu Gly Ile Val Asp Lys Gly Arg Val Cys Ile Val Gly Ala Ser Tyr
 50 55 60
 Gly Gly Tyr Ala Ala Met Trp Gly Ala Ile Arg Asn Pro Glu Arg Tyr
 65 70 75 80
 Arg Cys Ala Ala Ser Leu Ala Gly Val Ala Asp
 85 90

<210> 513
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 513
 nnatgcagac tagaagatgg catgacgggt ttggctggcg gtttcgggct atgcggcatt
 60
 ccagaaaatc tgattcaaga gatcaaacga cgccagactt gtgatttgac catagtgtca
 120
 aataactgtg gtgtagatgg ttttggttta ggggttttgc tagaagataa gcaagtacgc
 180
 aaaatgggtg cttcttatgt ggggtgaaaat gcactgtttg agaagcaatt attacaaggt
 240
 gagttggaag tcgagctcac tcctcaaggc actcttgccg aaaaactacg cgctggcggc
 300
 gcgggaattc ctgccttttt cacagcaacg ggtgtaggta cacctattgg tgagggtaaa
 360
 gacacgcgt
 369

<210> 514
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 514
 Xaa Cys Arg Leu Glu Asp Gly Met Thr Val Leu Ala Gly Gly Phe Gly

```

      1             5             10             15
Leu Cys Gly Ile Pro Glu Asn Leu Ile Gln Glu Ile Lys Arg Arg Gln
      20             25             30
Thr Cys Asp Leu Thr Ile Val Ser Asn Asn Cys Gly Val Asp Gly Phe
      35             40             45
Gly Leu Gly Val Leu Leu Glu Asp Lys Gln Val Arg Lys Met Val Ser
      50             55             60
Ser Tyr Val Gly Glu Asn Ala Leu Phe Glu Lys Gln Leu Leu Gln Gly
      65             70             75             80
Glu Leu Glu Val Glu Leu Thr Pro Gln Gly Thr Leu Ala Glu Lys Leu
      85             90             95
Arg Ala Gly Gly Ala Gly Ile Pro Ala Phe Phe Thr Ala Thr Gly Val
      100             105             110
Gly Thr Pro Ile Gly Glu Gly Lys Asp Thr Arg
      115             120

```

<210> 515
 <211> 387
 <212> DNA
 <213> Homo sapiens

```

<400> 515
gcggtgggacg agaagggcgc cggcaactgc gcgatcgact acgggttcca ccagatcctc
60
tccgacgtgc aggactcgtc gctgaccgcg atggacgagc tgatcaccga gggcgtgaca
120
tccttcaagc tcttcgtggc ctacaagggc gtcttctctc cggacgacgg gcagatcctg
180
cgggcggttc agaagggcgc cgacaacggc gcgatgatga tgatgcacgc cgagaacggc
240
gcgatcatcg acgtgctcgt gcagcaggcg ctcgaggccg ggaagaccac cccgtactac
300
cacggcatca gccggccgtg gcaggccgag gaggaggcca cccaccgcgc gatcatgac
360
gccgacctga ccggtgcgcc gttgtac
387

```

<210> 516
 <211> 129
 <212> PRT
 <213> Homo sapiens

```

<400> 516
Ala Trp Asp Glu Lys Ala Ala Gly Asn Cys Ala Ile Asp Tyr Gly Phe
1             5             10             15
His Gln Ile Leu Ser Asp Val Gln Asp Ser Ser Leu Thr Ala Met Asp
20             25             30
Glu Leu Ile Thr Glu Gly Val Thr Ser Phe Lys Leu Phe Val Ala Tyr
35             40             45
Lys Gly Val Phe Leu Ser Asp Asp Gly Gln Ile Leu Arg Ala Phe Gln
50             55             60
Lys Gly Ala Asp Asn Gly Ala Met Met Met Met His Ala Glu Asn Gly
65             70             75             80
Ala Ile Ile Asp Val Leu Val Gln Gln Ala Leu Glu Ala Gly Lys Thr

```

```

      85              90              95
Thr Pro Tyr Tyr His Gly Ile Ser Arg Pro Trp Gln Ala Glu Glu Glu
      100              105              110
Ala Thr His Arg Ala Ile Met Ile Ala Asp Leu Thr Gly Ala Pro Leu
      115              120              125
Tyr

```

<210> 517
 <211> 377
 <212> DNA
 <213> Homo sapiens

```

<400> 517
acgcgtgaag ggctggtggg caggccttgc gccccctctg gggacagctc tcctccaccc
60
agaccccttc gggccaacag tggggagggg ctgccgtctg agccactggt cgcacagggg
120
attcgcgagt tccgggggag ctgggggactg agctgcgggc ctctctgggct ggggctcttc
180
tccgaggttg gaggcagctt tagaaacttg agacccttag ctggagaggg cagaaggggt
240
ccctgagctt ccccaggaga agggggggcca atttgagct tgcttttcac ctgagatgag
300
gaatgggggt ggccaggccg agagcccagt ggggcatccc cagcacccat gaacatgcta
360
aggaagggga ggggccc
377

```

<210> 518
 <211> 118
 <212> PRT
 <213> Homo sapiens

```

<400> 518
Met Phe Met Gly Ala Gly Asp Ala Pro Leu Gly Ser Arg Pro Gly His
1      5      10      15
Pro His Ser Ser Ser Gln Val Lys Ser Lys Leu Gln Ile Gly Pro Pro
      20      25      30
Ser Pro Gly Glu Ala Gln Gly Pro Leu Leu Pro Ser Pro Ala Arg Gly
      35      40      45
Leu Lys Phe Leu Lys Leu Pro Pro Thr Ser Glu Lys Ser Pro Ser Pro
50      55      60
Gly Gly Pro Gln Leu Ser Pro Gln Leu Pro Arg Asn Ser Arg Ile Pro
65      70      75      80
Cys Arg Asn Ser Gly Ser Asp Gly Ser Pro Ser Pro Leu Leu Ala Arg
      85      90      95
Arg Gly Leu Gly Gly Gly Glu Leu Ser Pro Glu Gly Ala Gln Gly Leu
100      105      110
Pro Thr Ser Pro Ser Arg
115

```

<210> 519
 <211> 311

<212> DNA

<213> Homo sapiens

<400> 519

gcgcgccagg ggggaagggag agaaaacaca gaaaaatgag ggggaaatac cagatactga
60
agaatttaaa ttattataaa ggaacctttt ctgcaactct gaaaaatggtt agaatatcca
120
aagaaattga taattttcta ggaaaacatg acttaccaaa attaactcta gaaaagaatc
180
gatacacatc agtaacaaca gaagttgaga aagtagttaa catattgccca aacctggaat
240
tcatgattga attctttgag atctactgtg agtacatact ctgcctctgt tcagctgttc
300
cagaacttaa g
311

<210> 520

<211> 92

<212> PRT

<213> Homo sapiens

<400> 520

Met	Arg	Gly	Lys	Tyr	Gln	Ile	Leu	Lys	Asn	Leu	Asn	Tyr	Tyr	Lys	Gly
1				5				10						15	
Thr	Phe	Ser	Ala	Thr	Leu	Lys	Asn	Val	Arg	Ile	Ser	Lys	Glu	Ile	Asp
			20				25						30		
Asn	Phe	Leu	Gly	Lys	His	Asp	Leu	Pro	Lys	Leu	Thr	Leu	Glu	Lys	Asn
		35				40					45				
Arg	Tyr	Thr	Ser	Val	Thr	Thr	Glu	Val	Glu	Lys	Val	Val	Asn	Ile	Leu
	50				55					60					
Pro	Asn	Leu	Glu	Phe	Met	Ile	Glu	Phe	Phe	Glu	Ile	Tyr	Cys	Glu	Tyr
65				70				75						80	
Ile	Leu	Cys	Leu	Cys	Ser	Ala	Val	Pro	Glu	Leu	Lys				
			85					90							

<210> 521

<211> 352

<212> DNA

<213> Homo sapiens

<400> 521

nnngatgccca cgccggtcta cggaatctcc accggcttcg gcgcgcttgc ccgcgccac
60
attccagaag agatgcgcgc gcagctgcag ctgtccctgg tgcgctccca cgcgccgggc
120
accggccctg aggtggaaga agaagtaatt cgcgcgctca tgctgctgcg cctatccacc
180
ctgtgtaccg gccgtaccgg cgtgcgcccc gtggtggtag aaacttatgc caaggcgctc
240
aacgccggca tcgtgccggg ggtgcgcgaa tacgggtcgc tgggctgctc cggcgacttg
300
gccccgctgg ctcaactgcgc cctagcgctg ttgggtgagg gtgaggtacg cn
352

<210> 522
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 522
 Xaa Asp Ala Thr Pro Val Tyr Gly Ile Ser Thr Gly Phe Gly Ala Leu
 1 5 10 15
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 Asn Ala Gly Ile Val Pro Gly Val Arg Glu Tyr Gly Ser Leu Gly Cys
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<210> 530

<211> 802

<212> PRT

<213> Homo sapiens

<400> 530

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      20           25           30
Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro Glu Gly Cys
      35           40           45
Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly Ala Arg Gly Asp
      50           55           60
Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser Asp Pro Asp Gly Gly
65           70           75           80
Pro Arg Asp Arg Asn Phe Leu Phe Val Gly Val Met Thr Ala Gln Lys
      85           90           95
Tyr Leu Gln Thr Arg Ala Val Ala Ala Tyr Arg Thr Trp Ser Lys Thr
      100          105          110
Ile Pro Gly Lys Val Gln Phe Phe Ser Ser Glu Gly Ser Asp Thr Ser
      115          120          125
Val Pro Ile Pro Val Val Pro Leu Arg Gly Val Asp Asp Ser Tyr Pro
      130          135          140
Pro Gln Lys Lys Ser Phe Met Met Leu Lys Tyr Met His Asp His Tyr
145          150          155          160
Leu Asp Lys Tyr Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile
      165          170          175
Lys Gly Asp Arg Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu
      180          185          190
Pro Leu Phe Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly
      195          200          205
Lys Leu Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly
      210          215          220
Val Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
225          230          235          240
Lys Cys Leu Arg Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly
      245          250          255
Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser Tyr Glu
      260          265          270
Met Gln Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys Lys Gly Tyr
      275          280          285
Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala Ile Thr Leu His
      290          295          300
Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu His Ser Tyr Met Leu
305          310          315          320
Ser Arg Lys Ile Ser Glu Leu Arg His Arg Thr Ile Gln Leu His Arg
      325          330          335
Glu Ile Val Leu Met Ser Lys Tyr Ser Asn Thr Glu Ile His Lys Glu
      340          345          350
Asp Leu Gln Leu Gly Ile Pro Pro Ser Phe Met Arg Phe Gln Pro Arg
      355          360          365
Gln Arg Glu Glu Ile Leu Glu Trp Glu Phe Leu Thr Gly Lys Tyr Leu
      370          375          380
Tyr Ser Ala Val Asp Gly Gln Pro Pro Arg Arg Gly Met Asp Ser Ala
385          390          395          400
Gln Arg Glu Ala Leu Asp Asp Ile Val Met Gln Val Met Glu Met Ile

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405 410 415
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 420 425 430
 Gln Tyr Gly Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile
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 Leu Asp Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr
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 Val Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
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 Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys Arg
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 Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser Leu Lys
 500 505 510
 Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu His Lys Glu
 515 520 525
 Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu Ser Gly Arg Phe
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 Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu Lys Thr Cys Leu Ile
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 Pro Asn Gln Asn Val Lys Leu Val Val Leu Leu Phe Asn Ser Asp Ser
 565 570 575
 Asn Pro Asp Lys Ala Lys Gln Val Glu Leu Met Thr Asp Tyr Arg Ile
 580 585 590
 Lys Tyr Pro Lys Ala Asp Met Gln Ile Leu Pro Val Ser Gly Glu Phe
 595 600 605
 Ser Arg Ala Leu Ala Leu Glu Val Gly Ser Ser Gln Phe Asn Asn Glu
 610 615 620
 Ser Leu Leu Phe Phe Cys Asp Val Asp Leu Val Phe Thr Thr Glu Phe
 625 630 635 640
 Leu Gln Arg Cys Arg Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe
 645 650 655
 Pro Ile Ile Phe Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys
 660 665 670
 Val Pro Ser Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp
 675 680 685
 Arg Asn Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val
 690 695 700
 Arg Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp
 705 710 715 720
 Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe Arg
 725 730 735
 Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe Cys Asp
 740 745 750
 Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly Ser Lys Ala
 755 760 765
 Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met Trp Leu Glu Lys
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<210> 531

<211> 321

<212> DNA

<213> Homo sapiens

<400> 531

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<210> 532

<211> 96

<212> PRT

<213> Homo sapiens

<400> 532

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Lys	Gly	Leu	Leu	Phe	Arg	Asn	Asn	Lys	Gly	Leu	Glu	Leu	Arg	Gly	Arg
		20						25					30		
Ser	Val	Lys	Arg	Cys	Arg	Thr	Ser	Val	Ser	Asn	Ala	Pro	Glu	Val	Asn
		35					40				45				
Pro	Arg	Gly	Arg	Leu	Asn	Gln	Ala	Ser	Trp	Ala	Trp	Asp	Asp	Ser	Gly
		50				55				60					
Cys	Ser	Gly	Ser	Asn	Gly	Ala	Cys	Gly	Ser	Ala	Leu	Ile	Asp	Ser	Arg
65				70					75					80	
Gln	Ala	Pro	Ser	His	Ser	Ala	Trp	Pro	Ser	Phe	His	Thr	Cys	Trp	Cys
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<210> 533

<211> 335

<212> DNA

<213> Homo sapiens

<400> 533

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 180
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 240
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<210> 534
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 534

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Met Pro Arg Asp Ile Asp Phe Ser Glu Ala Asn Arg Ser Ile Ile Asp
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Asn Met Ala Thr Ala Ser Ile Pro Leu Phe Arg Thr His Lys Asn Trp
 20             25             30
Glu Thr Trp Ser Ser Gln Val Arg His Phe Ile Ser Leu Leu His Pro
 35             40             45
Lys Val Thr Leu Thr Asn Ile Asp Asn Val Leu Asn Lys Asp His Leu
 50             55             60
Arg Trp Leu His Phe Leu Leu Glu Gly Arg Leu Glu Pro Asn Val Arg
 65             70             75             80
Leu Ile Val Gln Gly Tyr Cys Ser Pro Gly Lys Leu Tyr Arg Lys Leu
 85             90             95
Glu Glu Leu Tyr Ala Pro Ser
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<210> 535
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 535

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<210> 536
 <211> 114
 <212> PRT
 <213> Homo sapiens

<400> 536

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Met Ala Leu His Thr Trp Arg Leu Val Asn Pro Glu Thr Val Asp Val
 1             5             10             15
Val Glu Leu Arg Gly Ala Asp Thr Gly Ser His Gln Val Gly Gly Val
 20             25             30
Ser Ser Ala Gly Gly Leu Ala Leu Trp Ser Ala Leu Ala Ile Ser Leu

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          35              40              45
Val Pro Ala Leu Trp Val Tyr Pro Val Ala Val Ala Val Gly Ile Leu
          50              55              60
Met Thr Arg Pro Arg Arg Leu Leu Leu Gly Ser Ile Val Val Leu Gly
65              70              75              80
Pro Leu Leu Val Ile Ser Pro Trp Ile Pro Arg Leu Ile Thr Glu Pro
          85              90              95
Gly Arg Met Ala Thr Gly Ala Glu Pro Val Leu Ser Pro Ala Val Glu
          100              105              110
Thr Arg

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<210> 537

<211> 404

<212> DNA

<213> Homo sapiens

<400> 537

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cagcgtgctg ggcactggct tgccatggaa gtggaagaaa ccaagatcca gctcaccat
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caagacagcc gccacgtgcc gctggaccgc atcgaagcgg gcctgagcgt agacctgagc
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404

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<210> 538

<211> 118

<212> PRT

<213> Homo sapiens

<400> 538

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Met Pro Thr Ser His His Met Asn Leu Ala Thr Trp His Thr Ile Asn
          20          25          30
Ser Val Tyr Ser Gln Lys Ser Gln Leu Ala Leu Gly Ser Met Arg Tyr
          35          40          45
Asp Ile Glu Asp Thr Gly Gly Ile Asp Arg Leu Phe Lys Leu Ile Glu
50          55          60
Gln Arg Ala Gly His Trp Leu Ala Met Glu Val Glu Glu Thr Lys Ile
65          70          75          80
Gln Leu Thr His Gln Asp Ser Arg His Val Pro Leu Asp Arg Ile Glu
          85          90          95
Ala Gly Leu Ser Val Asp Leu Ser Arg Ala Leu Phe Glu Ser Ser Ile
          100          105          110
Asp Asn Leu Leu Glu Arg

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115

<210> 539
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 539
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 ttacttgcca tttatggaaa aaagggggat acaagcaaca tcatcacagt aagagtggct
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 gatggggcaaa cagtgcgaagg ggaagtctgg aaaacaacgc cttaccaagt ggctgctgaa
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 360
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 420
 tacattatat aagaggccac atattgaatt cacgaatggt gagttttttg ggggtttcta
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<210> 540
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 540
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 20 25 30
 Ile Leu Lys Lys Asp His Gln Leu Leu Ala Ile Tyr Gly Lys Lys
 35 40 45
 Gly Asp Thr Ser Asn Ile Ile Thr Val Arg Val Ala Asp Gly Gln Thr
 50 55 60
 Val Gln Gly Glu Val Trp Lys Thr Thr Pro Tyr Gln Val Ala Ala Glu
 65 70 75 80
 Ile Ser Gln Glu Leu Ala Glu Ser Thr Val Ile Ala Lys Val Asn Gly
 85 90 95
 Glu Leu Trp Asp Leu Asp Arg Pro Leu Glu Gly Asp Ser Ser Leu Glu
 100 105 110
 Leu Leu Thr Phe Asp Asn Glu Glu Ala Gln Ala Val Ser Ile Leu Lys
 115 120 125
 Pro Asp Ser Gln Thr Leu Gly Ser Tyr Val Val Asn Tyr Ile Ile
 130 135 140

<210> 541
 <211> 551

<212> DNA

<213> Homo sapiens

<400> 541

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551

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<210> 542

<211> 168

<212> PRT

<213> Homo sapiens

<400> 542

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Gly Thr Pro Glu Asn Ser Ala Pro Val Glu Ser Glu Pro Ser Gln Trp
          20           25           30
Ala Cys Lys Val Cys Ser Ala Thr Phe Leu Glu Leu Gln Leu Leu Asn
          35           40           45
Gly Lys Glu Asp Val Trp Gly Ala Pro Val Val Lys Leu Leu Cys Arg
          50           55           60
Phe Leu Ser Asp Leu Arg Cys His Leu Ser Ala Ala Val Gly Gly Val
65           70           75           80
Pro Asp Phe Val Leu Ser Ala Pro Leu Pro His Asn Val Val Ala Arg
          85           90           95
Thr Lys Ala Phe Ser Gly Phe Lys Ala Ser Gly Gln Ser Arg Phe Pro
          100          105          110
Pro Pro Thr Pro Ala Gly Leu Thr Pro His Ser Ser Trp Leu Gly Ser
          115          120          125
Cys Ile Ser Ala Gly Arg Leu Asp Ser Gly Ala Leu Ala Gly Ala Arg
          130          135          140
Gly Gln Glu Pro Ala Val Ala Cys Val Val His Ser Cys Leu Cys Cys
145          150          155          160
Leu Tyr Leu Thr Ala Pro Ser Arg
          165

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<210> 543
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 543
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 120
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 180
 caggacgtct ggatcattga gcaaaacctg ccccatagct taaacgagca cctggctggg
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<210> 544
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 544
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 Ile Ile Leu Ala Gly Gly Lys Gly Ser Arg Leu Ala Pro Met Thr Asp
 20 25 30
 Gln Val Ala Lys Pro Ala Val Pro Phe Met Gly Thr Tyr Arg Leu Ile
 35 40 45
 Asp Phe Ser Leu Ser Asn Ile Val His Ser Gly Leu Gln Asp Val Trp
 50 55 60
 Ile Ile Glu Gln Asn Leu Pro His Ser Leu Asn Glu His Leu Ala Gly
 65 70 75 80
 Gly Arg Ser Trp Asp Leu Asp Arg Thr Arg Gly Gly Leu Lys Val Met
 85 90 95
 Pro Pro Phe Ser Gly Pro Ala Asp Glu Asp Gly Gly Phe Ser Glu Gly
 100 105 110
 Asn Ala His Ala
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<210> 545
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 545
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 120
 ccaaataaag caggctcaaa tccagaaggt tctattgcaa cgcgttttat tgcagaaaca
 180

atgtataacg aactcaaaac agtggattta actattcaaa atgctggcgg tgtacgcgca
 240
 gatattttac cggggaatgt aacctttaac gatgcttata ctttcttacc tttcgggaat
 300
 acgttatata cctataaaat ggaaagttca ttagtgaaac aagtgcctga agatgcaatg
 360
 ctatttgctt tgggtcccc ccccccccc
 390

<210> 546

<211> 130

<212> PRT

<213> Homo sapiens

<400> 546

His	Asp	Ala	Lys	Thr	Asp	Met	Leu	Ile	Ser	Lys	Tyr	Lys	Ser	Glu	Lys
1				5					10					15	
Asp	Arg	Leu	Ala	Gln	Glu	Ile	Val	Gly	Val	Ile	Thr	Gly	Ser	Ala	Met
		20						25					30		
Pro	Gly	Gly	Ser	Ala	Asn	Arg	Ile	Pro	Asn	Lys	Ala	Gly	Ser	Asn	Pro
		35					40					45			
Glu	Gly	Ser	Ile	Ala	Thr	Arg	Phe	Ile	Ala	Glu	Thr	Met	Tyr	Asn	Glu
	50				55					60					
Leu	Lys	Thr	Val	Asp	Leu	Thr	Ile	Gln	Asn	Ala	Gly	Gly	Val	Arg	Ala
65				70					75					80	
Asp	Ile	Leu	Pro	Gly	Asn	Val	Thr	Phe	Asn	Asp	Ala	Tyr	Thr	Phe	Leu
		85						90					95		
Pro	Phe	Gly	Asn	Thr	Leu	Tyr	Thr	Tyr	Lys	Met	Glu	Ser	Ser	Leu	Val
		100					105					110			
Lys	Gln	Val	Leu	Glu	Asp	Ala	Met	Leu	Phe	Ala	Leu	Gly	Pro	Pro	Pro
	115						120					125			
Pro	Pro														
	130														

<210> 547

<211> 306

<212> DNA

<213> Homo sapiens

<400> 547

aagcttgttt ttctgatttt tattcaaattc tctatcatgg atgaagcatg cagtttcaga
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 atcagttcag tgttgacaac atatcaagat attctgcagt caatctcaat gtatgttcat
 120
 gaagcctcca acatatatttg tgggatacca tctttgtcag gcattgtgct aggcactgtc
 180
 cctgcagtga ataagaaaga caggatttct gtatttatgg ggcttagtac caagttgttc
 240
 tcaaactttc atgtttgtgt atacaaatca gctgaggcct tcaactaaact cnnnnnccnn
 300
 nnnccnn
 306

<210> 548

<211> 90
 <212> PRT
 <213> Homo sapiens

<400> 548
 Met Asp Glu Ala Cys Ser Phe Arg Ile Ser Ser Val Leu Thr Thr Tyr
 1 5 10 15
 Gln Asp Ile Leu Gln Ser Ile Ser Met Tyr Val His Glu Ala Ser Asn
 20 25 30
 Ile Phe Cys Gly Ile Pro Ser Leu Ser Gly Ile Val Leu Gly Thr Val
 35 40 45
 Pro Ala Val Asn Lys Lys Asp Arg Ile Ser Val Phe Met Gly Leu Ser
 50 55 60
 Thr Lys Leu Phe Ser Asn Phe His Val Cys Val Tyr Lys Ser Ala Glu
 65 70 75 80
 Ala Phe Thr Lys Leu Xaa Xaa Xaa Xaa Xaa
 85 90

<210> 549
 <211> 780
 <212> DNA
 <213> Homo sapiens

<400> 549
 nnacgcgtac ttccaacacc tatgctccag tatggaggac gggtaaagtc tcttgtaaat
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 gttttaatca tacacatatt gtctgtaagt atgaagagaa aggcatatca gaaatatttc
 120
 aattcagcga tttgaaatgt ttactttctg tttattgaaa atttttggtc tttttcacca
 180
 tggtattttt ttctcctcgt gtagaatcgg acagtagcaa caccgagcca tggagtatgg
 240
 gacatgcgag ggaaacaatt ccacacagga gttgaaatca aaatgtgggc tatcgcttgt
 300
 tttgccacac agaggcagtg cagagaagaa atattgaagg gtttcacaga ccagctgcgt
 360
 aagatttcta aggatgcagg gatgcccatc cagggccagc catgcttctg caaatatgca
 420
 cagggggcag acagcgtaga gcccatgttc cggcatctca agaacacata ttctggccta
 480
 cagcttatta tcgtcatcct gccggggaag acaccagtgt atgcggaagt gaaacgtgta
 540
 ggagacacac ttttgggtat ggctacacaa tgtgttcaag tcaagaatgt aataaaaaca
 600
 tctcctcaaa ctctgtcaaa cttgtgccta aagataaatg ttaaactcgg agggatcaat
 660
 aatattcttg tacctcatca aagaccttct gtgttccagc aaccagtgat ctttttggga
 720
 gccgatgtca ctcatccacc tgctggtgat ggaaagaagc cttctattgc tgctgttgta
 780

<210> 550
 <211> 192
 <212> PRT

<213> Homo sapiens

<400> 550

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Asn Arg Thr Val Ala Thr Pro Ser His Gly Val Trp Asp Met Arg Gly
 1           5           10           15
Lys Gln Phe His Thr Gly Val Glu Ile Lys Met Trp Ala Ile Ala Cys
           20           25           30
Phe Ala Thr Gln Arg Gln Cys Arg Glu Glu Ile Leu Lys Gly Phe Thr
           35           40           45
Asp Gln Leu Arg Lys Ile Ser Lys Asp Ala Gly Met Pro Ile Gln Gly
 50           55           60
Gln Pro Cys Phe Cys Lys Tyr Ala Gln Gly Ala Asp Ser Val Glu Pro
65           70           75           80
Met Phe Arg His Leu Lys Asn Thr Tyr Ser Gly Leu Gln Leu Ile Ile
           85           90           95
Val Ile Leu Pro Gly Lys Thr Pro Val Tyr Ala Glu Val Lys Arg Val
           100           105           110
Gly Asp Thr Leu Leu Gly Met Ala Thr Gln Cys Val Gln Val Lys Asn
           115           120           125
Val Ile Lys Thr Ser Pro Gln Thr Leu Ser Asn Leu Cys Leu Lys Ile
           130           135           140
Asn Val Lys Leu Gly Gly Ile Asn Asn Ile Leu Val Pro His Gln Arg
145           150           155           160
Pro Ser Val Phe Gln Gln Pro Val Ile Phe Leu Gly Ala Asp Val Thr
           165           170           175
His Pro Pro Ala Gly Asp Gly Lys Lys Pro Ser Ile Ala Ala Val Val
           180           185           190

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<210> 551

<211> 291

<212> DNA

<213> Homo sapiens

<400> 551

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nnggatccgg attatggggc tattgctaac aggtcaacgg ccatcaaggt gctcgttgcc
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gtggcaccgc cagccccgga gcctactcgc gagccaccga cgaactccgc tccttcgag
120
gaaccgtcct cgtcgtcaat cgcaccgggtc ccgcccggccc cgacgactgc agtaccacg
180
actagttcgt cgtcggggccg ctgaccgatg cgcccatcgg cgggctcatc tggctggcgc
240
tagcggggggc ttcgatgtcc ccataccaca gcgtccgcta aattgccnc c
291

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<210> 552

<211> 67

<212> PRT

<213> Homo sapiens

<400> 552

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Xaa Asp Pro Asp Tyr Gly Ala Ile Ala Asn Arg Ser Thr Ala Ile Lys
 1           5           10           15
Val Leu Val Ala Val Ala Pro Pro Ala Pro Glu Pro Thr Arg Glu Pro

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20 25 30
 Pro Thr Asn Ser Ala Pro Ser Glu Glu Pro Ser Ser Ser Ile Ala
 35 40 45
 Pro Val Pro Pro Ala Pro Thr Thr Ala Val Pro Thr Thr Ser Ser Ser
 50 55 60
 Ser Gly Arg
 65

<210> 553
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 553
 ctagccgatg taggattagt aggttttccg agcgtgggta aatctacctt actctcaata
 60
 gtatctaaag ccaaaccgaa aattggtgca tatcatttca ctacaattaa acctaactta
 120
 ggtgttggtt ccacaaaaga tcaacgtagt tttgttatgg cagatttacc aggtttaatt
 180
 gaaggtgcat ctgatggcgt tggattagga catcaatttt taagacatgt agagagaaca
 240
 aaagttattg ttcacatgat tgatatgagc ggttctgaag gtagagaacc tattgaagat
 300
 tataaagtca ttaatcaaga attagctgcg tacgagcaac gtttagaaga tagacctcaa
 360
 atcgtagtag ctaacaagat ggatttacct gaatcacaag ataatttaaa cttgttttaa
 420
 gaagaaattg gcgaagatgt gccagttatt ccagtttcaa caataacgcg t
 471

<210> 554
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 554
 Leu Ala Asp Val Gly Leu Val Gly Phe Pro Ser Val Gly Lys Ser Thr
 1 5 10 15
 Leu Leu Ser Ile Val Ser Lys Ala Lys Pro Lys Ile Gly Ala Tyr His
 20 25 30
 Phe Thr Thr Ile Lys Pro Asn Leu Gly Val Val Ser Thr Lys Asp Gln
 35 40 45
 Arg Ser Phe Val Met Ala Asp Leu Pro Gly Leu Ile Glu Gly Ala Ser
 50 55 60
 Asp Gly Val Gly Leu Gly His Gln Phe Leu Arg His Val Glu Arg Thr
 65 70 75 80
 Lys Val Ile Val His Met Ile Asp Met Ser Gly Ser Glu Gly Arg Glu
 85 90 95
 Pro Ile Glu Asp Tyr Lys Val Ile Asn Gln Glu Leu Ala Ala Tyr Glu
 100 105 110
 Gln Arg Leu Glu Asp Arg Pro Gln Ile Val Val Ala Asn Lys Met Asp
 115 120 125
 Leu Pro Glu Ser Gln Asp Asn Leu Asn Leu Phe Lys Glu Glu Ile Gly

130 135 140
 Glu Asp Val Pro Val Ile Pro Val Ser Thr Ile Thr Arg
 145 150 155

<210> 555
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 555
 tctagagatt gagaacaatt atggatacag aaatggttga ttccgtcaaa tatattcgag
 60
 attcggaatc atgtgaggct cgcgtgctgg agatcttagc cagaaggccg tccatgatgg
 120
 tgcagatctt gcgtggcgac ggcttaatta acgaagacca gagattagtc agattatggc
 180
 ttaataaagt acctagaatt gttcgctgc ttctccggct tagtggtggtc gtcgctgcgg
 240
 caataggtgc ccgtgcggta tgggcggcgg cttccggtaa tcccgatctt gttcacgcgt
 300

<210> 556
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 556
 Met Asp Thr Glu Met Val Asp Ser Val Lys Tyr Ile Arg Asp Ser Glu
 1 5 10 15
 Ser Cys Glu Ala Arg Val Leu Glu Ile Leu Ala Arg Arg Pro Ser Met
 20 25 30
 Met Val Gln Ile Leu Arg Gly Asp Gly Leu Ile Asn Glu Asp Gln Arg
 35 40 45
 Leu Val Arg Leu Trp Leu Asn Lys Val Pro Arg Ile Val Arg Leu Leu
 50 55 60
 Leu Arg Leu Ser Val Phe Val Ala Ala Ala Ile Gly Ala Arg Ala Val
 65 70 75 80
 Trp Ala Ala Ala Ser Gly Asn Pro Asp Leu Val His Ala
 85 90

<210> 557
 <211> 678
 <212> DNA
 <213> Homo sapiens

<400> 557
 atcttcccgg tttatgagga gaatgcgctg cgtgtcgagt ttttcggcga cgaaattgag
 60
 gccctcacga cgatgcaccc gctcaccggg gaggtcatca gcgaggacga gcaggtctac
 120
 gtgttcccgg ctaccacta tgtcgccggc ccggaacgta tggagcgggg catagcgtcc
 180
 atccagcagg agctcgagga gcgcctggcc gttctagagc gtgatgggaa actgttggag
 240

gcccaacggt tacgtatgcg tactacctac gatatcgaga tgatgcagca ggtcgggtgcc
 300
 tgtgctggca tcgaaaacta ttcgcggcac atcgacggac gcgctcccg ctcagccccc
 360
 aactgtctgc ttgactactt tccggaagat tttgtgctcg tcattgatga atcccacgtg
 420
 accgtcccg agattggcgg gatgtatgag ggggacatga gccgcaagcg gacattggta
 480
 gaacatgggt tccgactgcc cagcgcgatg gacaaccgtc ctctcaaatt cgacgagttc
 540
 acccagcgga tcggccagac tgtctacctg tccgccacgc ccggttcgta cgagaccgaa
 600
 cgagctcacg gcgtcgtcga acaaatcatt cgtcgcgacag gtctgggtgga tccggagatt
 660
 atcgtcaagc ctacgcgt
 678

<210> 558

<211> 226

<212> PRT

<213> Homo sapiens

<400> 558

Ile Phe Pro Val Tyr Glu Glu Asn Ala Leu Arg Val Glu Phe Phe Gly
 1 5 10 15
 Asp Glu Ile Glu Ala Leu Thr Thr Met His Pro Leu Thr Gly Glu Val
 20 25 30
 Ile Ser Glu Asp Glu Gln Val Tyr Val Phe Pro Ala Thr His Tyr Val
 35 40 45
 Ala Gly Pro Glu Arg Met Glu Arg Ala Ile Ala Ser Ile Gln Gln Glu
 50 55 60
 Leu Glu Glu Arg Leu Ala Val Leu Glu Arg Asp Gly Lys Leu Leu Glu
 65 70 75 80
 Ala Gln Arg Leu Arg Met Arg Thr Thr Tyr Asp Ile Glu Met Met Gln
 85 90 95
 Gln Val Gly Ala Cys Ala Gly Ile Glu Asn Tyr Ser Arg His Ile Asp
 100 105 110
 Gly Arg Ala Pro Gly Ser Ala Pro Asn Cys Leu Leu Asp Tyr Phe Pro
 115 120 125
 Glu Asp Phe Val Leu Val Ile Asp Glu Ser His Val Thr Val Pro Gln
 130 135 140
 Ile Gly Gly Met Tyr Glu Gly Asp Met Ser Arg Lys Arg Thr Leu Val
 145 150 155 160
 Glu His Gly Phe Arg Leu Pro Ser Ala Met Asp Asn Arg Pro Leu Lys
 165 170 175
 Phe Asp Glu Phe Thr Gln Arg Ile Gly Gln Thr Val Tyr Leu Ser Ala
 180 185 190
 Thr Pro Gly Ser Tyr Glu Thr Glu Arg Ala His Gly Val Val Glu Gln
 195 200 205
 Ile Ile Arg Pro Thr Gly Leu Val Asp Pro Glu Ile Ile Val Lys Pro
 210 215 220
 Thr Arg
 225

<210> 559
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 559
 ggatcctatg gagctcaagt tcaagaaaag aaactgtaaa catggagggt ttgtgataaa
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 tggaatgcag tcagagggaa ggaactgccn gcttaaagtg tcctatgctg cgctttccag
 120
 agcaatacag tacacagtgg agggcgctac catggagtct ctgggtgaaa gttaggatgg
 180
 tatgggtggca ccagccaaac ttctcagggt tcataggcag acagcagctc tggagtggaa
 240
 ctaaagtgtg tccaggagct gaagccctta atcagctagg gctcacacag agtcaaggta
 300
 ggggtcaaaaa cattcagtct gggaccatat ctaga
 335

<210> 560
 <211> 92
 <212> PRT
 <213> Homo sapiens

<400> 560
 Met Glu Cys Ser Gln Arg Glu Gly Thr Ala Xaa Leu Lys Cys Pro Met
 1 5 10 15
 Leu Arg Phe Pro Glu Gln Tyr Ser Thr Gln Trp Arg Ala Leu Pro Trp
 20 25 30
 Ser Leu Trp Val Lys Val Arg Met Val Trp Trp His Gln Pro Asn Phe
 35 40 45
 Ser Gly Phe Ile Gly Arg Gln Gln Leu Trp Ser Gly Thr Lys Val Tyr
 50 55 60
 Pro Gly Ala Glu Ala Leu Asn Gln Leu Gly Leu Thr Gln Ser Gln Gly
 65 70 75 80
 Arg Val Lys Asn Ile Gln Ser Gly Thr Ile Ser Arg
 85 90

<210> 561
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 561
 ngcgcgcccc ctccctccgat ggcgggcggag atccagccca agcctctgac ccgcaagccg
 60
 atcctgctgc agcggatgga ggggtcccgag gaggtggtga atatggccgt gatcgtgccc
 120
 aaagaggagg gcgtcatcag cgtctccgag gacaggacag ttcgtgtttg gttaaagaga
 180
 gacagtggac agtattggcc aagcgtatac catgcaatgc cttgagttta tattgtcaga
 240
 agattataac aagatgactc ctgtgaaaaa ctatcaagcg catcagagca gagtgcagat
 300

gatcctgttt gtccctggagc tggagtgggt gctgagcaca ggacaggaca agcaatttgc
 360
 ctggcactgc tctgagagtg ggcagcgcct gggaggttat cggaccagtg ctgtggcctc
 420
 aggccctgcaa tttgatgttg aaaccggca tgtgtttatc ggtgaccact caggcca
 477

<210> 562

<211> 74

<212> PRT

<213> Homo sapiens

<400> 562

Xaa	Ala	Pro	Pro	Pro	Pro	Met	Ala	Ala	Glu	Ile	Gln	Pro	Lys	Pro	Leu
1			5						10					15	
Thr	Arg	Lys	Pro	Ile	Leu	Leu	Gln	Arg	Met	Glu	Gly	Ser	Gln	Glu	Val
			20					25					30		
Val	Asn	Met	Ala	Val	Ile	Val	Pro	Lys	Glu	Glu	Gly	Val	Ile	Ser	Val
		35					40					45			
Ser	Glu	Asp	Arg	Thr	Val	Arg	Val	Trp	Leu	Lys	Arg	Asp	Ser	Gly	Gln
	50					55					60				
Tyr	Trp	Pro	Ser	Val	Tyr	His	Ala	Met	Pro						
65					70										

<210> 563

<211> 403

<212> DNA

<213> Homo sapiens

<400> 563

ccatggcaga cagggagctg agcggcctgc ggaccaggt gcaccagagc atggtgcccc
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 tgctcctaca cctgaaggac caatgcccaa ctgtcgccac gggcaatgcc caccccaaga
 120
 aaaggaaggg aaaaggcctc aaccttggtc agggctggaa cccacaggag gccagggtac
 180
 ggggcagacg gatggcagca gcactgcctg agagtgggg gagctccac ggggcagcaa
 240
 gtggcgggca gaggtcttg ccatctgcac tggtttctgt gaccacagtt ggctgccccg
 300
 ctccccact gcaccactga cgaagcgaga ccctgcctca aaaaaaaaaa caaaaacaaa
 360
 aacaaaaaca aaactcaaac ttcacactgg agatctgtgc aat
 403

<210> 564

<211> 105

<212> PRT

<213> Homo sapiens

<400> 564

Met	Ala	Asp	Arg	Glu	Leu	Ser	Gly	Leu	Arg	Thr	Gln	Val	His	Gln	Ser
1					5				10					15	
Met	Val	Pro	Leu	Leu	Leu	His	Leu	Lys	Asp	Gln	Cys	Pro	Thr	Val	Ala


```

                20                25                30
Thr Gly Asn Ala His Pro Lys Lys Arg Lys Gly Lys Gly Leu Asn Leu
      35                40                45
Gly Gln Gly Trp Asn Pro Gln Glu Ala Arg Val Arg Gly Arg Arg Met
      50                55                60
Ala Ala Ala Leu Pro Glu Ser Trp Gly Ser Ser His Gly Ala Ala Ser
65                70                75                80
Gly Gly Gln Arg Val Trp Pro Ser Ala Leu Val Ser Val Thr Thr Val
      85                90                95
Gly Leu Pro Ala Pro Pro Leu His His
      100                105

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<210> 565
 <211> 311
 <212> DNA
 <213> Homo sapiens

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<400> 565
ncctctccat ggagcagccc catcttcact cttcacctgg ggccaggcct tccacagcag
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120
gcacgatctc caccggcttt cccagctccc tgggtcagcc ccacgggacc tctctctctc
180
tctcccatat ctccaagcca gccttgcata tagtaagagc tgtgatcagg atggaaagag
240
gcttgggccg cacagacctg gacaatgtcc cagtgagggc tggaggtgct agaagggcac
300
aggaggcccc n
311

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<210> 566
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 566
Met Glu Gln Pro His Leu His Ser Ser Pro Gly Ala Arg Pro Ser Thr
1      5      10      15
Ala Ala Thr Thr Gln Arg Pro Gln Arg Gly Cys Ala Glu Asp Thr Gly
20      25      30
Glu Arg Glu Pro Thr Gly Thr Ile Ser Thr Gly Phe Pro Ser Ser Leu
35      40      45
Gly Gln Pro His Gly Thr Ser Pro Pro Leu Ser His Ile Ser Lys Pro
50      55      60
Ala Leu His Ile Val Arg Ala Val Ile Arg Met Glu Arg Gly Leu Gly
65      70      75      80
Arg Thr Asp Leu Asp Asn Val Pro Val Arg Ala Gly Gly Ala Arg Arg
85      90      95
Ala Gln Glu Ala Pro
100

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<210> 567
 <211> 929

<212> DNA

<213> Homo sapiens

<400> 567

atcacatcgg tcgctgaacc ccgacgagcc tcaccttgtc gaaatattca tccttgagat
 60
 cagcccacgt gccgtcgacc tctacctcgg tgagggctgc gggcgggtac caacagccga
 120
 cctcgtcctc ggtccactc atggcggcaa gttccgctgc cagtccgggg atcgtcgggg
 180
 catgggcgat gatgagcagg ttatccacat cgtcgtcgat ttctccgatg cgccgacgca
 240
 cggtatcagt gccgcagtaa tagagggtc gcatgaattc gaccggacaa tccagttgga
 300
 ggcagtccca ggtctggcgg gtgcgtaggg catcggagac cagagcatgt ccaacattgc
 360
 gcagtcctaa acgcgtgccg acctcacggg cctgacggcg cccacgctcg gtgagcggac
 420
 gctcccgatc ccgcccga gcatgggatg cgggctgtgc atgtctcatg aggaacagag
 480
 tgtgcatgga tccatcgttg cacttcgcgg tcgccgcggt tctacgatgt tggcatgccg
 540
 ttgacggatt tgggcattga tgaggcgcgt acctaccgcc cgaacgtccc tgaaccgat
 600
 ggtttcgact ctttttgggc cgagaccctc gatgagtatt ccggcgttcc ccaagatctg
 660
 acggcgggtgc ctttcgataa ccgtcaggct ctgatagata cctgggattt gtcgtgggtg
 720
 gggatcacaca actctcgggt gagcgggtga ttacatgccc cagccgctgt gaacggccca
 780
 ttcccccttg tcatcgagta cctcgggtac tcgagttcgc gtggtgtgcc gattggatca
 840
 gtcttcgctg ctgctggcta tgcacatata gtcgtcgatc cacgtgggtca ggggtggggc
 900
 caccacaacct tgacggaaaa ctgtccgga
 929

<210> 568

<211> 71

<212> PRT

<213> Homo sapiens

<400> 568

Met	Pro	Leu	Thr	Asp	Leu	Gly	Ile	Asp	Glu	Ala	Arg	Thr	Tyr	Arg	Pro
1				5					10					15	
Asn	Val	Pro	Glu	Pro	Asp	Gly	Phe	Asp	Ser	Phe	Trp	Ala	Glu	Thr	Leu
		20						25					30		
Asp	Glu	Tyr	Ser	Gly	Val	Pro	Gln	Asp	Leu	Thr	Ala	Val	Pro	Phe	Asp
		35					40					45			
Asn	Arg	Gln	Ala	Leu	Ile	Asp	Thr	Trp	Asp	Leu	Ser	Trp	Val	Gly	Tyr
	50					55					60				
His	Asn	Ser	Arg	Val	Ser	Gly									
65						70									

<210> 569
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 569
 ncgcaaactt caacggtgcc atctgccata ttccagggat gccagatttg gatggaaaat
 60
 accatatcac tctcgattca gaattcgtac ttgatttagt ggcctttaac aaaacgctac
 120
 ctgtcgatta cttaatggtc gaaggaacgg aacttggtga ttcaaactg gaagaactac
 180
 ctgaatgccc atattatcca aaagatcaaa agccaatcgt gattgggaaa aacacaaaac
 240
 tcaaggaaca accaacagcc gttgctctct tctcggatgt tgataaacgg ccagagatta
 300
 aatcaaaaat cttagaccgc tatgataatg atattgaaat ccgtacttgg ggcggtactt
 360
 cccatgtcta n
 371

<210> 570
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 570
 Met Pro Asp Leu Asp Gly Lys Tyr His Ile Thr Leu Asp Ser Glu Phe
 1 5 10 15
 Val Leu Asp Leu Val Ala Phe Asn Lys Thr Leu Pro Val Asp Tyr Leu
 20 25 30
 Met Val Glu Gly Thr Glu Leu Val Tyr Ser Asn Met Glu Glu Leu Pro
 35 40 45
 Glu Cys Pro Tyr Tyr Pro Lys Asp Gln Lys Pro Ile Val Ile Gly Lys
 50 55 60
 Asn Thr Lys Leu Lys Glu Gln Pro Thr Ala Val Ala Leu Phe Ser Asp
 65 70 75 80
 Val Asp Lys Arg Pro Glu Ile Lys Ser Lys Ile Leu Asp Arg Tyr Asp
 85 90 95
 Asn Asp Ile Glu Ile Arg Thr Trp Gly Gly Thr Ser His Val Xaa
 100 105 110

<210> 571
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 571
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 60
 ccgggccttg acgggcccac gcacgaagag gccaaagacac tgaccgagac tactgtttcc
 120
 gttccacact ccttcgccga cctcggcgtc cgagaagata tctgccaggc gctggaaggg
 180

gtgggaattg tctccccgtt cccgatccag gccatgtcga tccccgattgc cgtcgagggc
 240
 acggatctta ttgggcaggc gcgtactggc actggcaaaa cactcgccctt cggcattcacc
 300
 atcttgagc gcattaccct gcccggtgac gaaggttggg aagaactcac caccaaaggc
 360
 aagcccccaa gcactcgtga tgtgcccta cccgggagct aggtcgg
 407

<210> 572
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 572
 Leu Thr Glu Thr Thr Val Ser Val Pro Thr Ser Phe Ala Asp Leu Gly
 1 5 10 15
 Val Arg Glu Asp Ile Cys Gln Ala Leu Glu Gly Val Gly Ile Val Ser
 20 25 30
 Pro Phe Pro Ile Gln Ala Met Ser Ile Pro Ile Ala Val Glu Gly Thr
 35 40 45
 Asp Leu Ile Gly Gln Ala Arg Thr Gly Thr Gly Lys Thr Leu Ala Phe
 50 55 60
 Gly Ile Thr Ile Leu Gln Arg Ile Thr Leu Pro Gly Asp Glu Gly Trp
 65 70 75 80
 Glu Glu Leu Thr Thr Lys Gly Lys Pro Pro Ser Thr Arg Asp Val Pro
 85 90 95
 Leu Pro Gly Ser
 100

<210> 573
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 573
 acgcgtctac ctaggatcc atgaccttcc gcaagaccga ccaccacaag aacgccattg
 60
 actacgaggt cgccggacta atgtggctcg ctgctgcccg gccagatggg gccggcatcg
 120
 tcgaggtgct cgaccacggc aagggatggc tcaccgaacc cgaattgtcc actgggcacc
 180
 ccaccgcga ggcagccgag gactttggcc gccgactggc tcacacccac gcagccgggg
 240
 cctcacacct gggggctgca cctgacgggt ttgttcccga cgatgggtat atcggccgtg
 300
 ctcccctgcc actgccgtcc gaaccaatct cctcctgggg agagttttac gctcagtgcc
 360
 gcatcgaacc atatatggac agtctcgacg ctg
 393

<210> 574
 <211> 124
 <212> PRT

<213> Homo sapiens

<400> 574

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Met Thr Phe Arg Lys Thr Asp His His Lys Asn Ala Ile Asp Tyr Glu
 1           5           10           15
Val Ala Gly Leu Met Trp Leu Ala Ala Ala Arg Pro Asp Gly Ala Gly
          20           25           30
Ile Val Glu Val Leu Asp His Gly Lys Gly Trp Leu Thr Glu Pro Glu
          35           40           45
Leu Ser Thr Gly His Pro Thr Arg Glu Ala Ala Glu Asp Phe Gly Arg
          50           55           60
Arg Leu Ala His Thr His Ala Ala Gly Ala Ser His Leu Gly Ala Ala
 65           70           75           80
Pro Asp Gly Phe Val Pro Asp Asp Gly Tyr Ile Gly Arg Ala Pro Leu
          85           90           95
Pro Leu Pro Ser Glu Pro Ile Ser Ser Trp Gly Glu Phe Tyr Ala Gln
          100          105          110
Cys Arg Ile Glu Pro Tyr Met Asp Ser Leu Asp Ala
          115          120

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<210> 575

<211> 372

<212> DNA

<213> Homo sapiens

<400> 575

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nntatccatg cagacatggg accagggtct ctgagggcag gaagcaaagt gggtaggggg
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gatggggacaa gatgccctgg tgctaaggcc tctggagctg gagctgggta tagggatgat
 120
accaggcacc ctgagtcact cgcacctcac aatggggccg cttctggggag ccagtgggct
 180
tatggggctg gcaatgtgct gggttatgag gatggatcag aacttccagg gcctcagggg
 240
actgggggtca gaacagccta tggagaaagg tcaaggggccc ttgggcctag gagtacaggg
 300
ccaggggggtg aggcaggctt tagagatggt tcaggaggcc tccaaggaat gggatcagca
 360
gatggggccc gt
 372

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<210> 576

<211> 124

<212> PRT

<213> Homo sapiens

<400> 576

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Xaa Ile His Ala Asp Met Gly Pro Gly Ser Leu Arg Ala Gly Ser Lys
 1           5           10           15
Val Gly Glu Gly Asp Gly Thr Arg Cys Pro Gly Ala Lys Ala Ser Gly
          20           25           30
Ala Gly Ala Gly Tyr Arg Asp Asp Thr Arg His Pro Glu Ser Leu Ala
          35           40           45
Pro His Asn Gly Ala Ala Ser Gly Ser Gln Trp Ala Tyr Gly Ala Gly

```

```

      50              55              60
Asn Val Leu Gly Tyr Glu Asp Gly Ser Glu Leu Pro Gly Pro Gln Gly
65              70              75              80
Thr Gly Val Arg Thr Ala Tyr Gly Glu Arg Ser Arg Gly Leu Gly Pro
      85              90              95
Arg Ser Thr Gly Pro Gly Gly Glu Ala Gly Phe Arg Asp Gly Ser Gly
      100              105              110
Gly Leu Gln Gly Met Gly Ser Ala Asp Gly Pro Gly
      115              120

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<210> 577
 <211> 432
 <212> DNA
 <213> Homo sapiens

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<400> 577
nagcgcaatg tcatgatgtc ggatttgtca atgtcggatt tctcatccca gccatcaccc
60
ccgcagcgcc gggcgcggat gaccagcggc cagcgccgtg aacagctcat cagcgtggcc
120
cgtcgctctt tcgcagacaa tggcatggca gggacctccg tcgaggagat cgccgctacc
180
gcgggagtct ccaaaccggt catctacgag catttcgggt ccaaggatgg gctgtacgcc
240
gtcgtcgtag accgcgaggt acgccaccta caagattccc tcaacgccgc catgacccgc
300
ccaaagcaag gcccgaacg caccctggag tcagcggtag tggccctgct ggactacatc
360
gacgaccgtc cagacgggtt tcggatcate tcgcgagact cctcggtcgg ttcagccacc
420
ggttcgtacg cg
432

```

<210> 578
 <211> 118
 <212> PRT
 <213> Homo sapiens

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<400> 578
Met Thr Ser Gly Gln Arg Arg Glu Gln Leu Ile Ser Val Ala Arg Arg
1      5      10      15
Leu Phe Ala Asp Asn Gly Met Ala Gly Thr Ser Val Glu Glu Ile Ala
      20      25      30
Ala Thr Ala Gly Val Ser Lys Pro Val Ile Tyr Glu His Phe Gly Ser
      35      40      45
Lys Asp Gly Leu Tyr Ala Val Val Val Asp Arg Glu Val Arg His Leu
      50      55      60
Gln Asp Ser Leu Asn Ala Ala Met Thr Arg Pro Lys Gln Gly Pro Lys
65      70      75      80
Arg Thr Leu Glu Ser Ala Val Leu Ala Leu Leu Asp Tyr Ile Asp Asp
      85      90      95
Arg Pro Asp Gly Phe Arg Ile Ile Ser Arg Asp Ser Ser Val Gly Ser
      100      105      110
Ala Thr Gly Ser Tyr Ala

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115

<210> 579
 <211> 320
 <212> DNA
 <213> Homo sapiens

<400> 579
 ggccccaaac actccgacct cagctgggtcc agcatgctgg gcaccgtgct gctgctggcc
 60
 ctgctcccag ggatcaccac cttaccacagc gggccacctg ctcccccggt ccccgcggcg
 120
 cccggcccct ggctgcgag acccctcttc agcctgaagc tgtccgacac agaggacgtc
 180
 tttcctcgcc gcgcggggcc gctcgaggtc ccggccgaca gccgctgtt cgtgcaggcg
 240
 gccttgcccc gtccctcccc gcgctggggc ctggccctgc accgctgctc agtgacgccg
 300
 tcttcacgcc cggccccggg
 320

<210> 580
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 580
 Met Leu Gly Thr Val Leu Leu Leu Ala Leu Leu Pro Gly Ile Thr Thr
 1 5 10 15
 Leu Pro Ser Gly Pro Pro Ala Pro Pro Phe Pro Ala Ala Pro Gly Pro
 20 25 30
 Trp Leu Arg Arg Pro Leu Phe Ser Leu Lys Leu Ser Asp Thr Glu Asp
 35 40 45
 Val Phe Pro Arg Arg Ala Gly Pro Leu Glu Val Pro Ala Asp Ser Arg
 50 55 60
 Val Phe Val Gln Ala Ala Leu Ala Arg Pro Ser Pro Arg Trp Gly Leu
 65 70 75 80
 Ala Leu His Arg Cys Ser Val Thr Pro Ser Arg Pro Ala Pro
 85 90 95

<210> 581
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 581
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 cagctcggca tgggcttcaa gacgccagta cgcattgcaca gcgtcgaccc caagaccgcg
 120
 gaagcccgcg aggtgcattt ccgcccgtcg ctgttcaact atgccaagac cacggtggac
 180
 accaagcagc tgaccggcga cctgggtttc tccggtttca agctgttcaa ggcgccggaa
 240

ctggatcgcc atgacgtgct gtcgtttctc ggcgccagtt acttccgtgc ggtggacgca
 300
 acccgccagt acggcctctc cgcacgcggc ctggcgattg atacctacgc gaaaaaacgc
 360
 gaggaattcc ccgacttcac gcagttctgg ttcgaaaccc cgagcaagga cccacgcgt
 419

<210> 582

<211> 139

<212> PRT

<213> Homo sapiens

<400> 582

Xaa	Asp	Gly	Asn	His	Ser	Leu	Trp	Lys	Glu	Leu	Asn	Gly	Gln	Leu	Asp
1				5					10					15	
Val	Gln	Phe	Phe	His	Val	Gly	Met	Gly	Phe	Lys	Thr	Pro	Val	Arg	Met
			20					25					30		
His	Ser	Val	Asp	Pro	Lys	Thr	Arg	Glu	Ala	Arg	Glu	Val	His	Phe	Arg
		35				40					45				
Pro	Ser	Leu	Phe	Asn	Tyr	Ala	Lys	Thr	Thr	Val	Asp	Thr	Lys	Gln	Leu
	50					55				60					
Thr	Gly	Asp	Leu	Gly	Phe	Ser	Gly	Phe	Lys	Leu	Phe	Lys	Ala	Pro	Glu
65				70						75				80	
Leu	Asp	Arg	His	Asp	Val	Leu	Ser	Phe	Leu	Gly	Ala	Ser	Tyr	Phe	Arg
			85					90						95	
Ala	Val	Asp	Ala	Thr	Arg	Gln	Tyr	Gly	Leu	Ser	Ala	Arg	Gly	Leu	Ala
		100						105					110		
Ile	Asp	Thr	Tyr	Ala	Lys	Lys	Arg	Glu	Glu	Phe	Pro	Asp	Phe	Thr	Gln
	115					120						125			
Phe	Trp	Phe	Glu	Thr	Pro	Ser	Lys	Asp	Pro	Arg					
	130					135									

<210> 583

<211> 407

<212> DNA

<213> Homo sapiens

<400> 583

cttttgatca atgctgatgg cacgaagcta tcgaaaagggt cgggtgatgt ccgcgtagct
 60
 gattatatgg agcaggggatg ggagccggag acgctggtga acctagtgtc cctcacgggc
 120
 tatagctatg cgaatttgga gcatgctgat catgatgtca agacgatgaa cgaactcatc
 180
 cgtgactttg agcttactcg tatctcccat acgcgagcca cactcccat ggacaagctt
 240
 gtgtttttga acaagcatca cttgacaaat aagctggcgc tcgccacgac gtgtgagcag
 300
 accaaacaag acctattgtc gcgtatccgg ccgatcacta cctcgtggta cggcgattat
 360
 tcagatgatt atatcctgcg cgtcgttaaca ctgggacccc aacgcgt
 407

<210> 584

<211> 135
 <212> PRT
 <213> Homo sapiens

<400> 584
 Leu Leu Ile Asn Ala Asp Gly Thr Lys Leu Ser Lys Arg Ser Gly Asp
 1 5 10 15
 Val Arg Val Ala Asp Tyr Met Glu Gln Gly Trp Glu Pro Glu Thr Leu
 20 25 30
 Val Asn Leu Val Ala Leu Thr Gly Tyr Ser Tyr Ala Asn Leu Glu His
 35 40 45
 Ala Asp His Asp Val Lys Thr Met Asn Glu Leu Ile Arg Asp Phe Glu
 50 55 60
 Leu Thr Arg Ile Ser His Thr Arg Ala Thr Leu Pro Met Asp Lys Leu
 65 70 75 80
 Val Phe Leu Asn Lys His His Leu Thr Asn Lys Leu Ala Leu Ala Thr
 85 90 95
 Thr Cys Glu Gln Thr Lys Gln Asp Leu Leu Ser Arg Ile Arg Pro Ile
 100 105 110
 Thr Thr Ser Trp Tyr Gly Asp Tyr Ser Asp Asp Tyr Ile Leu Arg Val
 115 120 125
 Val Thr Leu Gly Pro Gln Arg
 130 135

<210> 585
 <211> 502
 <212> DNA
 <213> Homo sapiens

<400> 585
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 60
 gatattttgt tgtgcgcggt gggattgttg gttcagcacc gtgacatcac tgaggagatt
 120
 cgggctcggt accgacattt cgttgtcgac gaataccagg acgtttctcc gctgcagcat
 180
 aggttgcttg aactgtgggt tggcgatcga aatgatgtat gcgtcgtggg agatccgcac
 240
 caggccattc actcttatgc aggcgcacga gctgactacc tcctcgactt cgttgccgat
 300
 catcctggcg ctaaacgcat cgatttggtt cgcaactacc gctccactcc cgagatcggt
 360
 cagttggcca atgaagttct tgtcaaccgt atgactccag aggaggcttt ggaacatggc
 420
 aggggagtca cattgggttc gcggggtcga tccgggtccg agcccatcta tcaggctctc
 480
 ggggacgatg cctccgaagc tt
 502

<210> 586
 <211> 167
 <212> PRT
 <213> Homo sapiens

<400> 586
 Xaa Arg Val Leu Ala Gly Tyr Glu Ala Val Lys Arg Glu Arg Cys Val
 1 5 10 15
 Ile Asp Leu Asp Asp Ile Leu Leu Cys Ala Val Gly Leu Leu Val Gln
 20 25 30
 His Arg Asp Ile Thr Glu Glu Ile Arg Ala Arg Tyr Arg His Phe Val
 35 40 45
 Val Asp Glu Tyr Gln Asp Val Ser Pro Leu Gln His Arg Leu Leu Glu
 50 55 60
 Leu Trp Phe Gly Asp Arg Asn Asp Val Cys Val Val Gly Asp Pro His
 65 70 75 80
 Gln Ala Ile His Ser Tyr Ala Gly Ala Arg Ala Asp Tyr Leu Leu Asp
 85 90 95
 Phe Val Ala Asp His Pro Gly Ala Lys Arg Ile Asp Leu Val Arg Asn
 100 105 110
 Tyr Arg Ser Thr Pro Glu Ile Val Gln Leu Ala Asn Glu Val Leu Val
 115 120 125
 Asn Arg Met Thr Pro Glu Glu Ala Leu Glu His Gly Arg Gly Val Thr
 130 135 140
 Leu Val Ser Arg Gly Arg Ser Gly Pro Glu Pro Ile Tyr Gln Ala Leu
 145 150 155 160
 Gly Asp Asp Ala Ser Glu Ala
 165

<210> 587
 <211> 746
 <212> DNA
 <213> Homo sapiens

<400> 587
 gcgtcctgcc tcgagggcct cgggagcttc cgctgcctct gttggccagg ctacagcggc
 60
 gagctgtgcg aggtggacga ggacgagtgt gcatcgagcc cctgccagca tggggggccga
 120
 tgcctgcagc gctctgaccc ggccctctac ggggggtgtcc aggccgcctt ccctggcgcc
 180
 ttcagcttcc gccatgctgc gggtttcctg tgccactgcc ctctggctt tgagggagcc
 240
 gactgcggtg tggaggtgga cgagtgtgcc tcacggccat gcctcaatgg aggccactgc
 300
 caggacctgc ccaatggctt ccagtgtcac tgcccagatg gctacgcagg gccgacatgt
 360
 gaggaagatg tggatgaatg cctgtccgat ccctgcctgc acggcggaac ctgcagtgc
 420
 actgtggcag gctatatctg caggtgcccc gagacctggg gtgggcgcga ctgttctgtg
 480
 cagctcactg gctgccaggg ccacacctgc ccgctggctg ccacctgcat ccctatcttc
 540
 gagtctgggg tccacagtta cgtctgccac tgcccacctg gtacccatgg accgttctgt
 600
 ggccagaata ccaccttctc tgtgatggct gggagcccca ttcaggcatc agtgccagct
 660
 ggtggccccc tgggtctggc actgaggttt cgcaccacac tgcccgtgg gaccttggcc
 720

actcgcaatg acaccaagga aagctt
746

<210> 588

<211> 248

<212> PRT

<213> Homo sapiens

<400> 588

Ala	Ser	Cys	Leu	Glu	Gly	Leu	Gly	Ser	Phe	Arg	Cys	Leu	Cys	Trp	Pro
1			5					10					15		
Gly	Tyr	Ser	Gly	Glu	Leu	Cys	Glu	Val	Asp	Glu	Asp	Glu	Cys	Ala	Ser
			20				25					30			
Ser	Pro	Cys	Gln	His	Gly	Gly	Arg	Cys	Leu	Gln	Arg	Ser	Asp	Pro	Ala
		35				40					45				
Leu	Tyr	Gly	Gly	Val	Gln	Ala	Ala	Phe	Pro	Gly	Ala	Phe	Ser	Phe	Arg
	50					55				60					
His	Ala	Ala	Gly	Phe	Leu	Cys	His	Cys	Pro	Pro	Gly	Phe	Glu	Gly	Ala
65					70				75						80
Asp	Cys	Gly	Val	Glu	Val	Asp	Glu	Cys	Ala	Ser	Arg	Pro	Cys	Leu	Asn
			85					90					95		
Gly	Gly	His	Cys	Gln	Asp	Leu	Pro	Asn	Gly	Phe	Gln	Cys	His	Cys	Pro
		100					105					110			
Asp	Gly	Tyr	Ala	Gly	Pro	Thr	Cys	Glu	Glu	Asp	Val	Asp	Glu	Cys	Leu
	115					120					125				
Ser	Asp	Pro	Cys	Leu	His	Gly	Gly	Thr	Cys	Ser	Asp	Thr	Val	Ala	Gly
	130					135					140				
Tyr	Ile	Cys	Arg	Cys	Pro	Glu	Thr	Trp	Gly	Gly	Arg	Asp	Cys	Ser	Val
145					150				155						160
Gln	Leu	Thr	Gly	Cys	Gln	Gly	His	Thr	Cys	Pro	Leu	Ala	Ala	Thr	Cys
			165					170						175	
Ile	Pro	Ile	Phe	Glu	Ser	Gly	Val	His	Ser	Tyr	Val	Cys	His	Cys	Pro
		180						185				190			
Pro	Gly	Thr	His	Gly	Pro	Phe	Cys	Gly	Gln	Asn	Thr	Thr	Phe	Ser	Val
	195					200						205			
Met	Ala	Gly	Ser	Pro	Ile	Gln	Ala	Ser	Val	Pro	Ala	Gly	Gly	Pro	Leu
	210					215					220				
Gly	Leu	Ala	Leu	Arg	Phe	Arg	Thr	Thr	Leu	Pro	Ala	Gly	Thr	Leu	Ala
225					230				235						240
Thr	Arg	Asn	Asp	Thr	Lys	Glu	Ser								
				245											

<210> 589

<211> 381

<212> DNA

<213> Homo sapiens

<400> 589

atctcacaag tacaattaca gtctcaagaa ctgagctatc agcaaaagca aggtcttcag
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ccagtacctc tgcaagccac tatgagtgtc gcaactggta tccagccatc gcctgtaa
120
gtgggttggtg taacttcagc tttagggtcag cagccttcca tttccagttt ggctcaaccc
180

cagctaccat attctcaggc ggctcctcca gtgcaaactc cccttccagg ggcaccacca
 240
 ccccaacagt tacagtatgg acaacagcaa ccaatggttt ctacacagat ggccccaggc
 300
 catgtcaaatt cagtgactca aaatcctgct tcagagtatg tacaacagca gccaatcttt
 360
 caaacagcaa tgtcctccgg a
 381

<210> 590
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 590
 Ile Ser Gln Val Gln Leu Gln Ser Gln Glu Leu Ser Tyr Gln Gln Lys
 1 5 10 15
 Gln Gly Leu Gln Pro Val Pro Leu Gln Ala Thr Met Ser Ala Ala Thr
 20 25 30
 Gly Ile Gln Pro Ser Pro Val Asn Val Val Gly Val Thr Ser Ala Leu
 35 40 45
 Gly Gln Gln Pro Ser Ile Ser Ser Leu Ala Gln Pro Gln Leu Pro Tyr
 50 55 60
 Ser Gln Ala Ala Pro Pro Val Gln Thr Pro Leu Pro Gly Ala Pro Pro
 65 70 75 80
 Pro Gln Gln Leu Gln Tyr Gly Gln Gln Gln Pro Met Val Ser Thr Gln
 85 90 95
 Met Ala Pro Gly His Val Lys Ser Val Thr Gln Asn Pro Ala Ser Glu
 100 105 110
 Tyr Val Gln Gln Gln Pro Ile Leu Gln Thr Ala Met Ser Ser Gly
 115 120 125

<210> 591
 <211> 684
 <212> DNA
 <213> Homo sapiens

<400> 591
 tcgaccatgg atcatctgcg ccacggcatc cacctgcggtg gttatgcgca gaagaacccg
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 aagcaggaat acaagcgcgga gtcgttcacc ctgtttctccg agctgctgga ctcgatcaag
 120
 cgcgattcga ttcggttctt cttccacgtc cagggggccgg gggaaaaaatc cgtatcgaaa
 180
 naaaaagcgc gcctgcgta ggaagccgaa gccctggccc agcgcattgca gttcgagcac
 240
 gctgaagccc caggcctgga cgcgccggaa atcctcggtg aagaagtcga tgcgcacctg
 300
 gccaccgcg cggtacgcaa cgagcagaag ctggggccgta acgaactgtg ctactgcggt
 360
 tcggggcaaga agtacaagca ctgccacggt cagatcagct aaggtcttta ccggatactg
 420
 aaatacctgc gcgcgaccg gcattagccg tcgcggcggtt tttccatttg aaacactgcc
 480

cttgtgacgg cagtgcagat atcacattaa aaggagggca ttcattgggtg ttggttctgg
 540
 gtccttgccc tacgttgacac ccggttgccg gttttgaact cggatcgcgc tcggccggta
 600
 tcaagcgcgc tgggcgcaag gatgtggtgg cgatgcgctg cgccgaagggt tccacggtgg
 660
 cgggggtggt taccctcaac gcgt
 684

<210> 592

<211> 133

<212> PRT

<213> Homo sapiens

<400> 592

Ser	Thr	Met	Asp	His	Leu	Arg	His	Gly	Ile	His	Leu	Arg	Gly	Tyr	Ala
1				5					10					15	
Gln	Lys	Asn	Pro	Lys	Gln	Glu	Tyr	Lys	Arg	Glu	Ser	Phe	Thr	Leu	Phe
			20					25					30		
Ser	Glu	Leu	Leu	Asp	Ser	Ile	Lys	Arg	Asp	Ser	Ile	Arg	Val	Leu	Phe
		35					40					45			
His	Val	Gln	Gly	Pro	Gly	Glu	Lys	Ser	Val	Ser	Lys	Xaa	Lys	Ala	Arg
	50					55					60				
Leu	Arg	Gln	Glu	Ala	Glu	Ala	Leu	Ala	Gln	Arg	Met	Gln	Phe	Glu	His
65					70					75				80	
Ala	Glu	Ala	Pro	Gly	Leu	Asp	Ala	Pro	Glu	Ile	Leu	Gly	Glu	Glu	Val
				85					90					95	
Asp	Val	Ala	Leu	Ala	Thr	Ala	Pro	Val	Arg	Asn	Glu	Gln	Lys	Leu	Gly
			100					105					110		
Arg	Asn	Glu	Leu	Cys	Tyr	Cys	Gly	Ser	Gly	Lys	Lys	Tyr	Lys	His	Cys
		115					120					125			
His	Gly	Gln	Ile	Ser											
			130												

<210> 593

<211> 615

<212> DNA

<213> Homo sapiens

<400> 593

nnacgcgtgc agaccgcgcg gagtctcgct ccggtgcgga tagcgtagg ctcccaaacc
 60
 tgtgaaaccg tcacggtaga gcgtcgtggc gggctaccac ttagagcggc cggattcacc
 120
 gataccatcc ccgcgccgct aggccagcca cgatggtcga cggccaccat ccagacccca
 180
 gtcataccta ctacacgtgg tcgattcgtg atcgccccg tcatgatgcg caccatcgac
 240
 ccggtttggca tggcccgcca tcacaccgat ctcggtcagg ttgccgaagt cattgtcacg
 300
 ccaaggatcg tcgatttggg cgcctccggg gagctcgggg gtcagggatt cgacacaagg
 360
 tcctcagcga tccatgccgg acgacgtggt cccgacgatg ccatggtgcg cgattggcac
 420

accggagact cggcgcgacg cattcactgg cgctccaccg ctcaccgcgg ggacctcatg
 480
 gtccgatgcg aggagcaggc ctggaaccca tccgtcgta tegtgttgga ttctcgggct
 540
 cggcgtaacg ctggaactgg ccccgacgca tcctttgaat gggccgtcaa cgcgggtggca
 600
 tccatctcga cgcgt
 615

<210> 594
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 594
 Xaa Arg Val Gln Thr Ala Arg Ser Leu Ala Pro Val Arg Ile Ala Leu
 1 5 10 15
 Gly Ser Gln Thr Cys Glu Thr Val Thr Val Glu Arg Arg Gly Gly Leu
 20 25 30
 Pro Leu Arg Ala Ala Arg Phe Thr Asp Thr Ile Pro Ala Pro Leu Gly
 35 40 45
 Gln Pro Arg Trp Ser Thr Ala Thr Ile Gln Thr Pro Val Ile Pro Thr
 50 55 60
 Thr Arg Gly Arg Phe Val Ile Gly Pro Val Met Met Arg Thr Ile Asp
 65 70 75 80
 Pro Phe Gly Met Ala Arg His His Thr Asp Leu Gly Gln Val Ala Glu
 85 90 95
 Val Ile Val Thr Pro Arg Ile Val Asp Leu Gly Ala Ser Gly Glu Leu
 100 105 110
 Gly Gly Gln Gly Phe Asp Thr Arg Ser Ser Ala Ile His Ala Gly Arg
 115 120 125
 Arg Gly Pro Asp Asp Ala Met Val Arg Asp Trp His Thr Gly Asp Ser
 130 135 140
 Val Arg Arg Ile His Trp Arg Ser Thr Ala His Arg Gly Asp Leu Met
 145 150 155 160
 Val Arg Cys Glu Glu Gln Ala Trp Asn Pro Ser Val Val Ile Val Leu
 165 170 175
 Asp Ser Arg Ala Arg Arg His Ala Gly Thr Gly Pro Asp Ala Ser Phe
 180 185 190
 Glu Trp Ala Val Asn Ala Val Ala Ser Ile Ser Thr Arg
 195 200 205

<210> 595
 <211> 303
 <212> DNA
 <213> Homo sapiens

<400> 595
 acgcgtccta gccgcagtga atgttgctga accccggtga cctcacagtg gaggggaggc
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 cccatggggc catcggaaccg cgccgcgcgg gggcggttcgc cagggcctcc gcagaagccc
 120
 gcctgtgccc gcaaccgccc cgaaattctc tccttggcac cgtgtccgct ttacggagcc
 180

cggagcaagg ctcagaaaaa tgtcccagcc aaaaacatgg tacatgctg tcatcaggca
 240
 agtcttcaaa gagcggctgg gaccaggggc cgagggacct cgtttagagg cggcttaggg
 300
 gga
 303

<210> 596
 <211> 88
 <212> PRT
 <213> Homo sapiens

<400> 596
 Met Leu Leu Asn Pro Gly Asp Leu Thr Val Glu Gly Arg Pro His Gly
 1 5 10 15
 Ala Ile Gly Pro Arg Arg Ala Gly Ala Phe Ala Arg Ala Ser Ala Glu
 20 25 30
 Ala Arg Leu Cys Pro Gln Pro Pro Arg Asn Ser Leu Pro Gly Thr Val
 35 40 45
 Ser Ala Leu Arg Ser Pro Glu Gln Gly Ser Glu Lys Cys Pro Ser Gln
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<210> 597
 <211> 2709
 <212> DNA
 <213> Homo sapiens

<400> 597
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 360
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 420
 gttgagtgtg ggcattgtgg caaggccttc aggaaccagt caacgctgaa gacgcacatg
 480
 cgaagccaca cgggggagaa accgtacgaa tgcgatcact gtgggaaggc cttcagcata
 540
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 660

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1260
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1320
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1380
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aaacgtcact gttgctgagg ttgaaaataa tcatgcagtc attcctcaat tactgcctgc
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1680
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1740
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1980
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2220
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2280

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 2340
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 2460
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 aaaaaaaaaa
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<210> 598

<211> 240

<212> PRT

<213> Homo sapiens

<400> 598

Xaa	Ala	Cys	Thr	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Trp	Lys	Ser	Asn	Phe
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			20					25					30		
Glu	Cys	Gly	Lys	Ser	Phe	Gly	Asp	Leu	Val	Ser	Arg	Arg	Lys	His	Met
		35					40					45			
Arg	Ile	His	Ile	Val	Lys	Lys	Pro	Val	Glu	Cys	Arg	Gln	Cys	Gly	Lys
	50					55					60				
Thr	Phe	Arg	Asn	Gln	Ser	Ile	Leu	Lys	Thr	His	Met	Asn	Ser	His	Thr
65					70					75				80	
Gly	Glu	Lys	Pro	Tyr	Gly	Cys	Asp	Leu	Cys	Gly	Lys	Ala	Phe	Ser	Ala
				85					90					95	
Ser	Ser	Asn	Leu	Thr	Ala	His	Arg	Lys	Ile	His	Thr	Gln	Glu	Arg	Arg
			100					105					110		
Tyr	Glu	Cys	Ala	Ala	Cys	Gly	Lys	Val	Phe	Gly	Asp	Tyr	Leu	Ser	Arg
	115						120					125			
Arg	Arg	His	Met	Ser	Val	His	Leu	Val	Lys	Lys	Arg	Val	Glu	Cys	Arg
	130					135					140				
His	Cys	Gly	Lys	Ala	Phe	Arg	Asn	Gln	Ser	Thr	Leu	Lys	Thr	His	Met
145					150					155				160	
Arg	Ser	His	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asp	His	Cys	Gly	Lys
			165						170					175	
Ala	Phe	Ser	Ile	Gly	Ser	Asn	Leu	Asn	Val	His	Arg	Arg	Ile	His	Thr
			180					185					190		
Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Leu	Val	Cys	Gly	Lys	Ala	Phe	Ser	Asp
	195						200					205			
His	Ser	Ser	Leu	Arg	Ser	His	Val	Lys	Thr	His	Arg	Gly	Glu	Lys	Leu
	210					215					220				
Phe	Xaa	Cys	His	Pro	Cys	Gly	Lys	Gly	Ser	Ser	Glu	Arg	Ala	Xaa	Leu
225					230					235					240

<210> 599
 <211> 340
 <212> DNA
 <213> Homo sapiens

<400> 599
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 caggcatgtt tgccggggccg catcccttgc acttgcagtc cgtggcctat cggccgagggc
 180
 gcaggcctgc agttggagcc gtgcgtgggt gtcccgcgcg aggagcgtgt tggcagacta
 240
 tggggctcgt cggaggacga ggatgtgagt ggcgatggct ttgcgcgact gggcgtattc
 300
 caccggcgga tgggtgctcca gatcgtccag ggcattgatca
 340

<210> 600
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 600
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 Arg Ala Lys Pro Ser Pro Leu Thr Ser Ser Ser Asp Glu Pro His
 20 25 30
 Ser Leu Pro Thr Arg Ser Ser Arg Gly Thr Pro Thr His Gly Ser Asn
 35 40 45
 Cys Arg Pro Ala Pro Arg Pro Ile Gly His Gly Leu Gln Val Gln Gly
 50 55 60
 Met Arg Pro Gly Lys His Ala Trp Ala Lys Arg Cys Arg Leu Arg Cys
 65 70 75 80
 Thr Ala Thr Pro Ser Thr Cys Ala Met Thr Pro Asn Lys Arg Ser Asp
 85 90 95
 Thr Thr Glu Arg Ser His His Asp Val Lys Ser Arg Glu Ala Arg
 100 105 110

<210> 601
 <211> 421
 <212> DNA
 <213> Homo sapiens

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 120
 cagctgtcga tggccccgt gtctatcgggt aatctgcaat cgggtggacgt ggtgcgcggc
 180
 ggcggcgcgg tcgcgtacgg gccgcagaac gtcggcggcg tgatcaactt cgttaccgga
 240

gacattccca aaacgtttgg cggtgccgcc agcgtacaaa cccaggggtgc cagccacggc
 300
 ggccctgaaga ccctgaccag cgcctccgtg ggccggcaccg cagacaacgg cctcggcgcc
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 421

<210> 602

<211> 140

<212> PRT

<213> Homo sapiens

<400> 602

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Ser	Arg	Leu	Ser	Pro	Arg	Ser	Thr	Ile	Leu	Met	Asp	Gly	Val	Pro	Leu
			20					25					30		
Ala	Val	Ala	Pro	Tyr	Gly	Gln	Pro	Gln	Leu	Ser	Met	Ala	Pro	Leu	Ser
		35					40					45			
Ile	Gly	Asn	Leu	Gln	Ser	Val	Asp	Val	Val	Arg	Gly	Gly	Gly	Ala	Val
	50					55					60				
Arg	Tyr	Gly	Pro	Gln	Asn	Val	Gly	Gly	Val	Ile	Asn	Phe	Val	Thr	Arg
65					70					75				80	
Asp	Ile	Pro	Lys	Thr	Phe	Gly	Gly	Ala	Ala	Ser	Val	Gln	Thr	Gln	Gly
				85				90						95	
Ala	Ser	His	Gly	Gly	Leu	Lys	Thr	Leu	Thr	Ser	Ala	Ser	Val	Gly	Gly
			100					105					110		
Thr	Ala	Asp	Asn	Gly	Leu	Gly	Ala	Glu	Leu	Leu	Tyr	Ser	Gly	Leu	His
		115					120					125			
Gly	Gln	Gly	Tyr	Arg	Asp	Asn	Asn	Asp	Asn	Thr	Asp				
	130					135					140				

<210> 603

<211> 309

<212> DNA

<213> Homo sapiens

<400> 603

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 gtgctggatt acctgccggg cctgatgccg gctgacaaac ctcgttacct tatgggcggt
 180
 ggcaaaccgg aagacctcgt agaggggtgtg cgccgcggtg tggacatggt cgattgcgtg
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 309

<210> 604

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 604
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 Asp Lys Ile Gly Phe Asp Gly Leu Ala Ile Gly Gly Leu Ser Val Gly
 20 25 30
 Glu Pro Lys His Glu Met Ile Lys Val Leu Asp Tyr Leu Pro Gly Leu
 35 40 45
 Met Pro Ala Asp Lys Pro Arg Tyr Leu Met Gly Val Gly Lys Pro Glu
 50 55 60
 Asp Leu Val Glu Gly Val Arg Arg Gly Val Asp Met Phe Asp Cys Val
 65 70 75 80
 Met Pro Thr Arg Asn Ala Arg Asn Gly His Leu Phe Ile Asp Thr Gly
 85 90 95
 Val Leu Lys Ile Arg Asn Ala
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<210> 605
 <211> 428
 <212> DNA
 <213> Homo sapiens

<400> 605
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 120
 caccacatc acatttcagt accttggtta tcttcaatcg gaaaaaaga ttggagtaaa
 180
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 240
 attcccagtg caaagggtccc catgctacat cctgcgacaa tgaggccgtt agcacgttta
 300
 ttgcctcgtt gctttgccga acgccaacct ctgtaccgat acgctgatac tgattgttga
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 420
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 428

<210> 606
 <211> 135
 <212> PRT
 <213> Homo sapiens

<400> 606
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 Asn Asn Gln Tyr Gln Arg Ile Gly Thr Glu Val Gly Val Arg Gln Ser
 20 25 30
 Ser Glu Ala Ile Asn Val Leu Thr Ala Ser Leu Ser Gln Asp Val Ala

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      35              40              45
Trp Gly Pro Leu His Trp Glu Ser Val Ile Thr Phe Gln Asn Ser Ser
  50              55              60
Ser Gln Thr Ala Leu Pro Leu Pro Lys Leu Asn Ile Tyr Ser Asn Leu
  65              70              75              80
Phe Phe Arg Leu Lys Ile Ala Lys Val Leu Lys Cys Asp Val Gly Ala
      85              90              95
Asp Val Arg Tyr Phe Thr Lys Tyr Tyr Ala Pro Asp Tyr Ser Pro Ala
      100              105              110
Leu Gly Gln Phe Val Val Gln Glu Asn Thr Asp Arg Val Glu Ile Gly
      115              120              125
Asn Tyr Pro Ile Val Asn Ala
      130              135

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<210> 607
 <211> 366
 <212> DNA
 <213> Homo sapiens

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<400> 607
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  120
gttttcaacg gcaaacatta tcaaattgta aagaaagagg atgacctatt caaattgacc
  180
aaaagcaatt gttacaagtt gagcaacata aaatttaaca attggaaata cttgtacttg
  240
acaacgcacg gtgtgtacaa cgtgttcacc aacagctttc attcgagctg tccatttttg
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ttgggcacca cgttgccgca gacattcaag aagcccaccg acgaaaagta tttgcccag
  360
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  366

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<210> 608
 <211> 122
 <212> PRT
 <213> Homo sapiens

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<400> 608
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Asn Leu Pro Pro Asp Ile Val Cys Lys Gly Phe Phe Arg Lys Leu Glu
      20              25              30
Asn Val Val Thr Gly Val Asn Leu Val Phe Asn Gly Lys His Tyr Gln
      35              40              45
Ile Val Lys Lys Glu Asp Asp Leu Phe Lys Leu Thr Lys Ser Asn Cys
      50              55              60
Tyr Lys Leu Ser Asn Ile Lys Phe Asn Asn Trp Lys Tyr Leu Tyr Leu
  65              70              75              80
Thr Thr His Gly Val Tyr Asn Val Phe Thr Asn Ser Phe His Ser Ser
      85              90              95
Cys Pro Phe Leu Leu Gly Thr Thr Leu Pro Gln Thr Phe Lys Lys Pro

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100 105 110
 Thr Asp Glu Lys Tyr Leu Pro Glu Asp Ala
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<210> 609
 <211> 291
 <212> DNA
 <213> Homo sapiens

<400> 609
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 120
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 180
 ccgaagcctc aaacttcccc cgccccgtac gccggggccgg ctccgaagac accggccaca
 240
 cctggaccat ctggggcggg ggcgcgcggc tgggtggtggc ggggtggagcc g
 291

<210> 610
 <211> 69
 <212> PRT
 <213> Homo sapiens

<400> 610
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 Lys Gln Asp Pro His Ala Thr Glu Ser Pro Ala Ser Lys Ser Ser Pro
 20 25 30
 Pro Lys Pro Gln Thr Ser Pro Ala Pro Tyr Ala Gly Pro Ala Pro Lys
 35 40 45
 Thr Pro Ala Thr Pro Gly Pro Ser Gly Ala Gly Ala Pro Pro Trp Trp
 50 55 60
 Trp Arg Val Glu Pro
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<210> 611
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 611
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 120
 acgcgcacatca ggccgcacaa aggtcaggta gcgactcttg agcaagcgct tgatgcaggt
 180
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 240
 atggcaacgg ttctggagag ctatctgcgg gaagagtttc ccagtagcga aatcaggagc
 300

gattcgacaga acaagtccat tgacgagacc atctctatcg tccgctccta tctgcggtag
 360
 aggcaccagg gtgtcctcgg tgagggcaaa ttt
 393

<210> 612

<211> 119

<212> PRT

<213> Homo sapiens

<400> 612

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Ile	Met	Arg	Arg	Cys	Thr	Gln	Val	Glu	Arg	Cys	Ser	Met	Pro	His	Ser
		20						25					30		
Pro	Glu	Glu	Lys	Lys	Gln	Ala	Leu	Thr	Arg	Ile	Arg	Arg	Ile	Lys	Gly
		35					40					45			
Gln	Val	Ala	Thr	Leu	Glu	Gln	Ala	Leu	Asp	Ala	Gly	Ala	Lys	Cys	Pro
		50				55				60					
Ala	Ile	Leu	Gln	Gln	Leu	Ala	Ala	Val	Arg	Gly	Ala	Val	Asn	Gly	Leu
65					70				75					80	
Met	Ala	Thr	Val	Leu	Glu	Ser	Tyr	Leu	Arg	Glu	Glu	Phe	Pro	Ser	Ser
			85					90					95		
Glu	Ile	Arg	Ser	Asp	Ser	Gln	Asn	Lys	Ser	Ile	Asp	Glu	Thr	Ile	Ser
		100						105					110		
Ile	Val	Arg	Ser	Tyr	Leu	Arg									
						115									

<210> 613

<211> 567

<212> DNA

<213> Homo sapiens

<400> 613

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 aacttgata aagagagtgg agaaagcctc agagtttgca gtgtcaaata cattttttac
 180
 tagaaattca gatttaccta gaagtccttg gggccaaatc acagatttga aaacatctga
 240
 gcaaatagag gatcatgatg aaatctatgc agaagctcag gagctgggtca atgactgggt
 300
 agacacaaaa cttaagcaag aattagcaag tgaggaagaa ggtgatgcta aaaacactgt
 360
 gtcaagtgtc actattatgc cggaagccaa tggccatttg aaatatgaca agtttgatga
 420
 tttatgtggc tatttggagg aagaagagga aagtaccacc gttcaaaaat ttatagacca
 480
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<210> 614
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 614
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 Leu Asn Arg Trp Lys Arg Phe Thr Arg Lys Pro Ser Pro Lys Pro Thr
 20 25 30
 Phe Gly Pro Asp Ser Val Glu His Trp Ile Lys Arg Val Glu Lys Ala
 35 40 45
 Ser Glu Phe Ala Val Ser Asn Ala Phe Phe Thr Arg Asn Ser Asp Leu
 50 55 60
 Pro Arg Ser Pro Trp Gly Gln Ile Thr Asp Leu Lys Thr Ser Glu Gln
 65 70 75 80
 Ile Glu Asp His Asp Glu Ile Tyr Ala Glu Ala Gln Glu Leu Val Asn
 85 90 95
 Asp Trp Leu Asp Thr Lys Leu Lys Gln Glu Leu Ala Ser Glu Glu Glu
 100 105 110
 Gly Asp Ala Lys Asn Thr Val Ser Ser Val Thr Ile Met Pro Glu Ala
 115 120 125
 Asn Gly His Leu Lys Tyr Asp Lys Phe Asp Asp Leu Cys Gly Tyr Leu
 130 135 140
 Glu Glu Glu Glu Glu Ser Thr Thr Val Gln Lys Phe Ile Asp His Leu
 145 150 155 160
 Leu His Lys Asn Val Val Asp Ser Ala Met Met Glu Asp Leu Gly Arg
 165 170 175
 Lys Glu Asn Gln Asp Lys Lys Gln Gln Lys Asp
 180 185

<210> 615
 <211> 685
 <212> DNA
 <213> Homo sapiens

<400> 615
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 ggccatgaac gggccctagc gagggccgga ctcgcccccg tggccggatg cgacgaggcg
 120
 gggcggggag cgtgtgcagg gccattggta gccgcagctg tcattcttga tgatcgcaga
 180
 tccggcagga ttgcggggct agcagattcc aagacactat ctgcggccaa gagagaggcc
 240
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 gaatgcgacg ggttggggat gcaggaggca gatatcagcg gcttgaggcg tgccgtggtg
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 420
 gttcccgatc tgggaatgtg gaagggcgat tcagtgtgtg cgtgtgtggc agctgcctcc
 480

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 540
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 660
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<210> 616

<211> 213

<212> PRT

<213> Homo sapiens

<400> 616

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Ala	Arg	Ala	Gly	Leu	Gly	Pro	Val	Ala	Gly	Cys	Asp	Glu	Ala	Gly	Arg
			20					25					30		
Gly	Ala	Cys	Ala	Gly	Pro	Leu	Val	Ala	Ala	Ala	Val	Ile	Leu	Asp	Asp
		35					40					45			
Arg	Arg	Ser	Gly	Arg	Ile	Ala	Gly	Leu	Ala	Asp	Ser	Lys	Thr	Leu	Ser
		50				55					60				
Ala	Ala	Lys	Arg	Glu	Ala	Leu	Phe	Asn	Val	Ile	Met	Asp	Lys	Ala	Leu
65					70					75				80	
Ala	Val	Ser	Trp	Val	Arg	Val	Glu	Ala	Asp	Glu	Cys	Asp	Arg	Leu	Gly
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Met	Gln	Glu	Ala	Asp	Ile	Ser	Gly	Leu	Arg	Arg	Ala	Val	Val	Arg	Leu
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Gly	Val	Glu	Pro	Gly	Tyr	Val	Leu	Ser	Asp	Gly	Phe	Pro	Val	Asp	Gly
		115					120						125		
Leu	Thr	Val	Pro	Asp	Leu	Gly	Met	Trp	Lys	Gly	Asp	Ser	Val	Cys	Ala
		130				135					140				
Cys	Val	Ala	Ala	Ala	Ser	Ile	Val	Ala	Lys	Val	Ala	Arg	Asp	Arg	Ile
145					150					155				160	
Met	Ile	Ala	Met	Asp	Ala	Glu	Ile	Pro	Gly	Tyr	Asp	Phe	Ala	Val	His
			165						170					175	
Lys	Gly	Tyr	Ala	Thr	Ala	Leu	His	Gln	Arg	Arg	Leu	Lys	Glu	Leu	Gly
			180					185					190		
Pro	Ser	Arg	Gln	His	Arg	Met	Ser	Tyr	Ala	Asn	Val	Arg	Arg	Ala	Ala
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Arg	Leu	His	Ser	Ser											
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<210> 617

<211> 337

<212> DNA

<213> Homo sapiens

<400> 617

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<210> 618
 <211> 112
 <212> PRT
 <213> Homo sapiens

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 Arg Cys Arg Ser Thr Thr Ser Ser Ser Ala Pro Thr Ala Ser Ala Arg
 35 40 45
 Pro Cys Ser Ser Lys Thr Phe Pro Ala Phe Pro Glu Arg Ile Leu Arg
 50 55 60
 Asn Phe Asp Leu Ser Gln Gln Asp Ser Ala Leu Val Ile Ser Ser Ser
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<210> 619
 <211> 425
 <212> DNA
 <213> Homo sapiens

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<210> 620

<211> 137

<212> PRT

<213> Homo sapiens

<400> 620

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      20             25             30
Glu Arg Ala Ser Ile Ala Cys Trp Glu Phe His Leu Ala Ile Glu Lys
      35             40             45
Ser Ile Lys Val Met Ile His Ser Lys Ser Gly Ser Gly Lys His Gly
      50             55             60
His Asn Leu Asp Asp Leu Ile Glu His Leu Ser Lys Phe Glu Ser Gly
      65             70             75             80
Ile Asp Ser Ser Gly Leu Ala Gly Leu Pro Ser Asp Lys Asp Ala Ile
      85             90             95
Lys Leu Arg Tyr Ala Glu Met Ile Lys Thr Pro Ile Asp Ala Phe Glu
      100            105            110
Tyr Tyr Leu Ile Ala Ile Arg Phe Val Ala Asp Ile Val Ser Arg Leu
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Glu His Lys Ile Gly Ile Lys Asn Ala
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<210> 621

<211> 453

<212> DNA

<213> Homo sapiens

<400> 621

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<210> 622

<211> 151

<212> PRT

<213> Homo sapiens

<400> 622

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Pro Gly Lys Gly Ala Ile Leu Thr Asn Met Ser Leu Trp Trp Phe Asp

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 35 40 45
 Pro Val Glu Cys Val Val Arg Gly Tyr Leu Thr Gly Ser Gly Trp Ala
 50 55 60
 Glu Tyr Gln Arg Asn Gln Ala Val Cys Gly Ile Arg Leu Pro Glu Gly
 65 70 75 80
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 Lys Ala Pro Gln Gly Glu His Asp Glu Asn Ile Asp Tyr Leu Arg Leu
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 Val Glu Leu Val Gly Pro Xaa Xaa Ser Ala Gln Leu His Asp Leu Ser
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<210> 623

<211> 345

<212> DNA

<213> Homo sapiens

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<211> 111

<212> PRT

<213> Homo sapiens

<400> 624

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 20 25 30
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 35 40 45
 Gly Ala Glu Leu Val Lys Ser Val Val Asn Ser Ile Thr Cys Val Ser
 50 55 60
 Pro Leu Tyr Ile Glu Asp Phe Thr Thr Ile Glu Ile Gln Gly Leu Gly

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65              70              75              80
Leu His Cys Val Arg Leu Trp Ala Pro Gly Leu Leu Ala Leu Ser Leu
              85              90              95
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<210> 625
 <211> 339
 <212> DNA
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20     25     30
Gln Ala Gly Arg Ala Cys Leu Ser Trp Glu Val Val Gly Trp Val Gly
35     40     45
Ala Gln Cys Lys Gly Arg Gln Thr Cys Trp Ser Leu Gly Tyr Asp Pro
50     55     60
Glu Gln Ser Gly Gly Ala Glu Ser Ser Cys Leu Trp Ala Ser Ile Ala
65     70     75     80
Leu Pro Val Asn Tyr Arg Pro Trp Lys Asn His Leu Cys Ile Gln Gln
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<210> 627
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<211> 1294

<212> PRT

<213> Homo sapiens

<400> 628

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Val	Ser	Val	Ala	Ser	Lys	Asn	Pro	Gln	Val	Pro	Ser	Asp	Gly	Gly	Val
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Arg	Leu	Asn	Lys	Ser	Lys	Thr	Asp	Leu	Leu	Val	Asn	Asp	Asn	Pro	Asp
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Leu	Asp	Ser	Lys	Ile	Leu	Ala	Leu	His	Asn	Met	Val	Gln	Phe	Ser	His		
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 675 680 685
 Gln Val Glu Glu Glu Ile Ser Arg His Tyr Arg Arg Ala His Ser Cys
 690 695 700
 Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr Gln Ser Leu
 705 710 715 720
 Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp Ile Thr Thr
 725 730 735
 Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile Lys Glu Glu
 740 745 750
 Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro Asp Ser Lys
 755 760 765
 Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu Lys Leu Glu
 770 775 780
 Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser Ser Ser Asp
 785 790 795 800
 Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu Arg Gly Ser
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 Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro Val Ser Gly
 820 825 830
 Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn Val Glu Ala
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 Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu Thr Lys Gly
 850 855 860
 Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly Ala Leu Pro
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 Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp Glu Ser Gln
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 980 985 990
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 Lys His Pro Asn Tyr Ser Pro Pro Gly Ser Pro Ile Glu Lys Tyr Gln

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Asn Pro His Tyr Leu Ser His Val Pro Gly Leu Pro Asn Pro Cys Gln
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Asn Tyr Val Pro Tyr Pro Thr Phe Asn Leu Pro Pro His Phe Ser Ala
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Val Gly Ser Asp Asn Asp Ile Pro Leu Asp Leu Ala Ile Lys His Ser
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Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys Gln His Leu
      1250              1255              1260
Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg Gly Leu His
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<210> 629
 <211> 411
 <212> DNA
 <213> Homo sapiens

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<210> 630
 <211> 137
 <212> PRT
 <213> Homo sapiens

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<400> 630
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35           40           45
Thr Leu Pro Gly Arg Asn Trp Ile Asn Leu Gly Leu Leu Val Val Ile
50           55           60
Ile Ala Cys Gly Ile Trp Phe Ser Asn Val Ser Gly Gly Ile Ala Trp
65           70           75           80
Leu Pro Leu Ala Leu Leu Thr Leu Ala Ser Leu Phe Leu Gly Phe His
85           90           95
Phe Val Ala Ala Ile Gly Gly Ala Asp Met Pro Val Val Ile Ser Met
100          105          110
Leu Asn Ser Tyr Ser Gly Trp Ala Ala Ala Phe Ser Gly Phe Ser Leu
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His Ile Pro Val Leu Ile Val Thr Gly
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<210> 631
 <211> 275
 <212> DNA
 <213> Homo sapiens

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275

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<210> 632
 <211> 87
 <212> PRT
 <213> Homo sapiens

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20           25           30
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35           40           45
Glu Arg Asp Gln Tyr Lys Leu Met Ala Asn Gln Leu Arg Glu Arg His
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<210> 633
 <211> 420
 <212> DNA
 <213> Homo sapiens

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 420

<210> 634
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 634
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 Val Asp Ala Val Val Asn Ala Val Glu His Tyr Ser Glu Leu Thr Pro
 35 40 45
 Gln Leu Leu Thr Thr Gly Gly Thr Ser Asp Gly Arg Phe Ile Ala Gln
 50 55 60
 Met Gly Xaa Gln Val Val Glu Leu Gly Pro Val Asn Ala Thr Ile His
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<210> 635
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 <212> DNA
 <213> Homo sapiens

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<210> 636

<211> 619

<212> PRT

<213> Homo sapiens

<400> 636

Xaa Pro Asn Arg Gln Pro Ile Gly Ile Val Leu Thr Val Leu Gly Val
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 Val Val Leu Asp Phe Ser Ala Asp Ala Thr Glu Gly Pro Ile Arg Ala
 20 25 30
 Tyr Leu Leu Asp Val Val Asp Ser Glu Glu Gln Asp Met Ala Leu Asn
 35 40 45
 Ile His Ala Phe Ser Ala Gly Leu Gly Gly Ala Ile Gly Tyr Val Leu
 50 55 60
 Gly Gly Leu Asp Trp Thr Gln Thr Phe Leu Gly Ser Trp Phe Arg Thr
 65 70 75 80
 Gln Asn Gln Val Leu Phe Phe Phe Ala Ala Ile Ile Phe Thr Val Ser
 85 90 95
 Val Ala Leu His Leu Phe Ser Ile Asp Glu Glu Gln Tyr Ser Pro Gln
 100 105 110
 Gln Glu Arg Ser Ala Glu Glu Pro Gly Ala Leu Asp Gly Gly Glu Pro
 115 120 125
 His Gly Val Pro Ala Phe Pro Asp Glu Val Gln Ser Glu His Glu Leu
 130 135 140
 Ala Leu Asp Tyr Pro Asp Val Asp Ile Met Arg Ser Lys Ser Asp Ser
 145 150 155 160
 Ala Leu His Val Pro Asp Thr Ala Leu Asp Leu Glu Pro Glu Leu Leu
 165 170 175
 Phe Leu His Asp Ile Glu Pro Ser Ile Phe His Asp Ala Ser Tyr Pro
 180 185 190
 Ala Thr Pro Arg Ser Thr Ser Gln Glu Leu Ala Lys Thr Lys Leu Pro
 195 200 205
 Arg Leu Ala Thr Phe Leu Lys Glu Ala Ala Lys Glu Asp Glu Thr Leu
 210 215 220
 Leu Asp Asn His Leu Asn Glu Ala Lys Val Pro Asn Gly Ser Gly Ser
 225 230 235 240
 Pro Thr Lys Asp Ala Leu Gly Gly Tyr Thr Arg Val Asp Thr Lys Pro
 245 250 255
 Ser Ala Thr Ser Ser Ser Met Arg Arg Arg Arg His Ala Phe Arg Arg
 260 265 270
 Gln Ala Ser Ser Thr Phe Ser Tyr Tyr Gly Lys Leu Gly Ser His Cys
 275 280 285
 Tyr Arg Tyr Arg Arg Ala Asn Ala Val Val Leu Ile Lys Pro Ser Arg

290		295		300
Ser Met Ser Asp Leu Tyr Asp Met Gln Lys Arg Gln Arg Gln His Arg				
305		310		315
His Arg Asn Gln Ser Gly Ala Thr Thr Ser Ser Gly Asp Thr Glu Ser				320
	325		330	335
Glu Glu Gly Glu Gly Glu Thr Thr Val Arg Leu Leu Trp Leu Ser Met				
	340		345	350
Leu Lys Met Pro Arg Glu Leu Met Arg Leu Cys Leu Cys His Leu Leu				
	355		360	365
Thr Trp Phe Ser Val Ile Ala Glu Ala Val Phe Tyr Thr Asp Phe Met				
	370		375	380
Gly Gln Val Ile Phe Glu Gly Asp Pro Lys Ala Pro Ser Asn Ser Thr				
385		390		395
Ala Trp Gln Ala Tyr Asn Ala Gly Val Lys Met Gly Cys Trp Gly Leu				400
	405		410	415
Val Ile Tyr Ala Ala Thr Gly Ala Ile Cys Ser Ala Leu Leu Gln Lys				
	420		425	430
Tyr Leu Asp Asn Tyr Asp Leu Ser Val Arg Val Ile Tyr Val Leu Gly				
	435		440	445
Thr Leu Gly Phe Ser Val Gly Thr Ala Val Met Ala Met Phe Pro Asn				
	450		455	460
Val Tyr Val Ala Met Val Thr Ile Ser Thr Met Gly Ile Val Ser Met				
465		470		475
Ser Ile Ser Tyr Cys Pro Tyr Ala Leu Leu Gly Gln Tyr His Asp Ile				
	485		490	495
Lys Gln Tyr Ile His His Ser Pro Gly Asn Ser Lys Arg Gly Phe Gly				
	500		505	510
Ile Asp Cys Ala Ile Leu Ser Cys Gln Val Tyr Ile Ser Gln Ile Leu				
	515		520	525
Val Ala Ser Ala Leu Gly Gly Val Val Asp Ala Val Gly Thr Val Arg				
	530		535	540
Val Ile Pro Met Val Ala Ser Val Gly Ser Phe Leu Gly Phe Leu Thr				
545		550		555
Ala Thr Phe Leu Val Ile Tyr Pro Asp Val Ser Glu Glu Ala Lys Glu				
	565		570	575
Glu Gln Lys Gly Leu Ser Ser Pro Leu Ala Gly Glu Gly Arg Ala Gly				
	580		585	590
Gly Asn Ser Glu Lys Pro Thr Val Leu Lys Leu Thr Arg Lys Glu Gly				
	595		600	605
Leu Gln Gly Pro Val Glu Thr Glu Ser Val Val				
	610		615	

<210> 637

<211> 370

<212> DNA

<213> Homo sapiens

<400> 637

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 tctcgatcgg tgatgatctg gaaaggaaaa atcatcgtga ctactacatc acccgctact
 120
 acgcaaagac cgtcagttgg caggaaagtt ggttctctgt cccttaatcc atggtgtttt
 180

tgtaggccct tattatTTTT cggaatgggt cggtttattg cgattccagt attcctcact
 240
 gtgccgaata tcattaatat cggaatccaa gccgcgggtgg tggcgattat ggccttcggt
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 370

<210> 638
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 638
 Met Ile Trp Lys Gly Lys Ile Ile Val Thr Thr Thr Ser Pro Ala Thr
 1 5 10 15
 Thr Gln Arg Pro Ser Val Gly Arg Lys Val Gly Ser Trp Ser Leu Asn
 20 25 30
 Pro Trp Cys Phe Cys Arg Pro Leu Leu Phe Phe Gly Met Val Arg Phe
 35 40 45
 Ile Ala Ile Pro Val Phe Leu Thr Val Pro Asn Ile Ile Asn Ile Gly
 50 55 60
 Ile Gln Ala Ala Val Val Ala Ile Met Ala Phe Gly Met Thr Phe Val
 65 70 75 80
 Ile Val Thr Ser Gly Ile Asp Leu Ser Val Gly Ser Val Ala Ala Leu
 85 90 95
 Ser Ala Met

<210> 639
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 639
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 120
 gaggcggggg acgcgcaggt ctacgacttc tgtgacaacc aggtgcccgg aaccaccgag
 180
 aaggatcggg actactggcg ggacgtggga actatcgatg cctaccacga cgcgcacatg
 240
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 300
 atccaggaac aggcaccggg agcgaaattt
 330

<210> 640
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 640

```

Xaa Ala Ser Met Gly Asn Tyr Ile Phe Ser Arg Asp Ala Leu Val Glu
 1           5           10           15
Ala Leu Phe Ala Asp Ser Gln Ser Ala Glu Ser Arg His Asp Met Gly
          20           25           30
Gly Asp Ile Ile Pro Arg Phe Val Glu Ala Gly Asp Ala Gln Val Tyr
          35           40           45
Asp Phe Cys Asp Asn Gln Val Pro Gly Thr Thr Glu Lys Asp Arg Asp
          50           55           60
Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala Tyr His Asp Ala His Met
65           70           75           80
Asp Leu Val Ser Val Glu Pro Glu Phe Asn Leu Tyr Asn' Pro Asp Trp
          85           90           95
Pro Ile Trp Ser Ile Gln Glu Gln Ala Pro Gly Ala Lys Phe
          100           105           110

```

<210> 641

<211> 491

<212> DNA

<213> Homo sapiens

<400> 641

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120
ggcgacatcc accgcaacaa gcgcaaggtc ttctccaaga tcttcagcca cgaggccctg
180
gagagttacc tgcccaagat ccagctggtg atccaggaca cactgcgcgc ctggagcagc
240
caccgccagg ccatcaacgt gtaccaggag gcgcagaagc tgaccttcg catggccatc
300
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360
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480
ctgcagtga c
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```

<210> 642

<211> 163

<212> PRT

<213> Homo sapiens

<400> 642

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Arg Val Thr Gly Ala Glu Asn Val Arg Lys Ile Leu Met Gly Glu His
 1           5           10           15
His Leu Val Ser Thr Glu Trp Pro Arg Ser Thr Arg Met Leu Leu Gly
          20           25           30
Pro Asn Thr Val Ser Asn Ser Ile Gly Asp Ile His Arg Asn Lys Arg
          35           40           45
Lys Val Phe Ser Lys Ile Phe Ser His Glu Ala Leu Glu Ser Tyr Leu

```

```

      50              55              60
Pro Lys Ile Gln Leu Val Ile Gln Asp Thr Leu Arg Ala Trp Ser Ser
65
His Pro Glu Ala Ile Asn Val Tyr Gln Glu Ala Gln Lys Leu Thr Phe
      70              75              80
      85              90              95
Arg Met Ala Ile Arg Val Leu Leu Gly Phe Ser Ile Pro Glu Glu Asp
      100              105              110
Leu Gly His Leu Phe Glu Val Tyr Gln Gln Phe Val Asp Asn Val Phe
      115              120              125
Ser Leu Pro Val Asp Leu Pro Phe Ser Gly Tyr Arg Arg Gly Ile Gln
      130              135              140
Ala Arg Gln Ile Leu Gln Lys Gly Leu Glu Lys Ala Ile Arg Glu Lys
145              150              155              160
Leu Gln Cys

```

<210> 643

<211> 628

<212> DNA

<213> Homo sapiens

<400> 643

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nagatctttg acatctacgt ggtcacccgt gactacctgc ccctaggggc tgagcaggat
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120
tggtttgtcc gcaccaagcc caccaagtcc agcccctcac ggcagggctg ggtgtcacca
180
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420
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480
cagtgcgaca cggacgacga cgtggccatg tgcttcatca agaaccaggc ggcctttgag
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<210> 644

<211> 209

<212> PRT

<213> Homo sapiens

<400> 644

```

Xaa Ile Phe Asp Ile Tyr Val Val Thr Ala Asp Tyr Leu Pro Leu Gly
1           5           10           15
Ala Glu Gln Asp Ala Ile Thr Leu Arg Glu Gly Gln Tyr Val Glu Val

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	20		25		30										
Leu	Asp	Ala	Ala	His	Pro	Leu	Arg	Trp	Leu	Val	Arg	Thr	Lys	Pro	Thr
	35		40		45										
Lys	Ser	Ser	Pro	Ser	Arg	Gln	Gly	Trp	Val	Ser	Pro	Ala	Tyr	Leu	Asp
	50		55		60										
Arg	Arg	Leu	Lys	Leu	Ser	Pro	Glu	Trp	Gly	Ala	Ala	Glu	Ala	Pro	Glu
65			70		75									80	
Phe	Pro	Gly	Glu	Ala	Val	Ser	Glu	Asp	Glu	Tyr	Lys	Ala	Arg	Leu	Ser
			85		90									95	
Ser	Val	Ile	Gln	Glu	Leu	Leu	Ser	Ser	Glu	Gln	Ala	Phe	Val	Glu	Glu
	100		105		110										
Leu	Gln	Phe	Leu	Gln	Ser	His	His	Leu	Gln	His	Leu	Glu	Arg	Cys	Pro
	115		120		125										
His	Val	Pro	Ile	Ala	Val	Ala	Gly	Gln	Lys	Ala	Val	Ile	Phe	Arg	Asn
	130		135		140										
Val	Arg	Asp	Ile	Gly	Arg	Phe	His	Ser	Ser	Phe	Leu	Gln	Glu	Leu	Gln
145			150		155									160	
Gln	Cys	Asp	Thr	Asp	Asp	Asp	Val	Ala	Met	Cys	Phe	Ile	Lys	Asn	Gln
			165		170									175	
Ala	Ala	Phe	Glu	Gln	Tyr	Leu	Glu	Phe	Leu	Val	Gly	Arg	Val	Gln	Ala
	180		185		190										
Glu	Ser	Val	Val	Val	Ser	Thr	Ala	Ile	Gln	Glu	Phe	Tyr	Lys	Lys	Tyr
	195		200		205										

Ala

<210> 645

<211> 417

<212> DNA

<213> Homo sapiens

<400> 645

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120
caagctcagg aatggtgggg gagacagttg gagccacggc agggacaatg gagctcagaa
180
ggtccctctg tcateccctt tggaacccat tgatctggaa aatttggggc agtgtccttt
240
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300
tagatgttat aactaccccc attttccaga tgaagaaact gagcctctgg gatctgcgga
360
agctcccaga gctggagcag ttagtccctg ggcctacac tcacagcaca gtttccc
417

<210> 646

<211> 95

<212> PRT

<213> Homo sapiens

<400> 646

Met Val Gly Glu Thr Val Gly Ala Thr Ala Gly Thr Met Glu Leu Arg

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1           5           10           15
Arg Ser Leu Cys His Pro Phe Trp Asn Pro Leu Ile Trp Lys Ile Trp
          20           25           30
Gly Ser Val Leu Phe Arg Arg Tyr Trp Arg His Trp Leu Asp Ile Leu
          35           40           45
Gln Pro Ser Gln Glu Ala Gln Lys Val Asp Val Ile Thr Thr Pro Ile
          50           55           60
Phe Gln Met Lys Lys Leu Ser Leu Trp Asp Leu Arg Lys Leu Pro Glu
65           70           75           80
Leu Glu Gln Leu Val Pro Gly Pro Tyr Thr His Ser Thr Val Ser
          85           90           95

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<210> 647
 <211> 421
 <212> DNA
 <213> Homo sapiens

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<400> 647
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cgcgagcag ggtgatcaga taggcgatat ccgcctcggt cagttgcacg gtgtcgttat
120
cggtagccat gcgtggcgaa ctcttttggc atgggaaaat cgggtgaggc caacgggcac
180
agcaacagga cgtgtccctt gcggcacgtg gcaacacgtc agtatagcgc gtttccgccc
240
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300
tacgatagcc gcggcgccac caggttggtt acattccaaa cgcaacgcag gaaccgcgat
360
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420
c
421

```

<210> 648
 <211> 90
 <212> PRT
 <213> Homo sapiens

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<400> 648
Met Gly Lys Ser Gly Glu Ala Asn Gly His Ser Asn Arg Thr Cys Pro
1           5           10           15
Leu Arg His Val Ala Thr Arg Gln Tyr Ser Ala Phe Pro Pro Gly Phe
          20           25           30
Pro Leu Asn Glu Gly Lys Lys Ser Gly Thr His Pro Pro Ala Thr Ala
          35           40           45
Arg Trp Tyr Asp Ser Arg Gly Ala Thr Arg Leu Ala Thr Phe Gln Thr
          50           55           60
Gln Arg Arg Asn Pro His Glu Gln Arg Phe Ser Gln Gln Thr Pro Tyr
65           70           75           80
Asp Ala Gly Ser Arg Ala Phe Gln Cys Arg
          85           90

```

<210> 649
 <211> 563
 <212> DNA
 <213> Homo sapiens

<400> 649
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 gacctcagtg tccaggettg tgcatttagg ggctcaggtt tgggctctgt gcctatgagc
 120
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 180
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 240
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 300
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 360
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 420
 tgcacaggca cgcaactcaaa tccccccctc catgtcctcc gcctgtgcac attcaggcaa
 480
 cccgaaacac acaaagacac gggtggacac agcggccacc tgtgcacaca ggaggtagca
 540
 catggagcgc atctgacccc ggg
 563

<210> 650
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 650
 Met His Lys His Met Cys Ser Ser Glu Thr Gln Leu Leu Pro Leu Pro
 1 5 10 15
 Ser Leu Asp Leu Ser Val Gln Ala Cys Ala Phe Arg Gly Ser Gly Leu
 20 25 30
 Gly Ser Val Pro Met Ser Gln Ser Met Cys Ala Leu Ser Val Cys Leu
 35 40 45
 Ser Val Cys Gln Gln Pro Ser Arg Pro Gln Glu Gly Lys Ala Pro Met
 50 55 60
 Glu Gly Gly Gly Arg Glu Gly Gly Ser Val Asp Lys Phe Gln Cys Leu
 65 70 75 80
 Ala Phe Pro Pro Gly Asn Pro Glu Leu Gly Leu Ala Pro Pro Ser Leu
 85 90 95
 Pro Val Ser Leu Ala Gln Ala Arg Pro Phe
 100 105

<210> 651
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 651

gaattcttca acaagctctc ctgctctagg atcaaggata gacctataca aggtccaaac
 60
 cataatggag tccatggggt caaagttatc tcttgagct cagcagttga tggatatggt
 120
 taggtgtcag cagcggaatt gtattcccat tggagagcag cttcagtcgg tgttggggcaa
 180
 ttctggatac aagcatatga ttggactaca atcctcatct accttaggaa ccttaaacia
 240
 gtcgtcctcc acaccttttc cttttagaac tggattgaca tctgggaacg tgactgaaaa
 300
 cttacaagcg tacattgata aaagtacaca actgcctggt ggagagaatt c
 351

<210> 652

<211> 95

<212> PRT

<213> Homo sapiens

<400> 652

Met	Glu	Ser	Met	Gly	Ser	Lys	Leu	Ser	Pro	Gly	Ala	Gln	Gln	Leu	Met
1				5					10					15	
Asp	Met	Val	Arg	Cys	Gln	Gln	Arg	Asn	Cys	Ile	Pro	Ile	Gly	Glu	Gln
			20					25					30		
Leu	Gln	Ser	Val	Leu	Gly	Asn	Ser	Gly	Tyr	Lys	His	Met	Ile	Gly	Leu
		35				40					45				
Gln	Ser	Ser	Ser	Thr	Leu	Gly	Thr	Leu	Asn	Lys	Ser	Ser	Ser	Thr	Pro
	50				55				60						
Phe	Pro	Phe	Arg	Thr	Gly	Leu	Thr	Ser	Gly	Asn	Val	Thr	Glu	Asn	Leu
65					70				75					80	
Gln	Ala	Tyr	Ile	Asp	Lys	Ser	Thr	Gln	Leu	Pro	Gly	Gly	Glu	Asn	
				85				90						95	

<210> 653

<211> 399

<212> DNA

<213> Homo sapiens

<400> 653

nncccggtg gggctgggt ggggccagca tcagaggagg acatgaccaa gctgtgcaac
 60
 caccggcgga aagctgttgc tatggcaact ctgtaccgca gcatggagac cacctgttca
 120
 cactcttctc ctggagaggg agcgagcccc caaatgttcc aactgtgtc cccagggccc
 180
 cctctgccc gccctccctg tcgagttcct cctacaactc cacttaatgg gggctcctggc
 240
 tcccttcccc cagaaccacc ctcagtttcc caggccttcc ccactctagc aggccctggg
 300
 gggcttttcc cccaaggct tgetgacca gtcccttctg ggggcagtag cagcccccg
 360
 ttctcccaa ggggcaatgc cccctctcca gcccaccc
 399

<210> 654

<211> 133
 <212> PRT
 <213> Homo sapiens

<400> 654
 Xaa Pro Gly Gly Ala Gly Val Gly Pro Ala Ser Glu Glu Asp Met Thr
 1 5 10 15
 Lys Leu Cys Asn His Arg Arg Lys Ala Val Ala Met Ala Thr Leu Tyr
 20 25 30
 Arg Ser Met Glu Thr Thr Cys Ser His Ser Ser Pro Gly Glu Gly Ala
 35 40 45
 Ser Pro Gln Met Phe His Thr Val Ser Pro Gly Pro Pro Ser Ala Arg
 50 55 60
 Pro Pro Cys Arg Val Pro Thr Thr Pro Leu Asn Gly Gly Pro Gly
 65 70 75 80
 Ser Leu Pro Pro Glu Pro Pro Ser Val Ser Gln Ala Phe Pro Thr Leu
 85 90 95
 Ala Gly Pro Gly Gly Leu Phe Pro Pro Arg Leu Ala Asp Pro Val Pro
 100 105 110
 Ser Gly Gly Ser Ser Ser Pro Arg Phe Leu Pro Arg Gly Asn Ala Pro
 115 120 125
 Ser Pro Ala Pro Pro
 130

<210> 655
 <211> 368
 <212> DNA
 <213> Homo sapiens

<400> 655
 tgaaggaaat tctctatggc ttgtgttcat catgtagaac agcccatgag gagaatagga
 60
 gatgaggttg gaagtgcact gggatctggg ggaagaagcc cggggttcaa gactcagcta
 120
 ctgactgcat ggtgtcaaag gattcgggca tcctctctga ggctgagtct tcagatgaca
 180
 gtgagaacag ggacacctgc cctgcccttc tcacggggcg tgtgggcacc catgagcatg
 240
 cttgacaaat gcaagggtgcc atacaaacag gaactgcaca atctcacgc cgggcctact
 300
 cagcattgtt atttttacct ttacatctat atgaagatgt agttccattc cttttaactg
 360
 ttgttttc
 368

<210> 656
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 656
 Met Ala Cys Val His His Val Glu Gln Pro Met Arg Arg Ile Gly Asp
 1 5 10 15
 Glu Val Gly Ser Ala Leu Gly Ser Gly Gly Arg Ser Pro Gly Phe Lys

20 25 30
 Thr Gln Leu Leu Thr Ala Trp Cys Gln Arg Ile Arg Ala Ser Ser Leu
 35 40 45
 Arg Leu Ser Leu Gln Met Thr Val Arg Thr Gly Thr Pro Ala Leu Pro
 50 55 60
 Phe Ser Arg Gly Val Trp Ala Pro Met Ser Met Leu Asp Lys Cys Lys
 65 70 75 80
 Val Pro Tyr Lys Gln Glu Leu His Asn Leu Thr Ala Arg Pro Thr Gln
 85 90 95
 His Cys Tyr Phe Tyr Leu Tyr Ile Tyr Met Lys Met
 100 105

<210> 657
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 657
 gtcgaccacg gcatgaaaaa gccgggggatg atcctcatca acaacccctg gggcgagtcc
 60
 aacgaggcgg gcttcaagcg cgccctcgaa gagcgtggca tggccaacgc cgggtgctgag
 120
 cgtattcagg acagcgacct ggacgtggtg ccgcaattga ccccgctga aaaacgccgg
 180
 tgccgacacc ttgctgatgg tcggcaacgt cggcccttcg gcacaggtgg tcaagtcctt
 240
 ggaccgcatg ggttgggacg tgctgtggt gtctcactgg gggccggccg gnggtcgtt
 300
 tggcgagctg gcggggccta acgcttctcg
 330

<210> 658
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 658
 Met Lys Lys Pro Gly Met Ile Leu Ile Asn Asn Pro Trp Gly Glu Ser
 1 5 10 15
 Asn Glu Ala Gly Phe Lys Arg Ala Leu Glu Glu Arg Gly Met Ala Asn
 20 25 30
 Ala Gly Val Glu Arg Ile Gln Asp Ser Asp Leu Asp Val Val Pro Gln
 35 40 45
 Leu Thr Pro Pro Glu Lys Arg Arg Cys Arg His Leu Ala Asp Gly Arg
 50 55 60
 Gln Arg Arg Pro Phe Gly Thr Gly Gly Gln Val Pro Gly Pro His Gly
 65 70 75 80
 Leu Gly Arg Ala Cys Gly Val Ser Leu Gly Ala Gly Arg Xaa Ser Leu
 85 90 95
 Trp Arg Ala Gly Gly Ala
 100

<210> 659
 <211> 1505

<212> DNA

<213> Homo sapiens

<400> 659

gccaggatca tgtccaccac cacatgccaa gtggtggcgt tctctctgtc catcctgggg
60
ctggccggct gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac
120
aaccctgtca cctccgtggt ccagtacgaa gggctctgga ggagctgcgt gaggcagagt
180
tcaggcttca ccgaatgcag gccctatttc accatcctgg gacttccagc catgctgcag
240
gcagtgcgag ccctgatgat cgtaggcatc gtcctgggtg ccattggcct cctggtatcc
300
atctttgccc tgaaatgcat ccgcattggc agcatggagg actctgccaa agccaacatg
360
acactgacct ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct
420
gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat gtacaccggc
480
atgggtggga tgggtgcagac tgttcagacc aggtacacat ttggtgcggc tctgttcgtg
540
ggctgggtcg ctggaggcct cacactaatt ggggggtgtga tgatgtgcat cgcctgccgg
600
ggcctggcac cagaagaaac caactacaaa gccgtttctt atcatgcctc aggccacagt
660
gttgccata agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac
720
aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta tcttccaag
780
cacgactatg tgtaatgtc taagacctc cagcacgggc ggaagaaact cccggagagc
840
tcacccaaaa aacaaggaga tcccatctag atttcttctt gcttttgact cacagctgga
900
agttagaaaa gcctcgattt catctttgga gaggccaagt ggtcttagcc tcagtctctg
960
tctctaaata ttccaccata aaacagctga gttatttatg aattagaagc tatagctcac
1020
attttcaatc ctctatttct ttttttaaat ataactttct actctgatga gagaatgtgg
1080
ttttaatctc tctctcacat tttgatgatt tagacagact cccctcttc ctcctagtca
1140
ataaacccat tgatgatcta tttcccagct tatccccaag aaaacttttg aaaggaaaga
1200
gtagacccaa agatgttatt ttctgctgtt tgaattttgt ctccccaccc ccaacttggc
1260
tagtaataaa cacttactga agaagaagca ataagagaaa gatatttgta atctctccag
1320
cccatgatct cggttttctt aactgtgat cttaaaagt accaaaccaa agtcattttc
1380
agtttgaggc aaccaaactt ttctactgct gttgacatct tcttattaca gcaacaccat
1440
tctaggagtt tctgagctc tccactggag tcttccctt ctgtcgtctt ctgcgagcgg
1500

taccc
1505

<210> 660
<211> 261
<212> PRT
<213> Homo sapiens

<400> 660
Met Ser Thr Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile Leu
1 5 10 15
Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp Ser Thr
20 25 30
Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln Tyr Glu Gly
35 40 45
Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe Thr Glu Cys Arg
50 55 60
Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met Leu Gln Ala Val Arg
65 70 75 80
Ala Leu Met Ile Val Gly Ile Val Leu Gly Ala Ile Gly Leu Leu Val
85 90 95
Ser Ile Phe Ala Leu Lys Cys Ile Arg Ile Gly Ser Met Glu Asp Ser
100 105 110
Ala Lys Ala Asn Met Thr Leu Thr Ser Gly Ile Met Phe Ile Val Ser
115 120 125
Gly Leu Cys Ala Ile Ala Gly Val Ser Val Phe Ala Asn Met Leu Val
130 135 140
Thr Asn Phe Trp Met Ser Thr Ala Asn Met Tyr Thr Gly Met Gly Gly
145 150 155 160
Met Val Gln Thr Val Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe
165 170 175
Val Gly Trp Val Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met
180 185 190
Cys Ile Ala Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala
195 200 205
Val Ser Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly
210 215 220
Phe Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
225 230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro Ser
245 250 255
Lys His Asp Tyr Val
260

<210> 661
<211> 451
<212> DNA
<213> Homo sapiens

<400> 661
nnacgcgtgt agtttgtgta tcggcgcgga actcgccgcg tctgatctcg aggagcttcc
60
cccatggacg agattttaac cttgcttgcc ggaggcgggtg acgacgagcc agagtggcat
120

gacaaggcat tatgtgcccc gactgatccg gaggcattct tccctgaaaa ggggtggatcc
 180
 acccgtgagg ccaagcgcac ctgtgagtcc tgtgagggtcc gccaggagtg cttggagtag
 240
 gcccttgcca atgacgagag gttcgggaatc tggggcggat tgtccgagat ggagaggcgt
 300
 cggctgcgca agcggggcgtg acctgacgtc ggagcgcggg tattgacacg gcccggtaaa
 360
 atgccctgtc tgcccgggat ggctgtctgc acgatgcggc atatgcatg atcgacagc
 420
 tgggtgtgcat cccgtgctcc atgacgtcga c
 451

<210> 662
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 662
 Met Asp Glu Ile Leu Thr Leu Leu Ala Gly Gly Gly Asp Asp Glu Pro
 1 5 10 15
 Glu Trp His Asp Lys Ala Leu Cys Ala Gln Thr Asp Pro Glu Ala Phe
 20 25 30
 Phe Pro Glu Lys Gly Gly Ser Thr Arg Glu Ala Lys Arg Ile Cys Glu
 35 40 45
 Ser Cys Glu Val Arg Gln Glu Cys Leu Glu Tyr Ala Leu Ala Asn Asp
 50 55 60
 Glu Arg Phe Gly Ile Trp Gly Gly Leu Ser Glu Met Glu Arg Arg Arg
 65 70 75 80
 Leu Arg Lys Arg Ala
 85

<210> 663
 <211> 552
 <212> DNA
 <213> Homo sapiens

<400> 663
 ctcgagcgtc tcgacgccga cgccgcccag ggagccaagg aagacctctc gcagcgcgac
 60
 ccctacgacg tgctcgtcgt aggggcgggt cccgccgggt ccgcggccgc cgtgtacgcg
 120
 gctcgtaagg gcattcgac cgccatgggtc gggctctcgga tcggcggcca ggtactcgat
 180
 accgaggcca tcgacaacct catctcgggt ccgcacacca ccggtccgcg tctggccgac
 240
 gccctccgca gccacgtcaa cgactacaac attgacgtta ttgacgtca gaccgccagc
 300
 gccatagaga ccaccggcgg tatgaccacc gtgcatctga ccgacggcga cctgcggggc
 360
 cgctcagtca tcgtggccac cgggtgccgc tggcgcaacc ttggcgtacc tggcgaggag
 420
 gaataccgca ccaagggtgt gacctactgc ccgcactgcg atggcccgt attcacaggc
 480

aaaaaggtgg ccgtcgtcgg aggtggaaac tccggtattg aggccgctat cgacctcgcc
 540
 ggcgtcgtcg ac
 552

<210> 664
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 664
 Leu Glu Arg Leu Asp Ala Asp Ala Ala Gln Gly Ala Lys Glu Asp Leu
 1 5 10 15
 Ser Gln Arg Asp Pro Tyr Asp Val Leu Val Val Gly Ala Gly Pro Ala
 20 25 30
 Gly Ala Ala Ala Ala Val Tyr Ala Ala Arg Lys Gly Ile Arg Thr Ala
 35 40 45
 Met Val Gly Ser Arg Ile Gly Gly Gln Val Leu Asp Thr Glu Ala Ile
 50 55 60
 Asp Asn Leu Ile Ser Val Pro His Thr Thr Gly Pro Arg Leu Ala Asp
 65 70 75 80
 Ala Leu Arg Ser His Val Asn Asp Tyr Asn Ile Asp Val Ile Glu Arg
 85 90 95
 Gln Thr Ala Ser Ala Ile Glu Thr Thr Gly Gly Met Thr Thr Val His
 100 105 110
 Leu Thr Asp Gly Asp Leu Arg Ala Arg Ser Val Ile Val Ala Thr Gly
 115 120 125
 Ala Arg Trp Arg Asn Leu Gly Val Pro Gly Glu Glu Glu Tyr Arg Thr
 130 135 140
 Lys Gly Val Thr Tyr Cys Pro His Cys Asp Gly Pro Leu Phe Thr Gly
 145 150 155 160
 Lys Lys Val Ala Val Val Gly Gly Gly Asn Ser Gly Ile Glu Ala Ala
 165 170 175
 Ile Asp Leu Ala Gly Val Val Asp
 180

<210> 665
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 665
 acgcgtacag ttccgctcgg aggttgaaca ccacgatcgg tgtaccgggc acttcgctga
 60
 acacgctctt catttcgccc ggcagcagtt cggcgccggc gcagacaaag gtccaggcct
 120
 cgctcacgcg gtggccccgg ccagcggctt ttccaggatc tcgaaacgca ggtcgtcgcg
 180
 cttgggggatg ccgaatcggt cgtcgccata cgggaacggc ttcttgatgc cgggtgcgcag
 240
 gtagccgcgg cgctcgtaga agcgatcaga tcgcgcgcac gtcgatcact gtcattctgca
 300
 ttaccggcac gttccattcg cgcgcggcgt gggcttcggc ggcgtccatc aa
 352

<210> 666
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 666
 Met Glu Arg Ala Gly Asn Ala Asp Asp Ser Asp Arg Arg Ala Arg Asp
 1 5 10 15
 Leu Ile Ala Ser Thr Ser Ala Ala Ala Thr Cys Ala Pro Ala Ser Arg
 20 25 30
 Ser Arg Ser Arg Met Ala Thr Asn Asp Ser Ala Ser Pro Ser Ala Thr
 35 40 45
 Thr Cys Val Ser Arg Ser Trp Lys Ser Arg Trp Pro Gly Pro Pro Arg
 50 55 60
 Glu Arg Gly Leu Asp Leu Cys Leu Arg Arg Arg Arg Thr Ala Ala Gly
 65 70 75 80
 Arg Asn Glu Glu Arg Val Arg Arg Ser Asp Arg Tyr Thr Asp Arg Gly
 85 90 95
 Val Gln Pro Arg Arg Arg Thr Val Arg
 100 105

<210> 667
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 667
 nacgcgtacg aatcggtggt gcgtcgcaac ccaggggagg ccgagttcca ccaggctgtg
 60
 cgaggagatct ttgaatctct cggcccgggtg ctcgacaaga atccgcagta cgtggaggca
 120
 gccgtgttgt cgcgcacatctg cgaaccggaa cgccagatca ttttccgggt gccgtgggtt
 180
 gacgacgagg gcaagatccg tatcaaccgt ggcttccgctg ttgaatatc gtcggtactg
 240
 gggccgtata aggggtggatt gcgattccac cctcgggtgt acttaggaac gattaagtcc
 300
 cttggttttg agcagatctt caaaaatgct ctgactggca tgccgatcgg tggcgcgaaag
 360
 ggtgggtcgg actttgatcc ccatgacgct t
 391

<210> 668
 <211> 130
 <212> PRT
 <213> Homo sapiens

<400> 668
 Xaa Ala Tyr Glu Ser Val Leu Arg Arg Asn Pro Gly Glu Ala Glu Phe
 1 5 10 15
 His Gln Ala Val Arg Glu Ile Phe Glu Ser Leu Gly Pro Val Leu Asp
 20 25 30
 Lys Asn Pro Gln Tyr Val Glu Ala Ala Val Leu Ser Arg Ile Cys Glu

```

      35          40          45
Pro Glu Arg Gln Ile Ile Phe Arg Val Pro Trp Val Asp Asp Glu Gly
  50          55          60
Lys Ile Arg Ile Asn Arg Gly Phe Arg Val Glu Tyr Ser Ser Val Leu
  65          70          75          80
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Tyr Leu Gly
      85          90          95
Thr Ile Lys Phe Leu Gly Phe Glu Gln Ile Phe Lys Asn Ala Leu Thr
      100          105          110
Gly Met Pro Ile Gly Gly Ala Lys Gly Gly Ser Asp Phe Asp Pro His
      115          120          125
Asp Ala
      130

```

<210> 669

<211> 707

<212> DNA

<213> Homo sapiens

<400> 669

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nngagtccgt tccccgtcta agctcatcgt ggtggtgctg gcatggccgt caacaaggga
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attgagaaca cccttgctgc cttcggccac gcggtcgagg tgggatgcac ctaccttgaa
  120
actgacgttc acgcgaccag cgacgggggtg ctagtggcct tccacgatcc gatactcgat
  180
cgcgtcactg aatcaggcgg agtcacgcc gccatgccgt ggcacaaggt caaacaagcc
  240
aaggttgggtg gcgaaccgat cccacacctta gatgagattt tcgacgcctt tcccgcgcg
  300
ttcatcaata tcgacatcaa gcatgatggc gccaccatgc cgctcatcga cgttcttttc
  360
cgtcaccggg cttggagtcg ggtttgcgtc gggtcgttca gcagtaaagc catccagacc
  420
ttcgcgcgcc tggttcaggg acgcactgcg actgcagtgg ggtcgggtggg agtcnnggct
  480
gggctgtcat cagccctcat agcatgcaga tggcacagtc ccatgggaat gcgtaccagg
  540
tgccgcaccg cttgaccggg tnatgggggtg ccccttgatga caccgacctt cattaaagct
  600
gcccatcgtc agggggcgagc tgttcatgtc tggacgggta atgagatctc tgaggctcga
  660
gaactgatgg atatgggggt cgacggcatc gtcacagatc gtccgga
  707

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<210> 670

<211> 170

<212> PRT

<213> Homo sapiens

<400> 670

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Met Ala Val Asn Lys Gly Ile Glu Asn Thr Leu Ala Ala Phe Gly His
  1          5          10          15
Ala Val Glu Val Gly Cys Thr Tyr Leu Glu Thr Asp Val His Ala Thr

```

```

          20          25          30
Ser Asp Gly Val Leu Val Ala Phe His Asp Pro Ile Leu Asp Arg Val
          35          40          45
Thr Glu Ser Gly Gly Val Ile Ala Ala Met Pro Trp His Lys Val Lys
          50          55          60
Gln Ala Lys Val Gly Gly Glu Pro Ile Pro Thr Leu Asp Glu Ile Phe
65          70          75          80
Asp Ala Phe Pro Asp Ala Phe Ile Asn Ile Asp Ile Lys His Asp Gly
          85          90          95
Ala Thr Met Pro Leu Ile Asp Val Leu Ser Arg His Arg Ala Trp Ser
          100          105          110
Arg Val Cys Val Gly Ser Phe Ser Ser Lys Arg Ile Gln Thr Phe Arg
          115          120          125
Arg Leu Val Gln Gly Arg Thr Ala Thr Ala Val Gly Ser Val Gly Val
          130          135          140
Xaa Ala Gly Leu Ser Ser Ala Leu Ile Ala Cys Arg Trp His Ser Pro
145          150          155          160
Met Gly Met Arg Thr Arg Cys Arg Thr Ala
          165          170

```

<210> 671

<211> 444

<212> DNA

<213> Homo sapiens

<400> 671

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acgcgtgggc cttcggggttg atgggatcag aaggggacgg gacctgtaga aaggggcctg
60
cagctcagag catggggcgg ccttggtctca ctacgcctgc agctgtgaat tcgttctccg
120
gtgctggaga gggatctggt tatctccatt ctcttgcttc cacgtggaaa ggaaggacgt
180
gcgctctcat cctacgtggt ttgagaaatc gcattgtccc cagctctgcg ggaggatctg
240
gggacgcagt ggggaaccag acaggcagtt ggaggtctag tgcgcgccag aagccagttc
300
ccaccaggg tgccatttgc tgggcgcctt agggagctgc gtgggcatcc agaggagtga
360
gtcgccccct gctctgctca gtgccactt ccccgggcag ggcaggcggtt attaacgtag
420
agggagaaca cccatgcaca caac
444

```

<210> 672

<211> 103

<212> PRT

<213> Homo sapiens

<400> 672

```

Met Gly Ser Glu Gly Asp Gly Thr Cys Arg Lys Gly Pro Ala Ala Gln
  1          5          10          15
Ser Met Gly Arg Pro Trp Leu Thr Thr Pro Ala Ala Val Asn Ser Phe
          20          25          30
Ser Gly Ala Gly Glu Gly Ser Gly Tyr Leu His Ser Leu Val Ser Thr

```

```

      35          40          45
Trp Lys Gly Arg Thr Cys Ala Leu Ile Leu Arg Val Leu Arg Asn Arg
      50          55          60
Ile Val Pro Ser Ser Ala Gly Gly Ser Gly Asp Ala Val Gly Asn Gln
65          70          75          80
Thr Gly Ser Trp Arg Ser Ser Ala Arg Gln Lys Pro Val Pro Thr Gln
      85          90          95
Gly Ala Ile Cys Trp Ala Pro
      100

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<210> 673
 <211> 452
 <212> DNA
 <213> Homo sapiens

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<400> 673
acgcgtccct gcagaaatcc tctcggccta ggcatccgc aagatgtggc agggcatgca
60
ccgtgaaagc cttcaagtct gccgcagcaa gaccgcacgc ctgctgaaat tcgcagttgt
120
gccgcggtcc ctgatgcgga caaactcggc caccacgatc agcctgacgc ttgcggacca
180
acgttcaaat actgtgcact tgaaacgtcc gggccgcacac acctgggtga ctttgtgcga
240
ccgacattac ttatgttcac gctctttcag ttcttgtcaa taccgtatatt ttcgtcgacg
300
tctccatcag aaaaatgtcg gtgttaccgc accgcagacg atgcgtaccc ttgcgctgac
360
gatggaggcc ttgaaaagtg cattagccac tactgggcca atctacggca aaaagctggt
420
actaggcggt gattggggag gcccgtagtg gc
452

```

<210> 674
 <211> 134
 <212> PRT
 <213> Homo sapiens

```

<400> 674
Met Trp Gln Gly Met His Arg Glu Ser Leu Gln Val Cys Arg Ser Lys
1          5          10          15
Thr Ala Arg Leu Leu Lys Phe Ala Val Val Pro Arg Ser Leu Met Arg
      20          25          30
Thr Asn Ser Ala Thr Thr Ile Ser Leu Thr Leu Ala Asp Gln Arg Ser
      35          40          45
Asn Thr Val His Leu Lys Arg Pro Gly Arg Ile Thr Trp Val Thr Leu
50          55          60
Cys Asp Arg His Tyr Leu Cys Ser Arg Ser Phe Ser Ser Cys Gln Tyr
65          70          75          80
Arg Ile Phe Arg Arg Arg Leu His Gln Lys Asn Val Gly Val Thr Ala
      85          90          95
Pro Gln Thr Met Arg Thr Leu Ala Leu Thr Met Glu Ala Leu Lys Ser
100          105          110
Ala Leu Ala Thr Thr Gly Arg Ile Tyr Gly Lys Lys Leu Leu Leu Gly

```


115
Gly Asp Trp Gly Gly Pro
130

120

125

<210> 675
<211> 8564
<212> DNA
<213> Homo sapiens

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 1205 1210 1215
 Arg Val Pro Ser Asp Ser Ala Ile Thr Tyr Arg Gly Ser Ile Thr His
 1220 1225 1230
 Gly Thr Pro Ala Asp Val Leu Tyr Lys Gly Thr Ile Thr Arg Ile Ile
 1235 1240 1245
 Gly Glu Asp Ser Pro Ser Arg Leu Asp Arg Gly Arg Glu Asp Ser Leu
 1250 1255 1260
 Pro Lys Gly His Val Ile Tyr Glu Gly Lys Lys Gly His Val Leu Ser
 1265 1270 1275 1280
 Tyr Glu Gly Gly Met Ser Val Thr Gln Cys Ser Lys Glu Asp Gly Arg
 1285 1290 1295
 Ser Ser Ser Gly Pro Pro His Glu Thr Ala Ala Pro Lys Arg Thr Tyr
 1300 1305 1310
 Asp Met Met Glu Gly Arg Val Gly Arg Ala Ile Ser Ser Ala Ser Ile
 1315 1320 1325
 Glu Gly Leu Met Gly Arg Ala Ile Pro Pro Glu Arg His Ser Pro His
 1330 1335 1340
 His Leu Lys Glu Gln His His Ile Arg Gly Ser Ile Thr Gln Gly Ile
 1345 1350 1355 1360
 Pro Arg Ser Tyr Val Glu Ala Gln Glu Asp Tyr Leu Arg Arg Glu Ala
 1365 1370 1375
 Lys Leu Leu Lys Arg Glu Gly Thr Pro Pro Pro Pro Pro Pro Ser Arg
 1380 1385 1390
 Asp Leu Thr Glu Ala Tyr Lys Thr Gln Ala Leu Gly Pro Leu Lys Leu
 1395 1400 1405
 Lys Pro Ala His Glu Gly Leu Val Ala Thr Val Lys Glu Ala Gly Arg
 1410 1415 1420
 Ser Ile His Glu Ile Pro Arg Glu Glu Leu Arg His Thr Pro Glu Leu
 1425 1430 1435 1440
 Pro Leu Ala Pro Arg Pro Leu Lys Glu Gly Ser Ile Thr Gln Gly Thr
 1445 1450 1455
 Pro Leu Lys Tyr Asp Thr Gly Ala Ser Thr Thr Gly Ser Lys Lys His

1460 1465 1470
 Asp Val Arg Ser Leu Ile Gly Ser Pro Gly Arg Thr Phe Pro Pro Val
 1475 1480 1485
 His Pro Leu Asp Val Met Ala Asp Ala Arg Ala Leu Glu Arg Ala Cys
 1490 1495 1500
 Tyr Glu Glu Ser Leu Lys Ser Arg Pro Gly Thr Ala Ser Ser Ser Gly
 1505 1510 1515 1520
 Gly Ser Ile Ala Arg Gly Ala Pro Val Ile Val Pro Glu Leu Gly Lys
 1525 1530 1535
 Pro Arg Gln Ser Pro Leu Thr Tyr Glu Asp His Gly Ala Pro Phe Ala
 1540 1545 1550
 Gly His Leu Pro Arg Gly Ser Pro Val Thr Thr Arg Glu Pro Thr Pro
 1555 1560 1565
 Arg Leu Gln Glu Gly Ser Leu Ser Ser Ser Lys Ala Ser Gln Asp Arg
 1570 1575 1580
 Lys Leu Thr Ser Thr Pro Arg Glu Ile Ala Lys Ser Pro His Ser Thr
 1585 1590 1595 1600
 Val Pro Glu His His Pro His Pro Ile Ser Pro Tyr Glu His Leu Leu
 1605 1610 1615
 Arg Gly Val Ser Gly Val Asp Leu Tyr Arg Ser His Ile Pro Leu Ala
 1620 1625 1630
 Phe Asp Pro Thr Ser Ile Pro Arg Gly Ile Pro Leu Asp Ala Ala Ala
 1635 1640 1645
 Ala Tyr Tyr Leu Pro Arg His Leu Ala Pro Asn Pro Thr Tyr Pro His
 1650 1655 1660
 Leu Tyr Pro Pro Tyr Leu Ile Arg Gly Tyr Pro Asp Thr Ala Ala Leu
 1665 1670 1675 1680
 Glu Asn Arg Gln Thr Ile Ile Asn Asp Tyr Ile Thr Ser Gln Gln Met
 1685 1690 1695
 His His Asn Thr Ala Thr Ala Met Ala Gln Arg Ala Asp Met Leu Arg
 1700 1705 1710
 Gly Leu Ser Pro Arg Glu Ser Ser Leu Ala Leu Asn Tyr Ala Ala Gly
 1715 1720 1725
 Pro Arg Gly Ile Ile Asp Leu Ser Gln Val Pro His Leu Pro Val Leu
 1730 1735 1740
 Val Pro Pro Thr Pro Gly Thr Pro Ala Thr Ala Met Asp Arg Leu Ala
 1745 1750 1755 1760
 Tyr Leu Pro Thr Ala Pro Gln Pro Phe Ser Ser Arg His Ser Ser Ser
 1765 1770 1775
 Pro Leu Ser Pro Gly Gly Pro Thr His Leu Thr Lys Pro Thr Thr Thr
 1780 1785 1790
 Ser Ser Ser Glu Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 1795 1800 1805
 Arg Glu Arg Glu Lys Ser Ile Leu Thr Ser Thr Thr Val Glu His
 1810 1815 1820
 Ala Pro Ile Trp Arg Pro Gly Thr Glu Gln Ser Ser Gly Ser Ser Gly
 1825 1830 1835 1840
 Ser Ser Gly Gly Gly Gly Gly Ser Ser Ser Arg Pro Ala Ser His Ser
 1845 1850 1855
 His Ala His Gln His Ser Pro Ile Ser Pro Arg Thr Gln Asp Ala Leu
 1860 1865 1870
 Gln Gln Arg Pro Ser Val Leu His Asn Thr Gly Met Lys Gly Ile Ile
 1875 1880 1885
 Thr Ala Val Glu Pro Ser Thr Pro Thr Val Leu Arg Ser Thr Ser Thr

1890	1895	1900
Ser Ser Pro Val Arg Pro Ala Ala Thr Phe Pro Pro Ala Thr His Cys		
1905	1910	1915
Pro Leu Gly Gly Thr Leu Asp Gly Val Tyr Pro Thr Leu Met Glu Pro		1920
	1925	1930
Val Leu Leu Pro Lys Glu Ala Pro Arg Val Ala Arg Pro Glu Arg Pro		1935
	1940	1945
Arg Ala Asp Thr Gly His Ala Phe Leu Ala Lys Pro Pro Ala Arg Ser		1950
	1955	1960
Gly Leu Glu Pro Ala Ser Ser Pro Ser Lys Gly Ser Glu Pro Arg Pro		1965
	1970	1975
Leu Val Pro Pro Val Ser Gly His Ala Thr Ile Ala Arg Thr Pro Ala		1980
1985	1990	1995
Lys Asn Leu Ala Pro His His Ala Ser Pro Asp Pro Pro Ala Pro Pro		2000
	2005	2010
Ala Ser Ala Ser Asp Pro His Arg Glu Lys Thr Gln Ser Lys Pro Phe		2015
	2020	2025
Ser Ile Gln Glu Leu Glu Leu Arg Ser Leu Gly Tyr His Gly Ser Ser		2030
	2035	2040
Tyr Ser Pro Glu Gly Val Glu Pro Val Ser Pro Val Ser Ser Pro Ser		2045
	2050	2055
Leu Thr His Asp Lys Gly Leu Pro Lys His Leu Glu Glu Leu Asp Lys		2060
2065	2070	2075
Ser His Leu Glu Gly Glu Leu Arg Pro Lys Gln Pro Gly Pro Val Lys		2080
	2085	2090
Leu Gly Gly Glu Ala Ala His Leu Pro His Leu Arg Pro Leu Pro Glu		2095
	2100	2105
Ser Gln Pro Ser Ser Ser Pro Leu Leu Gln Thr Ala Pro Gly Val Lys		2110
	2115	2120
Gly His Gln Arg Val Val Thr Leu Ala Gln His Ile Ser Glu Val Ile		2125
	2130	2135
Thr Gln Asp Tyr Thr Arg His His Pro Gln Gln Leu Ser Ala Pro Leu		2140
2145	2150	2155
Pro Ala Pro Leu Tyr Ser Phe Pro Gly Ala Ser Cys Pro Val Leu Asp		2160
	2165	2170
Leu Arg Arg Pro Pro Ser Asp Leu Tyr Leu Pro Pro Pro Asp His Gly		2175
	2180	2185
Ala Pro Ala Arg Gly Ser Pro His Ser Glu Gly Gly Lys Arg Ser Pro		2190
	2195	2200
Glu Pro Asn Lys Thr Ser Val Leu Gly Gly Gly Glu Asp Gly Ile Glu		2205
	2210	2215
Pro Val Ser Pro Pro Glu Gly Met Thr Glu Pro Gly His Ser Arg Ser		2220
2225	2230	2235
Ala Val Tyr Pro Leu Leu Tyr Arg Asp Gly Glu Gln Thr Glu Pro Ser		2240
	2245	2250
Arg Met Gly Ser Lys Ser Pro Gly Asn Thr Ser Gln Pro Pro Ala Phe		2255
	2260	2265
Phe Ser Lys Leu Thr Glu Ser Asn Ser Ala Met Val Lys Ser Lys Lys		2270
	2275	2280
Gln Glu Ile Asn Lys Lys Leu Asn Thr His Asn Arg Asn Glu Pro Glu		2285
	2290	2295
Tyr Asn Ile Ser Gln Pro Gly Thr Glu Ile Phe Asn Met Pro Ala Ile		2300
2305	2310	2315
Thr Gly Thr Gly Leu Met Thr Tyr Arg Ser Gln Ala Val Gln Glu His		2320

2325 2330 2335
 Ala Ser Thr Asn Met Gly Leu Glu Ala Ile Ile Arg Lys Ala Leu Met
 2340 2345 2350
 Gly Lys Tyr Asp Gln Trp Glu Glu Ser Pro Pro Leu Ser Ala Asn Ala
 2355 2360 2365
 Phe Asn Pro Leu Asn Ala Ser Ala Ser Leu Pro Ala Ala Met Pro Ile
 2370 2375 2380
 Thr Ala Ala Asp Gly Arg Ser Asp His Thr Leu Thr Ser Pro Gly Gly
 2385 2390 2395 2400
 Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala Lys
 2405 2410 2415
 Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val Ser
 2420 2425 2430
 Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr Asn
 2435 2440 2445
 Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe Pro
 2450 2455 2460
 Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser Pro
 2465 2470 2475 2480
 Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro His
 2485 2490 2495
 His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr Glu
 2500 2505 2510
 Thr Leu Ser Asp Ser Glu
 2515

<210> 677
 <211> 345
 <212> DNA
 <213> Homo sapiens

<400> 677
 gtaatgcaag gtgaacgccc aatggctgcg cagaacaaga gcattggtca gttcaccctt
 60
 gagggatatag ctccggcacg ccgtgggtgtt ccacagattg aagttacttt cgatatcgat
 120
 gccaacggta tcttgaatgt gagcgcaaag gataaggcta ccggtaagga acagaagatt
 180
 cgcatacgaag cttcaagtgg tttgagtcag gaagaaatcg acagaatgaa agctgaggca
 240
 gaacagaatg cagcagcagg caaggctgaa cgcgaaaaga ttgataagct gaaccaagct
 300
 gactcaatga tttccccccc cgaaaactcc tgaaagacaa cgatn
 345

<210> 678
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 678
 Val Met Gln Gly Glu Arg Pro Met Ala Ala Gln Asn Lys Ser Ile Gly
 1 5 10 15
 Gln Phe Thr Leu Glu Gly Ile Ala Pro Ala Arg Arg Gly Val Pro Gln

```

      20      25      30
Ile Glu Val Thr Phe Asp Ile Asp Ala Asn Gly Ile Leu Asn Val Ser
      35      40      45
Ala Lys Asp Lys Ala Thr Gly Lys Glu Gln Lys Ile Arg Ile Glu Ala
      50      55      60
Ser Ser Gly Leu Ser Gln Glu Glu Ile Asp Arg Met Lys Ala Glu Ala
65      70      75      80
Glu Gln Asn Ala Ala Ala Gly Lys Ala Glu Arg Glu Lys Ile Asp Lys
      85      90      95
Leu Asn Gln Ala Asp Ser Met Ile Ser Pro Pro Glu Asn Ser
      100      105      110

```

<210> 679

<211> 362

<212> DNA

<213> Homo sapiens

<400> 679

```

acgcgtgacg tcaccgctcc atggggaaga tgacgactat ccctgtgaaa gtaaagcata
60
atgggaaaaa tgtacgttaa atgtgctaac gcgcagtatg atgtatctat gaatcttgag
120
ggtacaggcc tggatttcaa gcgtgccatt gctgacgtca cgcatgtgcc acccgaacgc
180
caaaaagtac tcatcaaggg aggattgcta aaagacgata cccattagg taaagtgggt
240
gcgcgtgcag gacagcagtt catggtgctg ggtgctgtgg gtgagctgcc caaggcccca
300
gaaaaacctg tgctgttcct ggaggatttg ccggaagacg agctcaacaa ggctaaggat
360
cc
362

```

<210> 680

<211> 100

<212> PRT

<213> Homo sapiens

<400> 680

```

Met Gly Lys Met Tyr Val Lys Cys Ala Asn Ala Gln Tyr Asp Val Ser
 1      5      10      15
Met Asn Leu Glu Gly Thr Gly Leu Asp Phe Lys Arg Ala Ile Ala Asp
      20      25      30
Val Thr His Val Pro Pro Glu Arg Gln Lys Val Leu Ile Lys Gly Gly
      35      40      45
Leu Leu Lys Asp Asp Thr Pro Leu Gly Lys Val Gly Ala Arg Ala Gly
      50      55      60
Gln Gln Phe Met Val Leu Gly Ala Val Gly Glu Leu Pro Lys Ala Pro
65      70      75      80
Glu Lys Pro Val Leu Phe Leu Glu Asp Leu Pro Glu Asp Glu Leu Asn
      85      90      95
Lys Ala Lys Asp
      100

```

<210> 681
 <211> 357
 <212> DNA
 <213> Homo sapiens

<400> 681
 acgcgtccaa atggacaaac gcttgatgat ttctaccatg aaattagagc aaaatatcca
 60
 gaacaattac tgatggcaga ctgttcaaca gtagaagaaa tgattcacgc tgatgaactc
 120
 ggttttgatt ttatcggaag tacttttagta ggatatacaa aacaaagtaa aggtgacaaa
 180
 atcgaagaaa atgactttga aatcttgaga acagtttttag aacgaattaa acatccacta
 240
 attgcagaag gcaatatcga tacacctgaa aaggtgaaac gtgtgcttga gttaggcgcg
 300
 tatagtgtcg ttgtagggtc agcgattact cgtccacaac tcatcacgaa aaaattt
 357

<210> 682
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 682
 Thr Arg Pro Asn Gly Gln Thr Leu Asp Asp Phe Tyr His Glu Ile Arg
 1 5 10 15
 Ala Lys Tyr Pro Glu Gln Leu Leu Met Ala Asp Cys Ser Thr Val Glu
 20 25 30
 Glu Met Ile His Ala Asp Glu Leu Gly Phe Asp Phe Ile Gly Ser Thr
 35 40 45
 Leu Val Gly Tyr Thr Lys Gln Ser Lys Gly Asp Lys Ile Glu Glu Asn
 50 55 60
 Asp Phe Glu Ile Leu Arg Thr Val Leu Glu Arg Ile Lys His Pro Leu
 65 70 75 80
 Ile Ala Glu Gly Asn Ile Asp Thr Pro Glu Lys Val Lys Arg Val Leu
 85 90 95
 Glu Leu Gly Ala Tyr Ser Val Val Val Gly Ser Ala Ile Thr Arg Pro
 100 105 110
 Gln Leu Ile Thr Lys Lys Phe
 115

<210> 683
 <211> 411
 <212> DNA
 <213> Homo sapiens

<400> 683
 ntctccgacc gcgtggtaaa actggcgacc ttaattgctg aagatgagca agctgaaatg
 60
 aatattgttt tgcccgacgc gtggttgcat gattgcgtca gttaccctaa aaaccatgta
 120
 ttaagagcac aaagtgcatt acatgcagca gataaagcga ttgtattttt gcgcagtatt
 180

aattacccca aacaatactt attagcaatt catcatgcaa ttccagcgca cagtgtcagt
 240
 ggtaaaatac aggcaatgag tttagaagct caaatagtgc aagatgcaga tagattggat
 300
 gcgctagggg caattggcgt ggctcgttgc attcaagtaa gtagccagtt acagcgccca
 360
 ctatattctg aagttgaccc cttcagcgag acacgatctc tagtctgcat g
 411

<210> 684

<211> 137

<212> PRT

<213> Homo sapiens

<400> 684

Xaa	Ser	Asp	Arg	Val	Val	Lys	Leu	Ala	Thr	Leu	Ile	Ala	Glu	Asp	Glu
1				5				10					15		
Gln	Ala	Glu	Met	Asn	Ile	Val	Leu	Pro	Ala	Ala	Trp	Leu	His	Asp	Cys
			20					25					30		
Val	Ser	Tyr	Pro	Lys	Asn	His	Val	Leu	Arg	Ala	Gln	Ser	Ala	Leu	His
		35					40					45			
Ala	Ala	Asp	Lys	Ala	Ile	Val	Phe	Leu	Arg	Ser	Ile	Asn	Tyr	Pro	Lys
	50					55					60				
Gln	Tyr	Leu	Leu	Ala	Ile	His	His	Ala	Ile	Ser	Ala	His	Ser	Val	Ser
65					70				75					80	
Gly	Lys	Ile	Gln	Ala	Met	Ser	Leu	Glu	Ala	Gln	Ile	Val	Gln	Asp	Ala
			85					90					95		
Asp	Arg	Leu	Asp	Ala	Leu	Gly	Ala	Ile	Gly	Val	Ala	Arg	Cys	Ile	Gln
			100				105						110		
Val	Ser	Ser	Gln	Leu	Gln	Arg	Pro	Leu	Tyr	Ser	Glu	Val	Asp	Pro	Phe
		115				120					125				
Ser	Glu	Thr	Arg	Ser	Leu	Val	Cys	Met							
		130				135									

<210> 685

<211> 417

<212> DNA

<213> Homo sapiens

<400> 685

acgcgttgcg ttgcggagtg aaccgcgaac gatggatgga ttgacactat tcggcctggt
 60
 cgccgtcact gcgatgctgg tctgctatgc catggaggac cgcagccact ggttcgtgct
 120
 gctgttcgcg gccgcttggc gctcggttcg gcctacggct tcctccaagg cgctggccg
 180
 ttcggcttcg tcgaggcgat atgggcgctc gttgcctgcg gcgtggtgga cgatcaggcc
 240
 gcgatgaccg catcgtccgg cttaagcccg gaaacgaaac cgaccagtgc gctggtttga
 300
 tgggcggcgc gtcgctggat gcacagcgtc tcgacgcgag cgtgatgatg gcctcagcgc
 360
 gtgcatgccg acgctgtcgc tcatcgcgct acgctcgacc acggcgcgcg gcaatag
 417

<210> 686
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 686
 Met Pro Trp Arg Thr Ala Ala Thr Gly Ser Cys Cys Cys Ser Arg Pro
 1 5 10 15
 Leu Gly Ala Arg Phe Gly Leu Arg Leu Pro Pro Arg Arg Leu Ala Val
 20 25 30
 Arg Leu Arg Arg Gly Asp Met Gly Ala Arg Cys Leu Arg Arg Gly Gly
 35 40 45
 Arg Ser Gly Arg Asp Asp Arg Ile Val Arg Leu Lys Pro Gly Asn Glu
 50 55 60
 Thr Asp Gln Cys Ala Gly Leu Met Gly Gly Ala Ser Leu Asp Ala Gln
 65 70 75 80
 Arg Leu Asp Ala Ser Val Met Met Ala Ser Ala Arg Ala Cys Arg Arg
 85 90 95
 Cys Arg Ser Ser Arg Tyr Ala Arg Pro Arg Arg Ala Ala Ile
 100 105 110

<210> 687
 <211> 412
 <212> DNA
 <213> Homo sapiens

<400> 687
 nnacgcgtga ccgaccaact gcgagccacc ctgctcgcca tggctgctat ggggttgcac
 60
 gacggcatcg atattccgtc tggggcgatt attgaaagct gccgcacctt atcagccggt
 120
 ctcgatgaaa cccacgggtg tgcgacgac gagcttcggg taccacctgc gtgcgcgggt
 180
 caattggcgg ccattgagtc gggccccaac caccaccggg gcactccgcc caatgtggcc
 240
 gagaccgacc ctgtcacctt cctgcagttg gcaactgget tctcacactg gccagaaatg
 300
 cgctcagcag gacgggttca ggcgtctgga tcccacgtcg acgacgttgc tggcgtgttc
 360
 ccagtcgttg atatggccgg ggttttccgc gacatttttg ccgacgacta ga
 412

<210> 688
 <211> 136
 <212> PRT
 <213> Homo sapiens

<400> 688
 Xaa Arg Val Thr Asp Gln Leu Arg Ala Thr Leu Leu Ala Met Ala Ala
 1 5 10 15
 Met Gly Leu His Asp Gly Ile Asp Ile Pro Ser Gly Ala Ile Ile Glu
 20 25 30
 Ser Cys Arg Thr Leu Ser Ala Val Leu Asp Glu Thr His Gly Gly Arg


```

      35              40              45
Thr Ile Glu Leu Arg Val Pro Pro Ala Cys Ala Val Gln Leu Ala Ala
      50              55              60
Ile Glu Ser Gly Pro Asn His His Arg Gly Thr Pro Pro Asn Val Ala
65      70              75              80
Glu Thr Asp Pro Val Thr Phe Leu Gln Leu Ala Thr Gly Phe Ser His
      85              90              95
Trp Pro Glu Met Arg Ser Ala Gly Arg Val Gln Ala Ser Gly Ser His
      100             105             110
Val Asp Asp Val Ala Gly Val Phe Pro Val Val Asp Met Ala Gly Val
      115             120             125
Phe Arg Asp Ile Phe Ala Asp Asp
      130             135

```

<210> 689
 <211> 499
 <212> DNA
 <213> Homo sapiens

```

<400> 689
cgcgctgcggg tactcgacgt cgattttcat caccgtaacg gcacccagaa cattttttac
60
ccgcgcaatg acgtgatgtt catatcgctg caccggcgagc cggccgtgtc ctatccctac
120
tattcgggggt tcagcgatga agtcggcgca ggtgttggcg aagggttcaa cctcaactac
180
ccgctgccga aaaacaccgc ctgggatacc taccgcgacg ccctgctgca tgctgcagg
240
aaactccagc aattctcgcc gcaggatttg gtgatctcac tgggggtcga caccttcaag
300
gacgacccga tcagtcactt cctgctggaa ggcgaggatt tcatcgggat cggcgagctg
360
atagcgagtg tgggttgccc caccctgttt gtgatggaag gcggctatat ggtcgatgaa
420
atcggaatca acgcggtgaa cgtactgcat ggcttcgaga gcaagcgcgc ttgagcatcc
480
gcccgaagac ggcgtgata
499

```

<210> 690
 <211> 157
 <212> PRT
 <213> Homo sapiens

```

<400> 690
Arg Val Ala Val Leu Asp Val Asp Phe His His Gly Asn Gly Thr Gln
1      5      10      15
Asn Ile Phe Tyr Pro Arg Asn Asp Val Met Phe Ile Ser Leu His Gly
      20      25      30
Glu Pro Ala Val Ser Tyr Pro Tyr Tyr Ser Gly Phe Ser Asp Glu Val
      35      40      45
Gly Ala Gly Val Gly Glu Gly Phe Asn Leu Asn Tyr Pro Leu Pro Lys
      50      55      60
Asn Thr Ala Trp Asp Thr Tyr Arg Asp Ala Leu Leu His Ala Cys Arg

```

```

65          70          75          80
Lys Leu Gln Gln Phe Ser Pro Gln Val Leu Val Ile Ser Leu Gly Val
          85          90          95
Asp Thr Phe Lys Asp Asp Pro Ile Ser His Phe Leu Leu Glu Gly Glu
          100          105          110
Asp Phe Ile Gly Ile Gly Glu Leu Ile Ala Ser Val Gly Cys Pro Thr
          115          120          125
Leu Phe Val Met Glu Gly Gly Tyr Met Val Asp Glu Ile Gly Ile Asn
          130          135          140
Ala Val Asn Val Leu His Gly Phe Glu Ser Lys Arg Ala
145          150          155

```

<210> 691
 <211> 336
 <212> DNA
 <213> Homo sapiens

```

<400> 691
ntgctgctg aaaacgtgca gcgcggcgca tcagcgactg gcgagcgctt tggctggagt
60
tcgcaaaggc aaggcccctg ggagttggcc tgcgacatcg cgctgccgtg cgccaccag
120
aacgaactgg acgccgacgc cgcccgacgc ctgctgcgca acggctgcct ttgctggct
180
ggaggcgcca atatgccgcc cgcgcttgag gctgtggata tctttatcga ggcgggcatt
240
ctgttcgcgc ccggcaaggc atccaatgcc ggcggcgctg ccgtgagtgg cctggaaatg
300
tcgcagaacg ccatgcgcct gctgtggacc gccggc
336

```

<210> 692
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 692
Xaa Leu Arg Glu Asn Val Gln Arg Gly Ala Ser Ala Thr Gly Glu Arg
1          5          10          15
Phe Gly Trp Ser Ser Gln Arg Gln Gly Pro Trp Glu Leu Ala Cys Asp
          20          25          30
Ile Ala Leu Pro Cys Ala Thr Gln Asn Glu Leu Asp Ala Asp Ala Ala
          35          40          45
Arg Thr Leu Leu Arg Asn Gly Cys Leu Cys Val Ala Gly Gly Ala Asn
          50          55          60
Met Pro Pro Ala Leu Glu Ala Val Asp Ile Phe Ile Glu Ala Gly Ile
65          70          75          80
Leu Phe Ala Pro Gly Lys Ala Ser Asn Ala Gly Gly Val Ala Val Ser
          85          90          95
Gly Leu Glu Met Ser Gln Asn Ala Met Arg Leu Leu Trp Thr Ala Gly
          100          105          110

```

<210> 693
 <211> 580

<212> DNA

<213> Homo sapiens

<400> 693

```

ngggcaaccc ggaaggtccg gcgtcccagc cgcctacctc gctgggaccc tggctcttgc
60
gtcccccgcgt ggccctcctgc ccaagcgact gcggccagga tgggccggaa ggtgaccgtg
120
gccacctgcg cactcaacca gtgggccctg gacttcgagg gcaatttgca aagaatttta
180
aagagtattg aaattgccaa aaacagagga gcaagataca ggcttggacc agagctggaa
240
atatgctggct gcggatgttg ggatcattat tacgagtcgg acaccctctt gcactcgttt
300
caagtcctag cggcccttgt ggagtctccc gtcactcagg acatcatctg cgacgtgggg
360
atacctgtaa tgcaccgaaa cgtccgctac aactgcagag tgatattcct caacaggaag
420
atcctgctca tcagacccaa gatggccttg gccaatgaag gcaactaccg cgagctgcgc
480
tggttcaccc cgtggctcgag gagtcggtga gtcgggtgcc tgaccactcc tgggatgtgc
540
gttaagcacc tccgctgtgt gtagccttgg gtcctgatca
580

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<210> 694

<211> 136

<212> PRT

<213> Homo sapiens

<400> 694

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Met Gly Arg Lys Val Thr Val Ala Thr Cys Ala Leu Asn Gln Trp Ala
1           5           10           15
Leu Asp Phe Glu Gly Asn Leu Gln Arg Ile Leu Lys Ser Ile Glu Ile
20          25          30
Ala Lys Asn Arg Gly Ala Arg Tyr Arg Leu Gly Pro Glu Leu Glu Ile
35          40          45
Cys Gly Cys Gly Cys Trp Asp His Tyr Tyr Glu Ser Asp Thr Leu Leu
50          55          60
His Ser Phe Gln Val Leu Ala Ala Leu Val Glu Ser Pro Val Thr Gln
65          70          75          80
Asp Ile Ile Cys Asp Val Gly Ile Pro Val Met His Arg Asn Val Arg
85          90          95
Tyr Asn Cys Arg Val Ile Phe Leu Asn Arg Lys Ile Leu Leu Ile Arg
100         105         110
Pro Lys Met Ala Leu Ala Asn Glu Gly Asn Tyr Arg Glu Leu Arg Trp
115         120         125
Phe Thr Pro Trp Ser Arg Ser Arg
130         135

```

<210> 695

<211> 439

<212> DNA

<213> Homo sapiens

<400> 695

ntgggtgactc aggcgtccaa tggcacgatg gctgacgtcg tcaatatgcc gtcctcgacc
60
atcatggctc tgtcgagggc tgattacctg ctcgatatcg agacttcggt gcccgggtatc
120
ggcgacaagt tcgtcccggg cgtctggggc aaactcaaac tcggcaagga caacgagcac
180
accgctctgc cctggtactt cggcccgttc gtcgtgacgt acaacaagga cattttcaag
240
gatgttggcc tcgatcccga aatcccgcgc aagacgatga ccgagtacct cgacttcgcc
300
aagaaaatca ccgctgccgg caagcaggcg gtctatggca acacgtcgtg gtacatgctc
360
gcggaatggc gtgccctcgg cgtcaaggtc atgaatgacg acttcaccaa gttcactttt
420
gcctcgggaat ccaacgcgt
439

<210> 696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 696

Xaa	Val	Thr	Gln	Ala	Ser	Asn	Gly	Thr	Met	Ala	Asp	Val	Val	Asn	Met
1				5					10					15	
Pro	Ser	Ser	Thr	Ile	Met	Ala	Leu	Ser	Arg	Ala	Asp	Tyr	Leu	Leu	Asp
			20					25					30		
Ile	Glu	Thr	Ser	Val	Pro	Gly	Ile	Gly	Asp	Lys	Phe	Val	Pro	Asp	Val
		35					40					45			
Trp	Gly	Lys	Leu	Lys	Leu	Gly	Lys	Asp	Asn	Glu	His	Thr	Ala	Leu	Pro
	50				55						60				
Trp	Tyr	Phe	Gly	Pro	Phe	Val	Val	Thr	Tyr	Asn	Lys	Asp	Ile	Phe	Lys
65				70					75					80	
Asp	Val	Gly	Leu	Asp	Pro	Glu	Ile	Pro	Pro	Lys	Thr	Met	Thr	Glu	Tyr
			85					90					95		
Leu	Asp	Phe	Ala	Lys	Lys	Ile	Thr	Ala	Ala	Gly	Lys	Gln	Ala	Val	Tyr
		100						105					110		
Gly	Asn	Thr	Ser	Trp	Tyr	Met	Leu	Ala	Glu	Trp	Arg	Ala	Leu	Gly	Val
	115					120					125				
Lys	Val	Met	Asn	Asp	Asp	Phe	Thr	Lys	Phe	Thr	Phe	Ala	Ser	Glu	Ser
	130					135					140				
Asn	Ala														
145															

<210> 697

<211> 368

<212> DNA

<213> Homo sapiens

<400> 697

nggcaataac gccgtcgtcg aaatccgttc ccttgatctc gaacatgccg atgaagcggg
60

tgtcgggtgat ggggtcggag atgtcgccct cccacaactt gaacttgatc ggaccaaccc
 120
 tttccaccct ggagagactc gcctgccttg aaagtcttct tgcccttctt gggcaactga
 180
 tcgccctccc gaacgagata atccaagctc aagcgaccgc ccaccttgtc gcgcgcctcc
 240
 acaccgacgg aatgcgatgc cgggatcgca tcgatgctag cggcgggtgcg tgcaatgaca
 300
 atcttgtctt cacgcagcga tacgggcccc ccgttggaat cgaacacaaa caccttgaag
 360
 gcgttgtn
 368

<210> 698
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 698
 Met Pro Met Lys Arg Leu Ser Val Met Gly Ser Glu Met Ser Pro Ser
 1 5 10 15
 His Asn Leu Asn Leu Ile Gly Pro Thr Leu Ser Thr Leu Glu Arg Leu
 20 25 30
 Ala Cys Leu Glu Ser Leu Leu Ala Leu Leu Gly Gln Leu Ile Ala Leu
 35 40 45
 Pro Asn Glu Ile Ile Gln Ala Gln Ala Thr Ala His Leu Val Ala Arg
 50 55 60
 Leu His Thr Asp Gly Met Arg Cys Arg Asp Arg Ile Asp Ala Ser Gly
 65 70 75 80
 Gly Ala Cys Asn Asp Asn Leu Val Phe Thr Gln Arg Tyr Gly Pro Ala
 85 90 95
 Val Gly Ile Glu His Lys His Leu Glu Gly Val Val
 100 105

<210> 699
 <211> 363
 <212> DNA
 <213> Homo sapiens

<400> 699
 nacgcgtaca caaatagtat cggaatcatt tcctatcatg ctgctatgac gagatttctc
 60
 cacacctcag attggcaact ggggatgact cggcactacc tgtcgaagcg cggcgacgac
 120
 gaccacagg cacggtttac tgccgatcga atcgagacgg tgcgcaggct gggcgacgtt
 180
 gcccggaagg agggctgcga gtttgcgctc gtcgccggag atgtcttcga aaccacaaat
 240
 gtctccactc agatcattgc ccgcgcgtgt gaggcgatag cctccattga tctccccgtg
 300
 tacctgctgc ccggaaatca cgacagctta gagccggggg gtctctggga tgggcccagaa
 360
 ttc
 363

<210> 700
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 700
 Xaa Ala Tyr Thr Asn Ser Ile Gly Ile Ile Ser Tyr His Ala Ala Met
 1 5 10 15
 Thr Arg Phe Leu His Thr Ser Asp Trp Gln Leu Gly Met Thr Arg His
 20 25 30
 Tyr Leu Ser Lys Arg Gly Asp Asp Asp Pro Gln Ala Arg Phe Thr Ala
 35 40 45
 Asp Arg Ile Glu Thr Val Arg Arg Leu Gly Asp Val Ala Arg Lys Glu
 50 55 60
 Gly Cys Glu Phe Val Val Val Ala Gly Asp Val Phe Glu Thr His Asn
 65 70 75 80
 Val Ser Thr Gln Ile Ile Ala Arg Ala Cys Glu Ala Ile Ala Ser Ile
 85 90 95
 Asp Leu Pro Val Tyr Leu Leu Pro Gly Asn His Asp Ser Leu Glu Pro
 100 105 110
 Gly Cys Leu Trp Asp Gly Pro Glu Phe
 115 120

<210> 701
 <211> 585
 <212> DNA
 <213> Homo sapiens

<400> 701
 nacgcgtccg ggcacaccgt caccgaggcg acgttccacg gccacccac gctgatctat
 60
 ttcggctacg tccattgcgc ggatgtctgc ccgctgacac tgggcaacat ggtctcggcc
 120
 ctcgatcgcc tggggtcccg ggcggacggc atcgttccga tcttcatctc cgtcgatccg
 180
 gccgcgcaca caccgcgcgt ggtcggacag tatgtcgcgc atttctcgcc gcggatcgtc
 240
 gggctgaccg gcaccgcagc gcagctggcg ccggtactgg cggagttcca catcaccgcg
 300
 cgcgccgaac ctgcggcaca cgacatggcc gccgacatgt atgccgtcga ccacagcgcc
 360
 ctctctatc tgatggacgg caacaaccgc ctgttgcggg tgatggcggt cagcgccgac
 420
 gctgcctcgc tgacgcacca gctggcgggc ggccctggccg gggcaagaat gagaccatga
 480
 aagcgatcgg accgacggac gccccgaac aggcagcgcc gggctggctg ttcggcatca
 540
 tcctgctgct cggcatcgcc ggcattgctg atttcgtcga ccggt
 585

<210> 702
 <211> 159
 <212> PRT

<213> Homo sapiens

<400> 702

```

Xaa Ala Ser Gly His Thr Val Thr Glu Ala Thr Phe His Gly His Pro
 1           5           10           15
Thr Leu Ile Tyr Phe Gly Tyr Val His Cys Ala Asp Val Cys Pro Leu
          20           25           30
Thr Leu Gly Asn Met Val Ser Ala Leu Asp Arg Leu Gly Ser Arg Ala
          35           40           45
Asp Gly Ile Val Pro Ile Phe Ile Ser Val Asp Pro Ala Arg Asp Thr
          50           55           60
Pro Ala Leu Val Gly Gln Tyr Val Ala His Phe Ser Pro Arg Ile Val
65           70           75           80
Gly Leu Thr Gly Thr Ala Ala Gln Leu Ala Pro Val Leu Ala Glu Phe
          85           90           95
His Ile Thr Ala Arg Ala Glu Pro Ala Ala His Asp Met Ala Ala Asp
          100          105          110
Met Tyr Ala Val Asp His Ser Ala Leu Leu Tyr Leu Met Asp Gly Asn
          115          120          125
Asn Arg Leu Leu Arg Val Met Ala Val Ser Ala Asp Ala Ala Ser Leu
          130          135          140
Thr His Gln Leu Ala Ala Gly Leu Ala Gly Ala Arg Met Arg Pro
145          150          155

```

<210> 703

<211> 390

<212> DNA

<213> Homo sapiens

<400> 703

```

ttctctgctc catacacacc tcagcagaat ggcacgccc agcgcaagaa cataactctt
60
attgagatgg cccgaacgat gcttgatgag tacaagactc cgcggaagtt ctggcctgaa
120
gccattgata ctgcttgta caccatcaac cgcgtttatc ttcacaaggt tttggagaaa
180
acctcttatg agttcctaac tggttaagaaa cccaatgtaa gctatttcag agtatttggt
240
gctaggtgct ggatcaagga tcctcatcac acttcaaaaat ttgcaccgaa agcacatgaa
300
ggtttttatgc ttggttacgg aaaggattcg cactcctaca gagtcttcaa cctctttcac
360
tataaagtgg ttcaaactgt ggatgtgcn
390

```

<210> 704

<211> 130

<212> PRT

<213> Homo sapiens

<400> 704

```

Phe Ser Ala Pro Tyr Thr Pro Gln Gln Asn Gly Ile Ala Glu Arg Lys
 1           5           10           15
Asn Ile Thr Leu Ile Glu Met Ala Arg Thr Met Leu Asp Glu Tyr Lys

```

```

      20      25      30
Thr Pro Arg Lys Phe Trp Pro Glu Ala Ile Asp Thr Ala Cys His Thr
      35      40      45
Ile Asn Arg Val Tyr Leu His Lys Val Leu Glu Lys Thr Ser Tyr Glu
      50      55      60
Phe Leu Thr Gly Lys Lys Pro Asn Val Ser Tyr Phe Arg Val Phe Gly
65      70      75      80
Ala Arg Cys Trp Ile Lys Asp Pro His His Thr Ser Lys Phe Ala Pro
      85      90      95
Lys Ala His Glu Gly Phe Met Leu Gly Tyr Gly Lys Asp Ser His Ser
      100      105      110
Tyr Arg Val Phe Asn Leu Phe His Tyr Lys Val Val Gln Thr Val Asp
      115      120      125
Val Arg
      130

```

<210> 705

<211> 513

<212> DNA

<213> Homo sapiens

<400> 705

```

acgcgtat ttt cgtccaaatg attcaaatca aaacgccgcc gttaaaaacg atgcaggcga
60
agacaatg cg aataaaaaaag gtggtaaata agcatgagtt ttaaaatgac acaatctcaa
120
tacacaagtc tttatggacc aactgtagga gactccgtga gattaggaga tacgaacttg
180
tttgcaaacg ttgagaaaga ctatgcaaat tatgggggatg aagctacttt cggtggcgga
240
aaatcaattc gtgatgggat ggctcaaaat cctaattgtga caagagatga taaaaatgta
300
gccgatttag ttttaactaa cgcattaatt attgattatg acaagattgt taaagcagat
360
atcggtatta aaaatgggta tatttttaag attggtaaag ctggaaaccc agatataatg
420
gataacgttg acatcatcat tgggtgcaaca actgatatta ttgctgctga aggtaaaatt
480
gttactgccg gcggtatcga tacacacgtg cac
513

```

<210> 706

<211> 140

<212> PRT

<213> Homo sapiens

<400> 706

```

Met Ser Phe Lys Met Thr Gln Ser Gln Tyr Thr Ser Leu Tyr Gly Pro
1      5      10      15
Thr Val Gly Asp Ser Val Arg Leu Gly Asp Thr Asn Leu Phe Ala Gln
      20      25      30
Val Glu Lys Asp Tyr Ala Asn Tyr Gly Asp Glu Ala Thr Phe Gly Gly
      35      40      45
Gly Lys Ser Ile Arg Asp Gly Met Ala Gln Asn Pro Asn Val Thr Arg

```


50	55	60
Asp Asp Lys Asn Val Ala Asp Leu Val Leu Thr Asn Ala Leu Ile Ile		
65	70	75
Asp Tyr Asp Lys Ile Val Lys Ala Asp Ile Gly Ile Lys Asn Gly Tyr		80
	85	90
Ile Phe Lys Ile Gly Lys Ala Gly Asn Pro Asp Ile Met Asp Asn Val		95
	100	105
Asp Ile Ile Ile Gly Ala Thr Thr Asp Ile Ile Ala Ala Glu Gly Lys		110
	115	120
Ile Val Thr Ala Gly Gly Ile Asp Thr His Val His		125
	130	135
		140

<210> 707

<211> 409

<212> DNA

<213> Homo sapiens

<400> 707

acgcgtggca tcctcagacc accaaagaca atcctgtcct gggaggcagg gagaaagccg
60
gcacactaca cagtgcacag gtgaagccct caggggggtcc tggagcaggg ccacctccct
120
gggggatccc caggtgccat tttcatggca gtgtctatgg acggctcccc ttggcatggt
180
gctgggtggc aatcctggct gtagctgccca cccctgccc tttttgcttc cctccgaggg
240
cattgtgatc atcagtgtga gtctgttggg aaggagagcc aggtccccag gtttgggaaa
300
ggagtagggg tcccagcct gtctggccat cccccccag cccagcccct cctgctgggt
360
gacgtgtca gttcgcccc tgctgtactg ggagggggct aggagcata
409

<210> 708

<211> 136

<212> PRT

<213> Homo sapiens

<400> 708

Met Leu Leu Ala Pro Ser Gln Tyr Ser Arg Gly Arg Thr Glu His Val	
1	5
Thr Gln Gln Glu Gly Leu Gly Trp Gly Val Met Ala Arg Gln Ala Gly	
	20
Lys Pro Tyr Ser Phe Pro Lys Pro Gly Asp Leu Ala Leu Leu Pro Asn	
	35
Arg Leu Thr Leu Met Ile Thr Met Pro Ser Glu Gly Ser Lys Lys Gly	
	50
Arg Gly Trp Gln Leu Gln Pro Gly Leu Pro Pro Ser Thr Met Pro Arg	
65	70
Gly Ala Val His Arg His Cys His Glu Asn Gly Thr Trp Gly Ser Pro	
	85
Arg Glu Val Ala Leu Leu Gln Asp Pro Leu Arg Ala Ser Pro Val His	
	100
Cys Val Val Cys Arg Leu Ser Pro Cys Leu Pro Gly Gln Asp Cys Leu	

125

400> 710															
Met	Ser	Glu	Ala	Ser	Ser	Ala	Lys	Asp	Thr	Pro	Leu	Phe	Arg	Met	Glu
1				5					10					15	
Gly	Glu	Asp	Ala	Leu	Val	Thr	Gln	Tyr	Gln	Ser	Lys	Ala	Ser	Asp	His
			20					25					30		
Glu	Gly	Leu	Leu	Ser	Asp	Pro	Leu	Ser	Asp	Leu	Gln	Leu	Val	Ser	Asp
		35					40					45			
Phe	Lys	Ser	Pro	Ile	Met	Ala	Asp	Leu	Asn	Leu	Ser	Leu	Pro	Ser	Ile
	50					55				60					
Pro	Glu	Val	Ala	Ser	Asp	Asp	Glu	Arg	Ile	Asp	Gln	Val	Glu	Asp	Asp
65					70					75				80	
Gly	Asp	Gln	Val	Glu	Asp	Asp	Gly	Glu	Thr	Ala	Lys	Ser	Ser	Thr	Leu

```

      85              90              95
Asp Ile Gly Ala Leu Ser Leu Gly Leu Val Val Pro Cys Pro Glu Arg
      100              105              110
Gly Lys Gly Pro Ser Gly Glu Ala Asp Arg Leu Val Leu Gly Glu Gly
      115              120              125
Leu Cys Asp Phe Arg Leu Gln Ala Pro Gln Ala Ser Val Thr Ala Pro
      130              135              140
Ser Glu Gln Thr Thr Glu Phe Gly Ile His Lys Pro His Leu Gly Lys
      145              150              155
Ser Ser Ser Leu Asp Lys Gln Leu Pro Gly Pro Ser Gly Gly Glu Glu
      165              170              175
Glu Lys Pro Met Gly Asn Gly Ser Pro Ser Pro Pro Pro Gly Thr Ser
      180              185              190
Leu Asp Asn Pro Val Pro Ser Pro Ser Pro Ser Glu Ile
      195              200              205

```

<210> 711
 <211> 432
 <212> DNA
 <213> Homo sapiens

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<400> 711
nnggatccga cggcgcaaag ccttaatgaa gggtaggcag ttacctcttt ttctgtagga
60
attctcctgt tttatatcta ctcccccta ggttcacccat actccctcat cttctgagct
120
aatgtgcccg ctttatttgc acttgcatgg aatatgatta tgaacacagt ttttatcatt
180
gatgaccacc ccgttatcag gttggcgatt cgtatgttgt tggaacacga ggggtataag
240
gtcgttggtg aaacggacaa cggttgtgac gcgatccaaa tggttcgaga atgcctgccg
300
gacctgatca tcttgatat cagcatcccg aaactcgacg gcctcgaagt gctctgccga
360
ttcaacgcca tgaacacatc catgaaaacc ctgattctta ccgccagag tccgacgttg
420
ttcgccacgc gt
432

```

<210> 712
 <211> 93
 <212> PRT
 <213> Homo sapiens

```

<400> 712
Met Ile Met Asn Thr Val Phe Ile Ile Asp Asp His Pro Val Ile Arg
1      5      10      15
Leu Ala Ile Arg Met Leu Leu Glu His Glu Gly Tyr Lys Val Val Gly
20     25     30
Glu Thr Asp Asn Gly Cys Asp Ala Ile Gln Met Val Arg Glu Cys Leu
35     40     45
Pro Asp Leu Ile Ile Leu Asp Ile Ser Ile Pro Lys Leu Asp Gly Leu
50     55     60
Glu Val Leu Cys Arg Phe Asn Ala Met Asn Thr Ser Met Lys Thr Leu

```

65 70 75 80
Ile Leu Thr Ala Gln Ser Pro Thr Leu Phe Ala Thr Arg
 85 90

```
<210> 713
<211> 465
<212> DNA
<213> Homo sapiens
```

```
<400> 713
atcctgatcg ccaacggtgg tatgcagaac ccggtgggcg cgggtgttcaa ccccgacacc
60
atgcgcgatgg aaatgaccga cttegccgcg gtgatcttca acccggtggc gcaggccaag
120
ttcgtgcata cggtcagcgc gggctacgtg gccggcgcca tgttcgtcat gtcgatcagc
180
gcctgggtacc tgetcaaggg ccgccacacc gacctggcca agcgctcgat ggcggtcgcc
240
gccagcttcg gcctggcgtc ggcgctgtcg gtcgtcgtgc tgggtgacga aagcggttat
300
ctcaccaccg aacaccagaa gatgaagatc gcggccatgg aatccatgtg gcacaccgag
360
ccggcgcccc cgtccttcaa cctgatcgcg ctgcccaacc aggccgaacg caagaacgac
420
ttcgccatcg agattcccta cgtcatgngc ctcatcggca cgcgt
465
```

```
<210> 714
<211> 155
<212> PRT
<213> Homo sapiens
```

```

<400> 714
Ile Leu Ile Ala Asn Gly Gly Met Gln Asn Pro Val Gly Ala Val Phe
 1          5          10          15
Asn Pro Asp Thr Met Arg Met Glu Met Thr Asp Phe Ala Ala Val Ile
 20          25          30
Phe Asn Pro Val Ala Gln Ala Lys Phe Val His Thr Val Ser Ala Gly
 35          40          45
Tyr Val Ala Gly Ala Met Phe Val Met Ser Ile Ser Ala Trp Tyr Leu
 50          55          60
Leu Lys Gly Arg His Thr Asp Leu Ala Lys Arg Ser Met Ala Val Ala
 65          70          75          80
Ala Ser Phe Gly Leu Ala Ser Ala Leu Ser Val Val Val Leu Gly Asp
 85          90          95
Glu Ser Gly Tyr Leu Thr Thr Glu His Gln Lys Met Lys Ile Ala Ala
 100          105          110
Met Glu Ser Met Trp His Thr Glu Pro Ala Pro Ala Ser Phe Asn Leu
 115          120          125
Ile Ala Leu Pro Asn Gln Ala Glu Arg Lys Asn Asp Phe Ala Ile Glu
 130          135          140
Ile Pro Tyr Val Met Xaa Leu Ile Gly Thr Arg
145          150          155

```

<210> 715
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 715
 nnaccggtgg atgccaacga atatcgtggc gagctgaaag tcggcgccat caccaccgcc
 60
 cagaccggcc tgctgcctca ggcactggtg cgtttgcgcc aggcagcgcc gacggtggag
 120
 tgcaagttgg taccgggggt ttccctggag ttgctcagcc aggtggacgc aggcgagctg
 180
 gactcggcga tcatcattcg cccgcccttt gatttgccca aggagttgca cgtacaggta
 240
 ctgcgcaagg agccgtttgt gttgatcgtg cccagggcgg tcgggggtga tgaccctgtg
 300
 caactgctcg aagctcatcc ccacgtgcgc tacgaccgcg cttcgtttgg cggg
 354

<210> 716
 <211> 118
 <212> PRT
 <213> Homo sapiens

<400> 716
 Xaa Pro Val Asp Ala Asn Glu Tyr Arg Gly Glu Leu Lys Val Gly Ala
 1 5 10 15
 Ile Thr Thr Ala Gln Thr Gly Leu Leu Pro Gln Ala Leu Val Arg Leu
 20 25 30
 Arg Gln Ala Ala Pro Thr Val Glu Cys Lys Leu Val Pro Gly Val Ser
 35 40 45
 Leu Glu Leu Leu Ser Gln Val Asp Ala Gly Glu Leu Asp Ser Ala Ile
 50 55 60
 Ile Ile Arg Pro Pro Phe Asp Leu Pro Lys Glu Leu His Val Gln Val
 65 70 75 80
 Leu Arg Lys Glu Pro Phe Val Leu Ile Val Pro Gln Ala Val Gly Gly
 85 90 95
 Asp Asp Pro Leu Gln Leu Leu Glu Ala His Pro His Val Arg Tyr Asp
 100 105 110
 Arg Ala Ser Phe Gly Gly
 115

<210> 717
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 717
 acgcgtatct tttcggtaaa cctactaatt tttcattcaa cgctcgacgc ccaggtaaag
 60
 ccgttaagtc atctaaatag gccattctgt ggctctccat cagtaagaac caaatccata
 120
 ggagaagttg agcggatagt aatgcatcaa attgatgctg agaaaccgaa aaatgggaca
 180

atataatcaa gctgacaata ctgatcaaac cactcgcacg aaagctacta ccgcttgacc
 240
 accaagcaga aaaaaccaat gaaatgctta aaaataaaat cgtccaaagt aaaaagctag
 300
 accaggtggg agccagatta aaaataggcc gctctagaaa atgaaaagaa atccaatgag
 360
 attcaacggc gtagcaccag cacagcaaca tagccactag t
 401

<210> 718

<211> 130

<212> PRT

<213> Homo sapiens

<400> 718

Met	Leu	Leu	Cys	Trp	Cys	Tyr	Ala	Val	Glu	Ser	His	Trp	Ile	Ser	Phe
1			5					10					15		
His	Phe	Leu	Glu	Arg	Pro	Ile	Phe	Asn	Leu	Ala	Thr	Thr	Trp	Ser	Ser
		20					25					30			
Phe	Leu	Leu	Trp	Thr	Ile	Leu	Phe	Leu	Ser	Ile	Ser	Leu	Val	Phe	Ser
	35					40					45				
Ala	Trp	Trp	Ser	Ser	Gly	Ser	Ser	Phe	His	Ala	Ser	Gly	Leu	Ile	Ser
	50				55					60					
Ile	Val	Ser	Leu	Ile	Ile	Leu	Ser	His	Phe	Ser	Val	Ser	Gln	His	Gln
65				70					75				80		
Phe	Asp	Ala	Leu	Leu	Ser	Ala	Gln	Leu	Leu	Trp	Ile	Trp	Phe	Leu	
			85					90					95		
Leu	Met	Glu	Ser	His	Arg	Met	Ala	Tyr	Leu	Asp	Asp	Leu	Thr	Ala	Leu
		100					105					110			
Pro	Gly	Arg	Arg	Ala	Leu	Asn	Glu	Lys	Leu	Val	Gly	Leu	Pro	Lys	Arg
	115					120					125				
Tyr	Ala														
	130														

<210> 719

<211> 685

<212> DNA

<213> Homo sapiens

<400> 719

tatatagggc tatctacctt attcacagca cattccatct acacaacctt gtagcggtca
 60
 ctcttgaagg cggattttca taggcgctgc gcctctcata ttcaagcatc aaggcaatcc
 120
 aatctccctg cgttggtaac tgggcaaaaag aaagacctct gcagtcacgc aacctcatcg
 180
 tgcaaatgcc gtggcggtgg caactctgac ggcttggaag ctgcagacct tgtcaaagga
 240
 cctcggccga aattcaccct tgatctcttt gtcttgtcca actcttgtcc ctgagaatga
 300
 aactgtcttc tgagagtcca tcaatgcgac gctgactcgt gagaagtgct gaatcacgtc
 360
 gccattttgg agacctgcca acgcagctct ggaacctgcc aggacgcctt ccacaacacc
 420

agaacgcagc gactttgcgt taaatccaag ctcaaacacc tcttgctcca caggcctgag
 480
 cataaaaagg tattctgcga cgggaaatgt aaagtctgag cttaggtgca gagtaccgcc
 540
 atcgatcagt gtctgatact gcttgctccgc gacttctttg ccgagcaatg ggtatagcgt
 600
 tttcaaccaa gtggaagcag tcgtttgctc accctggcga ttccggcgag ttagggacat
 660
 gaccacgtca tcgatgggat tttgc
 685

<210> 720
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 720
 Met Ser Leu Thr Arg Arg Asn Arg Gln Gly Glu Gln Thr Thr Ala Ser
 1 5 10 15
 Thr Trp Leu Lys Thr Leu Tyr Pro Leu Leu Gly Lys Glu Val Ala Asp
 20 25 30
 Lys Gln Tyr Gln Thr Leu Ile Asp Gly Gly Thr Leu His Leu Ser Ser
 35 40 45
 Asp Phe Thr Phe Pro Val Ala Glu Tyr Leu Phe Met Leu Arg Pro Val
 50 55 60
 Glu Gln Glu Val Phe Glu Leu Gly Phe Asn Ala Lys Ser Leu Arg Ser
 65 70 75 80
 Gly Val Val Glu Gly Val Leu Ala Gly Ser Arg Ala Ala Leu Ala Gly
 85 90 95
 Leu Gln Asn Gly Asp Val Ile Gln His Phe Ser Arg Val Ser Val Ala
 100 105 110
 Leu Met Asp Ser Gln Lys Thr Val Ser Phe Ser Gly Thr Arg Val Gly
 115 120 125
 Gln Asp Lys Glu Ile Lys Gly Glu Phe Arg Pro Arg Ser Phe Asp Lys
 130 135 140
 Val Cys Ser Phe Gln Ala Val Arg Val Asp His Ala Thr Ala Phe Ala
 145 150 155 160
 Arg

<210> 721
 <211> 579
 <212> DNA
 <213> Homo sapiens

<400> 721
 aagcttggga tcagggtgtg gcagtgtggc gggagtgtgg aggtcctgcc ctgctcacgg
 60
 attgcccaca ttgagcgagc ccacaagccc tacacagagg acctcaccgc ccatgtccgc
 120
 aggaacgctc tcagggtggc tgaagtctgg atggatgaat ttaaaagcca cgtctactgg
 180
 catggaacat accaggagga ctcaggaatt gacattgggg acatcactgc aaggaaggct
 240

ctcaggaaac agctgcagtg caagaccttc cgggtggtacc tggtcagcgt gtacccagag
 300
 atgaggatgt actccgacat cattgcctat ggagtgtctgc agaattctct gaagactgat
 360
 ttgtgtcttg accagggggcc agatacagag aatgtcccca tcatgtacat ctgccatggg
 420
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 480
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 35 40 45
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 50 55 60
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 65 70 75 80
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 50 55 60
 Glu Trp Cys Ile Gly Gly Leu Gln Ala Leu Leu Gly Ser Arg Cys Ser
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35 40 45
Ala His Val His Gly Ser Leu Asp Gly Gln Val Gly Val Phe Phe Val
50 55 60
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<211> 797

<212> PRT

<213> Homo sapiens

<400> 730

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Val	Thr	Arg	Leu	Pro	Ser	Pro	Thr	Ser	Pro	Phe	Ser	Ser	Leu	Ser	Gln
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 Phe Ser Arg Pro Pro Gln Leu Val Ser Thr Ser Asn Arg Ala Tyr
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 Lys Gly Ala Ala Met Ile Ile Glu Ser Leu Gly Leu Cys Tyr His Leu
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 His Cys Phe Lys Cys Val Ala Cys Glu Cys Asp Leu Gly Gly Ser Ser
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 <212> DNA
 <213> Homo sapiens

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<210> 732

<211> 113
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<400> 732

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Leu Ile Leu Pro Pro Pro Leu His Thr Tyr Leu Glu Leu Lys Glu Gln
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<210> 733
 <211> 4366
 <212> DNA
 <213> Homo sapiens

<400> 733

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780

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 4366

<210> 734

<211> 364

<212> PRT

<213> Homo sapiens

<400> 734

Met	Val	Val	Pro	Ser	Leu	Lys	Leu	Gln	Asp	Leu	Ile	Glu	Glu	Ile	Arg
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Gly	Ala	Lys	Thr	Gln	Ala	Gln	Glu	Arg	Glu	Val	Ile	Gln	Lys	Glu	Cys
			20				25					30			
Ala	His	Ile	Arg	Ala	Ser	Phe	Arg	Asp	Gly	Asp	Pro	Val	His	Arg	His
		35				40					45				
Arg	Gln	Leu	Ala	Lys	Leu	Leu	Tyr	Val	His	Met	Leu	Gly	Tyr	Pro	Ala
		50			55					60					
His	Phe	Gly	Gln	Met	Glu	Cys	Leu	Lys	Leu	Ile	Ala	Ser	Ser	Arg	Phe
65				70				75						80	
Thr	Asp	Lys	Arg	Val	Gly	Tyr	Leu	Gly	Ala	Met	Leu	Leu	Leu	Asp	Glu
			85					90						95	
Arg	His	Asp	Ala	His	Leu	Leu	Ile	Thr	Asn	Ser	Ile	Lys	Asn	Asp	Leu
			100					105					110		
Ser	Gln	Gly	Ile	Gln	Pro	Val	Gln	Gly	Leu	Ala	Leu	Cys	Thr	Leu	Ser
		115				120						125			
Thr	Met	Gly	Ser	Ala	Glu	Met	Cys	Arg	Asp	Leu	Ala	Pro	Glu	Val	Glu
		130				135				140					
Lys	Leu	Leu	Leu	Gln	Pro	Ser	Pro	Tyr	Val	Arg	Lys	Lys	Ala	Ile	Leu
145				150				155						160	
Thr	Ala	Val	His	Met	Ile	Arg	Lys	Val	Pro	Glu	Leu	Ser	Ser	Val	Phe
			165					170						175	
Leu	Pro	Pro	Cys	Ala	Gln	Leu	Leu	His	Glu	Arg	His	His	Gly	Ile	Leu
			180					185					190		
Leu	Gly	Thr	Ile	Thr	Leu	Ile	Thr	Glu	Leu	Cys	Glu	Arg	Ser	Pro	Ala
		195				200						205			
Ala	Leu	Arg	His	Phe	Arg	Lys	Val	Val	Pro	Gln	Leu	Val	His	Ile	Leu
		210				215					220				
Arg	Thr	Leu	Val	Thr	Met	Gly	Tyr	Ser	Thr	Glu	His	Ser	Ile	Ser	Gly
225					230					235				240	
Val	Ser	Asp	Pro	Phe	Leu	Gln	Val	Gln	Ile	Leu	Arg	Leu	Leu	Arg	Ile
			245					250						255	
Leu	Gly	Arg	Asn	His	Glu	Glu	Ser	Ser	Glu	Thr	Met	Asn	Asp	Leu	Leu
			260					265					270		
Ala	Gln	Val	Ala	Thr	Asn	Thr	Asp	Thr	Ser	Arg	Asn	Ala	Gly	Asn	Ala

275	280	285
Val Leu Phe Glu Thr	Val Leu Thr Ile Met Asp	Ile Arg Ser Ala Ala
290	295	300
Gly Leu Arg Val Leu Ala	Val Asn Ile Leu Gly Arg Phe Leu Leu Asn	
305	310	315
Ser Asp Arg Asn Ile Arg Tyr	Val Ala Leu Thr Ser Leu Leu Arg Leu	320
325	330	335
Val Gln Ser Asp His Ser Ala	Val Gln Arg His Arg Pro Thr Val Val	
340	345	350
Glu Cys Leu Arg Glu Thr Asp	Ala Ser Leu Ser Arg	
355	360	

<210> 735
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 735
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 120
 tgcttggtgt cctcgatccc gctctgaccg cccactggac cgctcaaccc aggacatcct
 180
 cagtgccatc cacgacgtgg ctgcaccgct ggcactaccc atcttcgtgg tgggtgccac
 240
 agcgcgcgac attctgctga cacacgtggt cggtatcgag accggacgtg ccacgctcga
 300
 cgtggatttc gccgttgccg tagaacattg gccgcagttc gaaaacatca agcagcacct
 360
 gctagccaac gaccatttcg actctgccgc cagcatcacc catcgactgc tctatcgcac
 420
 gagcgacaac acgatcgccc ggccaatcga tctcatccca ttcggcggca tcgaacagcc
 480
 gccagccacc atcaaattggc cgcccgacat ggctgtcatg atgaatgttg ctggctacgc
 540
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 597

<210> 736
 <211> 175
 <212> PRT
 <213> Homo sapiens

<400> 736
 Met Asp Ser Arg Asn Leu Glu Thr Ala Asn Leu Ile Pro Glu Lys Ile
 1 5 10 15
 Ile Ala Trp Cys Pro Arg Ser Arg Ser Asp Arg Pro Leu Asp Arg Ser
 20 25 30
 Thr Gln Asp Ile Leu Ser Ala Ile His Asp Val Ala Ala Pro Leu Ala
 35 40 45
 Leu Pro Ile Phe Val Val Gly Ala Thr Ala Arg Asp Ile Leu Leu Thr
 50 55 60
 His Val Phe Gly Ile Glu Thr Gly Arg Ala Thr Leu Asp Val Asp Phe

```

65          70          75          80
Ala Val Ala Val Glu His Trp Pro Gln Phe Glu Asn Ile Lys Gln His
          85          90          95
Leu Leu Ala Asn Asp His Phe Asp Ser Ala Ala Ser Ile Thr His Arg
          100          105          110
Leu Leu Tyr Arg Thr Ser Asp Asn Thr Ile Ala Arg Pro Ile Asp Leu
          115          120          125
Ile Pro Phe Gly Gly Ile Glu Gln Pro Pro Ala Thr Ile Lys Trp Pro
          130          135          140
Pro Asp Met Ala Val Met Met Asn Val Ala Gly Tyr Ala Asp Ala Trp
145          150          155          160
Arg Ala Ala Val Glu Val Glu Phe Val Pro Gly Arg Ser Ile Arg
          165          170          175

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<210> 737
 <211> 497
 <212> DNA
 <213> Homo sapiens

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<400> 737
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120
caccctgccc tgctctggat cagccacgta accttcgtta aaactgtcag tgtgggggat
180
accatcggtc acggcagaac atggacagcc agcgaaacga caaaaatcgc caccgtccca
240
gtcgggttacg ccgacggact gtcccaggga ctgtcaaata aaggacacgt tctcattaga
300
gggtccgttc atcccatcgt cggtcggatac tgcattggacc aattcatggt cgatcttggc
360
cccgattcga acgtcacggt gggagatgag gtggtgctca ttggaaccca ggaggacgaa
420
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497

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<210> 738
 <211> 165
 <212> PRT
 <213> Homo sapiens

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<400> 738
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Thr Ser Met Val Arg Ala Gly Ile Val Gly Tyr Gly Tyr Asp Pro Asn
          20          25          30
Pro His Ala Asp Arg Ala Asp Leu His Pro Ala Leu Ser Trp Ile Ser
          35          40          45
His Val Thr Phe Val Lys Thr Val Ser Val Gly Asp Thr Ile Gly Tyr
          50          55          60
Gly Arg Thr Trp Thr Ala Ser Glu Thr Thr Lys Ile Ala Thr Val Pro

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65		70		75		80									
Val	Gly	Tyr	Ala	Asp	Gly	Leu	Ser	Arg	Gly	Leu	Ser	Asn	Lys	Gly	His
			85						90					95	
Val	Leu	Ile	Arg	Gly	Ser	Val	His	Pro	Ile	Val	Gly	Arg	Ile	Cys	Met
			100					105					110		
Asp	Gln	Phe	Met	Val	Asp	Leu	Gly	Pro	Asp	Ser	Asn	Val	Thr	Val	Gly
		115					120					125			
Asp	Glu	Val	Val	Leu	Ile	Gly	Thr	Gln	Glu	Asp	Glu	Thr	Leu	Thr	Ala
	130					135					140				
Asp	Asp	Met	Ala	Glu	Leu	Leu	Gly	Thr	Ile	Ser	Tyr	Glu	Ile	Thr	Cys
145					150					155					160
Ala	Ile	Ser	Lys	Arg											
				165											

<210> 739
 <211> 438
 <212> DNA
 <213> Homo sapiens

<400> 739
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 120
 cagagcagcg gggaggagga gctgcagctc cagctggccc tggccatgag caaggaggag
 180
 gccgaccagc ccccgctctg cggccccgag gacgacgcc agctccagct ggcccttagt
 240
 ttgagccgag aagagcatga taaggaggag cggatccgct gcggggatga cctgcggctg
 300
 cagatggcaa tcgaggagag caagagggag actgggggca aggaggagtc gtcctcatg
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 420
 ccagcaccca tggctgct
 438

<210> 740
 <211> 146
 <212> PRT
 <213> Homo sapiens

Arg	Leu	Arg	Glu	Glu	Arg	Ala	His	Ala	Leu	Lys	Thr	Lys	Glu	Lys	Leu
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Ala	Gln	Thr	Ala	Thr	Ala	Ser	Ser	Ala	Ala	Val	Gly	Ser	Gly	Pro	Pro
			20					25					30		
Pro	Glu	Ala	Glu	Gln	Ala	Trp	Pro	Gln	Ser	Ser	Gly	Glu	Glu	Glu	Leu
		35				40					45				
Gln	Leu	Gln	Leu	Ala	Leu	Ala	Met	Ser	Lys	Glu	Glu	Ala	Asp	Gln	Pro
	50				55					60					
Pro	Ser	Cys	Gly	Pro	Glu	Asp	Asp	Ala	Gln	Leu	Gln	Leu	Ala	Leu	Ser
65					70				75					80	
Leu	Ser	Arg	Glu	Glu	His	Asp	Lys	Glu	Glu	Arg	Ile	Arg	Arg	Gly	Asp

				85						90					95				
Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr	Gly				
				100						105					110				
Gly	Lys	Glu	Glu	Ser	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	Pro				
		115					120					125							
Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro	Met				
	130					135						140							
Ala	Ala																		
145																			

<210> 741

<211> 726

<212> DNA

<213> Homo sapiens

<400> 741

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120
cgagtgtgcc gccgcttgta tgcgatgag caccgcgccg aaattattaa tactgactcg
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720
gtcgac
726

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<210> 742

<211> 242

<212> PRT

<213> Homo sapiens

<400> 742

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1				5				10						15					
Asn	Glu	Tyr	Val	Asn	Leu	Pro	Val	Ile	Cys	Leu	Val	Gly	Pro	Thr	Ala				
			20				25					30							
Ser	Gly	Lys	Ser	Gly	Leu	Ala	Val	Arg	Val	Cys	Arg	Arg	Leu	Tyr	Val				


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      35              40              45
Asp Glu His Pro Ala Glu Ile Ile Asn Thr Asp Ser Met Val Val Tyr
      50              55              60
Arg Gly Met Asp Ile Gly Thr Ala Thr Pro Thr Leu Arg Glu Gln Arg
      65              70              75              80
Thr Val Val His His Leu Val Ser Ile Leu Asp Val Thr Val Pro Ser
      85              90              95
Ser Leu Val Leu Met Gln Thr Leu Ala Arg Asp Ala Val Glu Asp Cys
      100             105             110
Leu Ser Arg Gly Val Ile Pro Val Leu Val Gly Gly Ser Ala Leu Tyr
      115             120             125
Thr Lys Ala Ile Ile Asp Glu Met Ser Ile Pro Pro Thr Asp Pro Glu
      130             135             140
Val Arg Ala Arg Trp Gln Glu Lys Leu Asp Ala Glu Gly Pro Arg Val
      145             150             155             160
Leu His Asp Glu Leu Ala Arg Arg Asp Pro Lys Ala Ala Glu Ser Ile
      165             170             175
Leu Pro Gly Asn Gly Arg Arg Ile Val Ser Cys Pro Arg Ser Leu Leu
      180             185             190
Thr Leu Thr Gly Ser Phe Thr Ala Thr Asp Pro Arg Arg Asp Pro Pro
      195             200             205
Leu Ala Lys Thr Val Gln Met Gly Leu Glu Leu Ser Arg Lys Asp Ile
      210             215             220
Asp Gln Arg Ile Ala Asp Arg Val Asp Gln Met Trp Ala Tyr Gly Phe
      225             230             235             240
Val Asp

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<210> 743
 <211> 430
 <212> DNA
 <213> Homo sapiens

<400> 743
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 120
 aagctatttg tacgagtgtg cccggcgac gtgtactcag aggagcccga tggcactatt
 180
 tccgtggagt acgcagcgtg tctggagtgt ggcacttgtc tggcggttgc tgcgccaggg
 240
 tcgcttgaat ggcactatcc cgcaggtgca atgggtattt cgttcagaga aggatgaagt
 300
 ccttggtggc gactgtaaag cgacatggcc gtcgctcggt aggaggaatt gtggtgtccg
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 420
 ctggtcgcga
 430

<210> 744
 <211> 98
 <212> PRT

<213> Homo sapiens

<400> 744

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Xaa Lys Ser Asp Gly Phe Gly Ser Val Ala Ser Arg Leu Ala Arg Asn
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His Tyr Asp Val Asp Glu Gly Asn Ser Xaa Ile His Val Asn Gln Asp
      20           25           30
Ile Ala Arg Arg Thr Gly Thr Gly Lys Leu Leu Val Arg Val Cys Pro
      35           40           45
Ala His Val Tyr Ser Glu Glu Pro Asp Gly Thr Ile Ser Val Glu Tyr
      50           55           60
Ala Ala Cys Leu Glu Cys Gly Thr Cys Leu Ala Val Ala,Ala Pro Gly
65           70           75           80
Ser Leu Glu Trp His Tyr Pro Ala Gly Ala Met Gly Ile Ser Phe Arg
      85           90           95
Glu Gly

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<210> 745

<211> 362

<212> DNA

<213> Homo sapiens

<400> 745

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120
tatgagcagg cggcgtttac ccgcatctg gaaagctcgc tgatcaaggg cctgatcctc
180
gcccagccga acaactactc cgaagaactg cgcgacgtac tcggcgtgaa gctgccgcat
240
tacttgattc gcgcgcggca gtacatccac gacaacgcc gcgaagccgt gcatctggaa
300
gacctggaaa ccgctgccgg ggtatcgcgg ttcaagttgt tcgatgcgtt tcgcaaatac
360
tt
362

```

<210> 746

<211> 108

<212> PRT

<213> Homo sapiens

<400> 746

```

Met Asp Ala Val Asp Gly Ala Ser Ala Ser Trp Trp Arg Met Ala Arg
 1           5           10           15
Tyr Phe Ile Ala Glu Leu Glu Arg Ser Ser Glu Leu Tyr Glu Gln Ala
      20           25           30
Ala Phe Thr Arg Asp Leu Glu Ser Ser Leu Ile Lys Gly Leu Ile Leu
      35           40           45
Ala Gln Pro Asn Asn Tyr Ser Glu Glu Leu Arg Asp Val Leu Gly Val
      50           55           60
Lys Leu Pro His Tyr Leu Ile Arg Ala Arg Gln Tyr Ile His Asp Asn

```

```

65              70              75              80
Ala Arg Glu Ala Val His Leu Glu Asp Leu Glu Thr Ala Ala Gly Val
              85              90              95
Ser Arg Phe Lys Leu Phe Asp Ala Phe Arg Lys Tyr
              100              105

```

<210> 747
 <211> 416
 <212> DNA
 <213> Homo sapiens

```

<400> 747
nagcgcgttga tcgccgccga ccgtttcatc ccgcaatcac ccgacatggc ggcctatattt
60
ctgaatgccg atggcacgcc taaagccacc ggcacgctgc tcaagaaccc agcgctggcc
120
gccgtgttca aacgtatcgc caaggaagga ccggacgcgc tgtaccacgg gccgattgcc
180
gacgagatcg cgcgcaaggt tcagggcaac cgcaatgcgg gcagcctgtc gcaagcggac
240
ctcaaggctt acaccgcca ggaacgcacg ccgctgtgca ccgactacaa gcaatatcag
300
gtgtgcggca tgccaccgcc gtcgtcaggc gggattgcgg tggcgcagat cctcggcacg
360
ctgcaggccg tggaagcccg cgaccacgc ctggccatcg ccccatgaa accggt
416

```

<210> 748
 <211> 138
 <212> PRT
 <213> Homo sapiens

```

<400> 748
Xaa Ala Leu Ile Ala Ala Asp Arg Phe Ile Pro Gln Ser Pro Asp Met
1              5              10              15
Ala Ala Tyr Phe Leu Asn Ala Asp Gly Thr Pro Lys Ala Thr Gly Thr
              20              25              30
Leu Leu Lys Asn Pro Ala Leu Ala Val Phe Lys Arg Ile Ala Lys
              35              40              45
Glu Gly Pro Asp Ala Leu Tyr His Gly Pro Ile Ala Asp Glu Ile Ala
50              55              60
Arg Lys Val Gln Gly Asn Arg Asn Ala Gly Ser Leu Ser Gln Ala Asp
65              70              75              80
Leu Lys Ala Tyr Thr Ala Lys Glu Arg Thr Pro Leu Cys Thr Asp Tyr
              85              90              95
Lys Gln Tyr Gln Val Cys Gly Met Pro Pro Pro Ser Ser Gly Gly Ile
              100              105              110
Ala Val Ala Gln Ile Leu Gly Thr Leu Gln Ala Val Glu Ala Arg Asp
              115              120              125
Pro Arg Leu Ala Ile Ala Pro Met Lys Pro
              130              135

```

<210> 749
 <211> 1211

<212> DNA

<213> Homo sapiens

<400> 749

nagtcctaga cgccagaccc gctcagaccc tcctgccagg tgacagccgc caagatgggg
60
tcttggggccc tgetgtggcc tcccctgctg ttcaccgggc tgctcgccg acccccgggg
120
accatggccc agggccagta ctgctctgtg aacaaggaca tctttgaagt agaggagaac
180
acaaatgtca ccgagccgct ggtggacatc cacgtcccgg agggccagga ggtgaccctc
240
ggagccttgt ccacccctt tgcatttcgg atccagggaa accagctgtt tctcaacgtg
300
actcctgatt acgaggagaa gtcactgctt gaggctcagc tgctgtgtca gagcggaggc
360
acattggtga cccagctaag ggtgttcgtg tcagtgtgtg acgtcaatga caatgcccc
420
gaattcccct ttaagaccaa ggagataagg gtggaggagg acacgaaagt gaactccacc
480
gtcatccccg agacgcaact gcaggctgag gaccgcgaca aggacgacat tctgttctac
540
accctccagg aaatgacagc aggtgccagt gactacttct ccctgggtgag tgtaaaccgt
600
cccgccctga ggctggaccg gccctggac ttctacgagc ggccgaacat gaccttctgg
660
ctgtggtgac gggacactcc gggggagaat gtggaacca gccacactgc caccgccaca
720
ctagtgtgta acgtggtgcc cgccgacctg cggcccccggt gggttcctgcc ctgcaccttc
780
tcagatggct acgtctgcat tcaagctcag taccacgggg ctgtccccac ggggcacata
840
ctgccatctc ccctcgctct gcgtcccga cccatctacg ctgaggacgg agaccgcggc
900
atcaaccagc ccatcatcta cagcatcttt aggggaaacg tgaatggtac attcatcatc
960
caccagact cgggcaacct caccgtggcc aggagtgtcc ccagccccat gaccttcttc
1020
ctgtggtgta agggccaaca ggccgacctt gcccgctact cagtgacca ggtcacctgt
1080
gagggtgtg gctgcggccg ggagcccgcc ccgcttcccc cagagcctgt atcgtggcac
1140
cgtggcgctg ggcgtggag cgggcgttgt ggtcaaggat gcagctgccc cttttcagcc
1200
tctgaggatc c
1211

<210> 750

<211> 385

<212> PRT

<213> Homo sapiens

<400> 750

Met Gly Ser Trp Ala Leu Leu Trp Pro Pro Leu Leu Phe Thr Gly Leu

```

1           5           10           15
Leu Val Arg Pro Pro Gly Thr Met Ala Gln Ala Gln Tyr Cys Ser Val
20           25           30
Asn Lys Asp Ile Phe Glu Val Glu Glu Asn Thr Asn Val Thr Glu Pro
35           40           45
Leu Val Asp Ile His Val Pro Glu Gly Gln Glu Val Thr Leu Gly Ala
50           55           60
Leu Ser Thr Pro Phe Ala Phe Arg Ile Gln Gly Asn Gln Leu Phe Leu
65           70           75           80
Asn Val Thr Pro Asp Tyr Glu Glu Lys Ser Leu Leu Glu Ala Gln Leu
85           90           95
Leu Cys Gln Ser Gly Gly Thr Leu Val Thr Gln Leu Arg Val Phe Val
100          105          110
Ser Val Leu Asp Val Asn Asp Asn Ala Pro Glu Phe Pro Phe Lys Thr
115          120          125
Lys Glu Ile Arg Val Glu Glu Asp Thr Lys Val Asn Ser Thr Val Ile
130          135          140
Pro Glu Thr Gln Leu Gln Ala Glu Asp Arg Asp Lys Asp Asp Ile Leu
145          150          155          160
Phe Tyr Thr Leu Gln Glu Met Thr Ala Gly Ala Ser Asp Tyr Phe Ser
165          170          175
Leu Val Ser Val Asn Arg Pro Ala Leu Arg Leu Asp Arg Pro Leu Asp
180          185          190
Phe Tyr Glu Arg Pro Asn Met Thr Phe Trp Leu Leu Val Arg Asp Thr
195          200          205
Pro Gly Glu Asn Val Glu Pro Ser His Thr Ala Thr Ala Thr Leu Val
210          215          220
Leu Asn Val Val Pro Ala Asp Leu Arg Pro Pro Trp Phe Leu Pro Cys
225          230          235          240
Thr Phe Ser Asp Gly Tyr Val Cys Ile Gln Ala Gln Tyr His Gly Ala
245          250          255
Val Pro Thr Gly His Ile Leu Pro Ser Pro Leu Val Leu Arg Pro Gly
260          265          270
Pro Ile Tyr Ala Glu Asp Gly Asp Arg Gly Ile Asn Gln Pro Ile Ile
275          280          285
Tyr Ser Ile Phe Arg Gly Asn Val Asn Gly Thr Phe Ile Ile His Pro
290          295          300
Asp Ser Gly Asn Leu Thr Val Ala Arg Ser Val Pro Ser Pro Met Thr
305          310          315          320
Phe Leu Leu Leu Val Lys Gly Gln Gln Ala Asp Leu Ala Arg Tyr Ser
325          330          335
Val Thr Gln Val Thr Val Glu Gly Cys Gly Cys Gly Arg Glu Pro Ala
340          345          350
Pro Leu Pro Pro Glu Pro Val Ser Trp His Arg Gly Ala Trp Arg Trp
355          360          365
Ser Gly Arg Cys Gly Gln Gly Cys Ser Cys Pro Phe Ser Ala Ser Glu
370          375          380
Asp
385

```

```

<210> 751
<211> 345
<212> DNA
<213> Homo sapiens

```

<400> 751

cgcgctcgcg tcacgtcaa cgacatgagc gaggtcaaca tcgacgcggc gctggtggcg
 60
 gcaggcggcg ggctgtcgcg caccgaggag aagctcgctg agatgtcgaa cggtgcacg
 120
 tgctgcacgc tgcgcgacga cctgatgcag gaagtggcga gactggcggg cgaaggccgc
 180
 ttcgatgcgc tggatcatga gagcaccggc gtgtccgagc cgatgccggg cgcgcaccg
 240
 ttcgatttcc gtgaccagga cggcgtctcg ctccgccgacg tcgcgcggtt ggataccatg
 300
 gtcaccgtcg tcgacgcgcg gtccttcctg cgcgactacg gctcg
 345

<210> 752

<211> 115

<212> PRT

<213> Homo sapiens

<400> 752

Arg	Val	Ala	Val	Ile	Val	Asn	Asp	Met	Ser	Glu	Val	Asn	Ile	Asp	Ala
1				5					10					15	
Ala	Leu	Val	Ala	Ala	Gly	Gly	Gly	Leu	Ser	Arg	Thr	Glu	Glu	Lys	Leu
		20						25					30		
Val	Glu	Met	Ser	Asn	Gly	Cys	Ile	Cys	Cys	Thr	Leu	Arg	Asp	Asp	Leu
		35					40					45			
Met	Gln	Glu	Val	Ala	Arg	Leu	Ala	Gly	Glu	Gly	Arg	Phe	Asp	Ala	Leu
	50					55					60				
Val	Ile	Glu	Ser	Thr	Gly	Val	Ser	Glu	Pro	Met	Pro	Val	Ala	Ala	Thr
65					70					75				80	
Phe	Asp	Phe	Arg	Asp	Gln	Asp	Gly	Val	Ser	Leu	Ala	Asp	Val	Ala	Arg
			85					90					95		
Leu	Asp	Thr	Met	Val	Thr	Val	Val	Asp	Ala	Ala	Ser	Phe	Leu	Arg	Asp
			100					105					110		
Tyr	Gly	Ser													
		115													

<210> 753

<211> 352

<212> DNA

<213> Homo sapiens

<400> 753

gcgcgccagt acgccaagac cgtccgcaag gaccgcaagg gcgaacggcg gcgtcggggc
 60
 gcgtcggact agtccacgat gcatccgaac cgcgccttcc gctttgccga tgatgtctcg
 120
 atgctcgatt tcgcggccaa gcgagccttt gcgcacatct tcgtgagcac gcccgagggg
 180
 cctatggtag cgcattgccc ggttacgccc ttgcacggag ccttccgctt ccatgtcgcg
 240
 cgcggcaatc ggatcgcgcg gcacctggat ggcgcgacgc tgctgctcag catcagcgcg
 300

accgacggct atatcagccc gagctggtac gccgaccgc agggaccaca gt
352

<210> 754
<211> 91
<212> PRT
<213> Homo sapiens

<400> 754
Met His Pro Asn Arg Ala Phe Arg Phe Ala Asp Asp Val Ser Met Leu
1 5 10 15
Asp Phe Ala Ala Lys Arg Ala Phe Ala His Ile Phe Val Ser Thr Pro
20 25 30
Glu Gly Pro Met Val Ala His Ala Pro Val Thr Pro Phe Asp Gly Ala
35 40 45
Phe Arg Phe His Val Ala Arg Gly Asn Arg Ile Ala Arg His Leu Asp
50 55 60
Gly Ala Thr Leu Leu Leu Ser Ile Ser Ala Thr Asp Gly Tyr Ile Ser
65 70 75 80
Pro Ser Trp Tyr Ala Asp Pro Gln Gly Pro Gln
85 90

<210> 755
<211> 301
<212> DNA
<213> Homo sapiens

<400> 755
tgggatgcag ggtctttctt ctccaaggat ttcattcctg gagggagaaa agggccccag
60
ctgtctgcc a tcaaaccggg ttgccgggct ggagctcctc ccaggcccgt gtgaggaaga
120
gcaaaggccg gcaggggctc gatggggacca gtcgctcgct caggcccagg aaaaccacac
180
agctgggggc tgtcaggatt ggaccagggt caggccggcc aggcgatggc gggaaaagca
240
ggcccactct gcagacctca atgtctcagg tgcactgcag ggcaaccccg cctacccccg
300
g
301

<210> 756
<211> 99
<212> PRT
<213> Homo sapiens

<400> 756
Met Gln Gly Leu Ser Ser Pro Arg Ile Ser Phe Leu Glu Gly Glu Lys
1 5 10 15
Gly Pro Ser Cys Leu Pro Ser Asn Arg Val Ala Gly Leu Glu Leu Leu
20 25 30
Pro Gly Pro Cys Glu Glu Glu Gln Arg Pro Ala Gly Ala Arg Trp Asp
35 40 45
Gln Ser Leu Ala Gln Ala Gln Glu Asn His Thr Ala Gly Gly Cys Gln

50 55 60
 Asp Trp Thr Arg Val Arg Pro Ala Arg Arg Trp Arg Glu Lys Gln Ala
 65 70 75 80
 His Ser Ala Asp Leu Asn Val Ser Gly Ala Leu Gln Gly Asn Pro Ala
 85 90 95
 Tyr Pro Gly

<210> 757
 <211> 311
 <212> DNA
 <213> Homo sapiens

<400> 757
 actgaggcga tcgccagagg ggtgggctg cgagggctgc tcaacatcca gtctgccctg
 60
 gtctccgatg ttctctacgt catcgaggcc aaccccaggg catcgcgac agtccccctc
 120
 gtctcaaagg catccggcgt gcagctcgcc aaagcggcgg ccctcatcat gacaggggag
 180
 acgatcgct cgctcaggcg ctccggccac ctgcccagg cgcacgcgc cgtcaccgat
 240
 cccgatgacc cgatcgccgt caaggaggcg gtcctaccct tcaaacgatt ccgcaccacc
 300
 gagggacgcg t
 311

<210> 758
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 758
 Thr Glu Ala Ile Ala Arg Gly Val Gly Val Arg Gly Leu Leu Asn Ile
 1 5 10 15
 Gln Phe Ala Leu Val Ser Asp Val Leu Tyr Val Ile Glu Ala Asn Pro
 20 25 30
 Arg Ala Ser Arg Thr Val Pro Phe Val Ser Lys Ala Ser Gly Val Gln
 35 40 45
 Leu Ala Lys Ala Ala Ala Leu Ile Met Thr Gly Glu Thr Ile Ala Ser
 50 55 60
 Leu Arg Arg Ser Gly His Leu Pro Glu Ala Asp Ala Ala Val Thr Asp
 65 70 75 80
 Pro Asp Asp Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Lys Arg
 85 90 95
 Phe Arg Thr Thr Glu Gly Arg
 100

<210> 759
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 759

gtgcacaccg gcaagctggg gtggaactgg gacagcggca acccggaacga cactacgccg
60
attgccgagg gcaagaccta caccgcaac tcgccgaaca tgtgggtccat gttcgccgtc
120
gacgaaaaac tcggcatgct ctacctgccg atgggcaacc agacccccga ccagttcggg
180
ggctaccgca cgctcgctc ggaactgcac gctgccggcc tgacagcgct ggatatcgac
240
actggtaaag tgcgctggca ctaccagttc acccaccatg acctgtggga catggacgtg
300
ggcggccagc cgagcctgat cgacatcaag accgccgccg gcgtgaaaca agccgtgatg
360
gcctcgacca agcaaggcag catctacgct t
391

<210> 760
<211> 130
<212> PRT
<213> Homo sapiens

<400> 760
Val His Thr Gly Lys Leu Val Trp Asn Trp Asp Ser Gly Asn Pro Asp
1 5 10 15
Asp Thr Thr Pro Ile Ala Glu Gly Lys Thr Tyr Thr Arg Asn Ser Pro
20 25 30
Asn Met Trp Ser Met Phe Ala Val Asp Glu Lys Leu Gly Met Leu Tyr
35 40 45
Leu Pro Met Gly Asn Gln Thr Pro Asp Gln Phe Gly Gly Tyr Arg Thr
50 55 60
Pro Ala Ser Glu Leu His Ala Ala Gly Leu Thr Ala Leu Asp Ile Asp
65 70 75 80
Thr Gly Lys Val Arg Trp His Tyr Gln Phe Thr His His Asp Leu Trp
85 90 95
Asp Met Asp Val Gly Gly Gln Pro Ser Leu Ile Asp Ile Lys Thr Ala
100 105 110
Ala Gly Val Lys Gln Ala Val Met Ala Ser Thr Lys Gln Gly Ser Ile
115 120 125
Tyr Ala
130

<210> 761
<211> 324
<212> DNA
<213> Homo sapiens

<400> 761
cctaggtagg cccaaagggg cctaactttc ttgctgccct ggtggagcaa gaaatatctt
60
ctaggagagg ccaatccttc cctgccccac agtccttct ctgcaaagct cagggggcaa
120
tcaggtacct cctgcccag agggcccccatt ggttcctcgc ctaaggaagg cagggcgagg
180
cattgggagc cgttgacagc tgggctcagc tggggggagg ggtcagtttg ggagcaggtg
240

cagatttcag ggaggggggg gcctaaaggg aagtagggat cttggtaggc tgcaaaattt
300

tcctcccat ccccatcca caga
324

<210> 762

<211> 105

<212> PRT

<213> Homo sapiens

<400> 762

Met	Gly	Asp	Gly	Glu	Glu	Asn	Phe	Ala	Ala	Tyr	Gln	Asp	Pro	Tyr	Phe
1				5					10					15	
Pro	Leu	Gly	Pro	Pro	Leu	Pro	Glu	Ile	Cys	Thr	Cys	Ser	Gln	Thr	Asp
			20				25						30		
Pro	Ser	Pro	Gln	Leu	Ser	Pro	Ala	Val	Asn	Gly	Ser	Gln	Cys	Pro	Ala
		35					40					45			
Leu	Pro	Ser	Leu	Gly	Glu	Glu	Pro	Trp	Gly	Pro	Leu	Gly	Gln	Glu	Val
	50				55					60					
Pro	Asp	Cys	Pro	Leu	Ser	Phe	Ala	Glu	Lys	Glu	Leu	Trp	Gly	Arg	Glu
65				70					75					80	
Gly	Leu	Ala	Ser	Pro	Arg	Arg	Tyr	Phe	Leu	Leu	His	Gln	Gly	Ser	Lys
			85				90							95	
Lys	Val	Arg	Pro	Leu	Trp	Ala	Tyr	Leu							
			100				105								

<210> 763

<211> 301

<212> DNA

<213> Homo sapiens

<400> 763

acgcgttatg ggcgccccgg atgggcgatg cgctatccca cacctcgatg atggcggaca
60
tcctcggcgg tgtgctggaa gtggcgccca atatcgcatg tactgcgggc gcgaccgctg
120
ccgcggtggc cgccaccggc tttaccgagg ccaccggcgg cctcggctgc ttctgctgg
180
gcgctgcctt gggcaccatt gccggcctgg ccatgagcaa cattggcgcg gacacagggc
240
tgaccaagat atgcaatgcc tttaacaacg ccttatttgc gccaccgtg catgcgaaca
300
t
301

<210> 764

<211> 100

<212> PRT

<213> Homo sapiens

<400> 764

Met	Phe	Ala	Cys	Thr	Val	Gly	Ala	Asn	Lys	Ala	Leu	Leu	Lys	Ala	Leu
1				5				10					15		
His	Ile	Leu	Val	Ser	Pro	Val	Ser	Ala	Pro	Met	Leu	Leu	Met	Ala	Arg

```

          20          25          30
Pro Ala Met Val Pro Lys Ala Ala Pro Ser Arg Lys Gln Pro Arg Pro
          35          40          45
Pro Val Ala Ser Val Lys Pro Val Ala Ala Thr Ala Ala Ala Val Ala
          50          55          60
Pro Ala Val Ile Ala Ile Leu Ala Ala Thr Ser Ser Thr Pro Pro Arg
65          70          75          80
Met Ser Ala Ile Ile Glu Val Trp Asp Ser Ala Ser Pro Ile Arg Ala
          85          90          95
Ala His Asn Ala
          100

```

<210> 765
 <211> 831
 <212> DNA
 <213> Homo sapiens

<400> 765
 ngcacactcc agcctctgtt ctttctctcc ttgtgccttt gcccttacca cggttcctca
 60
 taacattggt gttcctgtat ttaaggccct ataaacaggg agatgcgcca cctcatcagt
 120
 agcctccaga atcacaatca ccagctgaaa ggggaggtcc tgagatataa gcggaaattg
 180
 agagaagccc agtctgacct gaacaagaca cgcttgcgta gtggtagtgc cctcctgcag
 240
 tcccagtcta gtactgagga cccgaaggat gagcctgcgg agctaaaacc agattctggg
 300
 gacttatect ccagtcctc agcttcaaag gcattctcagg aggatgccaa tgaaatcaag
 360
 tctaaacggg atgaagaaga acgagaacga gaaaggaggg agaaggagag ggaacgagaa
 420
 agagaacggg agaaggagaa ggagagagaa cgagagaagc agaagctaaa agagtcagaa
 480
 aaagagagag attctgctaa ggataaagag aaaggcaaac atgatgatgg acggaaaaag
 540
 gaagcagaaa ttatcaaaca attgaagatt gaactcaaga aggcacagga gagccaaaag
 600
 gagatgaaac tattgctgga tatgtaccgt tctgccccaa aggaacagag agacaaagtt
 660
 cagctgatgg cagctgagaa gaagtctaag gcagagttgg aagatctaag gcaaagactc
 720
 aaggatctgg aagataaaga gaagaaagag aacaagaaaa tggctgatga ggatgccttg
 780
 aggaagatcc gggcagtgga ggagcagata gaatacctac agaagaagct a
 831

<210> 766
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 766
 Met Arg His Leu Ile Ser Ser Leu Gln Asn His Asn His Gln Leu Lys

```

      1           5           10           15
Gly Glu Val Leu Arg Tyr Lys Arg Lys Leu Arg Glu Ala Gln Ser Asp
      20           25           30
Leu Asn Lys Thr Arg Leu Arg Ser Gly Ser Ala Leu Leu Gln Ser Gln
      35           40           45
Ser Ser Thr Glu Asp Pro Lys Asp Glu Pro Ala Glu Leu Lys Pro Asp
      50           55           60
Ser Gly Asp Leu Ser Ser Gln Ser Ser Ala Ser Lys Ala Ser Gln Glu
      65           70           75           80
Asp Ala Asn Glu Ile Lys Ser Lys Arg Asp Glu Glu Glu Arg Glu Arg
      85           90           95
Glu Arg Arg Glu Lys Glu Arg Glu Arg Glu Arg Glu Arg Glu Lys Glu
      100          105          110
Lys Glu Arg Glu Arg Glu Lys Gln Lys Leu Lys Glu Ser Glu Lys Glu
      115          120          125
Arg Asp Ser Ala Lys Asp Lys Glu Lys Gly Lys His Asp Asp Gly Arg
      130          135          140
Lys Lys Glu Ala Glu Ile Ile Lys Gln Leu Lys Ile Glu Leu Lys Lys
      145          150          155          160
Ala Gln Glu Ser Gln Lys Glu Met Lys Leu Leu Leu Asp Met Tyr Arg
      165          170          175
Ser Ala Pro Lys Glu Gln Arg Asp Lys Val Gln Leu Met Ala Ala Glu
      180          185          190
Lys Lys Ser Lys Ala Glu Leu Glu Asp Leu Arg Gln Arg Leu Lys Asp
      195          200          205
Leu Glu Asp Lys Glu Lys Lys Glu Asn Lys Lys Met Ala Asp Glu Asp
      210          215          220
Ala Leu Arg Lys Ile Arg Ala Val Glu Glu Gln Ile Glu Tyr Leu Gln
      225          230          235          240
Lys Lys Leu

```

<210> 767

<211> 431

<212> DNA

<213> Homo sapiens

<400> 767

```

gctagctcgc tcgcactcat tctcgaggagg cttccccgcg ccggccgcgt cccgccccgt
60
ccccggcacc agaagttcct ctgcgcgtcc gacggcgaca tgggcgtccc caccgccccg
120
gaggccggca gctggcgctg gggatccctg ctcttcgctc tcttcctggc tgcgtcccta
180
ggtccggtgg cagccttcaa ggtcgccacg ccgtattccc tgtatgtctg tcccgagggg
240
cagaacgtca cctcacctg caggctcttg ggccctgtgg acaaagggca cgatgtgacc
300
ttctacaaga cgtggtaccg cagctcgagg ggcgaggtgc agacctgctc agagcgccgg
360
cccatccgca acctcacgtt ccaggacctt cacctgcacc atggaggcca ccaggctgcc
420
aacaccagcc a
431

```

<210> 768
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 768
 Met Gly Val Pro Thr Ala Pro Glu Ala Gly Ser Trp Arg Trp Gly Ser
 1 5 10 15
 Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val Ala Ala
 20 25 30
 Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro Glu Gly Gln
 35 40 45
 Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val Asp Lys Gly His
 50 55 60
 Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser Ser Arg Gly Glu Val
 65 70 75 80
 Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg Asn Leu Thr Phe Gln Asp
 85 90 95
 Leu His Leu His His Gly Gly His Gln Ala Ala Asn Thr Ser
 100 105 110

<210> 769
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 769
 tgtacacctc gtaatacatg atcgcgatac cgcccgcgat gaccctaagc aactcattct
 60
 cgacttcgaa ctccatcaag tgatttttgc ggtcgacgaa tctggtttcc gtatgaaaga
 120
 acggtatgtt ttgtatgtcg cggccctgcc actcaaacct caccgtgtca cccacctcaa
 180
 aaaaatcccg ggtcggccca caaataaatc aattgcgccg ctctccgag ttcttccatg
 240
 tcaacgatct cccctggctg ctcaagccaa ggccctcgcg gccgtgggac tccaagggtg
 300
 acgttgaccc gactgatttc ggaccagttg gcgtcggtat tgggggcagg gtagttaccg
 360
 cccatgtcga tgatctacat cgccaccggc agcgtgtctt cgtagtcgtc atgcctgac
 420
 an
 422

<210> 770
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 770
 Met Phe Cys Met Ser Arg Pro Cys His Ser Asn Leu Thr Val Ser Pro
 1 5 10 15
 Thr Ser Lys Lys Ser Arg Val Gly Pro Gln Ile Asn Gln Leu Arg Arg

```

          20          25          30
Ser Ser Glu Phe Phe His Val Asn Asp Leu Pro Trp Leu Leu Lys Pro
          35          40          45
Arg Pro Ser Arg Pro Trp Asp Ser Lys Val Asp Val Asp Pro Thr Asp
          50          55          60
Phe Gly Pro Val Gly Val Gly Ile Gly Gly Arg Val Val Thr Ala His
65          70          75          80
Val Asp Asp Leu His Arg His Arg Gln Arg Val Phe Val Val Val Met
          85          90          95
Pro Asp Xaa

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<210> 771
 <211> 369
 <212> DNA
 <213> Homo sapiens

```

<400> 771
gcctacgcgc aattcctcgc gggatatggcg tttaacaatg cgtctctcgg gtatgtgcat
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gcaatggcgc atcagctggg cggtttttac gatctgccgc acggcgtgtg caatgcgata
120
ctgttgccac acgtgcagac gtttaactgc aaagtggcgg cctcgcgcct gcgtgattgc
180
gcccaggcca tgggtgtcga tgtcagtcaa atgacagcag aacagggcgc acaggcgtgt
240
atcgcagaga ttcgctctct ggcacgtcag gtgaatatcc cggtgggatt gcgtgacctc
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aacgtgaagg aagcggactt cccgattctg gcgaccaacg cgctaaaaga ccctgtgggt
360
ttgattaat
369

```

<210> 772
 <211> 123
 <212> PRT
 <213> Homo sapiens

```

<400> 772
Ala Tyr Ala Gln Phe Leu Ala Gly Met Ala Phe Asn Asn Ala Ser Leu
1          5          10          15
Gly Tyr Val His Ala Met Ala His Gln Leu Gly Gly Phe Tyr Asp Leu
          20          25          30
Pro His Gly Val Cys Asn Ala Ile Leu Leu Pro His Val Gln Thr Phe
          35          40          45
Asn Cys Lys Val Ala Ala Ser Arg Leu Arg Asp Cys Ala Gln Ala Met
          50          55          60
Gly Val Asp Val Ser Gln Met Thr Ala Glu Gln Gly Ala Gln Ala Cys
65          70          75          80
Ile Ala Glu Ile Arg Ser Leu Ala Arg Gln Val Asn Ile Pro Val Gly
          85          90          95
Leu Arg Asp Leu Asn Val Lys Glu Ala Asp Phe Pro Ile Leu Ala Thr
          100          105          110
Asn Ala Leu Lys Asp Pro Val Gly Leu Ile Asn

```

115

120

<210> 773
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 773
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 60
 ggttacttga tccgcgtgga gccggggcgta caaactccgg aattcacctt ggaaaacgcc
 120
 tccggttcct gccgggattc ggcgtgggtg ctggtgcaac tgctgcgcaa cctgggcctg
 180
 gcggcgcgat ttgtgtctgg ctatctgac caactgaccg ccgacgtcaa agccctcgac
 240
 ggcccgctccg gcaccgaggt ggatttcacc gacctgcatg cctggtgcga agtgattttg
 300
 cccggcgcc
 309

<210> 774
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 774
 Pro Pro Leu Pro Ala Val Asp Phe Leu Val Gly Leu Asn Gln Arg Leu
 1 5 10 15
 Ala Ala Asp Ile Gly Tyr Leu Ile Arg Val Glu Pro Gly Val Gln Thr
 20 25 30
 Pro Glu Phe Thr Leu Glu Asn Ala Ser Gly Ser Cys Arg Asp Ser Ala
 35 40 45
 Trp Leu Leu Val Gln Leu Leu Arg Asn Leu Gly Leu Ala Ala Arg Phe
 50 55 60
 Val Ser Gly Tyr Leu Ile Gln Leu Thr Ala Asp Val Lys Ala Leu Asp
 65 70 75 80
 Gly Pro Ser Gly Thr Glu Val Asp Phe Thr Asp Leu His Ala Trp Cys
 85 90 95
 Glu Val Tyr Leu Pro Gly Ala
 100

<210> 775
 <211> 4125
 <212> DNA
 <213> Homo sapiens

<400> 775
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 60
 atctcatctg acgtgagttc aagtacagat cacacgcca ctaaagcca gaagaatgtg
 120
 gctaccagcg aagactccga cctgagcatg cgcacactga gcacgccag cccagccctg
 180

atatgtccac cgaatctccc aggatttcag aatggaaggg gctcgtccac ctctcgtcc
240
tccatcacccg gggagacggg ggccatgggtg cactccccgc ccccgacccg cctcacacac
300
ccgctcatcc ggctcgccctc cagacccag aaggatcagg ccagcataga ccggctccccg
360
gaccactcca tgggtgcagat cttctccttc ctgcccacca accagctgtg ccgctgcgcg
420
cgagtgtgcc gccgctggta caacctggcc tgggacccgc ggctctggag gactatccgc
480
ctgacgggcg agaccatcaa cgtggaccgc gccctcaagg tgctgacccg cagactctgc
540
caggacaccc ccaacgtgtg tctcatgctg gaaaccgtaa ctgtcagtgg ctgcaggcgg
600
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660
gtctcaggct gttacaatat ctccaacgag gccgtctttg atgtgggtgtc cctctgccct
720
aatctggagc acctggatgt gtcaggatgc tccaaagtga cctgcatcag cttgacccgg
780
gaggcctcca ttaaactgtc acccttgcac ggcaaacaga tttccatccg ctacctggac
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1260
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1320
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1380
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1440
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1500
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1620
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1680
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1740
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1800

gcccctttccc tcgcacacag gccccacccc cacagttcca cgcceccccc ccaaggccac
1860
accctccctc cctagagcag cagcgaggat ccatcatcag aatcacagtg ctctccagac
1920
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1980
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2040
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2100
tgactatgac cttggccaaa gcacttcact gctctgggct gcagcttcca gcactgaatc
2160
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2280
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2340
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2400
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 3600
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 3660
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 3720
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 3780
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 3840
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 3900
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 3960
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 4020
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 4080
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 4125

<210> 776

<211> 483

<212> PRT

<213> Homo sapiens

<400> 776

Tyr	Gly	Ser	Glu	Gly	Lys	Gly	Ser	Ser	Ser	Ile	Ser	Ser	Asp	Val	Ser
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Ser	Ser	Thr	Asp	His	Thr	Pro	Thr	Lys	Ala	Gln	Lys	Asn	Val	Ala	Thr
			20					25					30		
Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro
	35						40					45			
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly
	50					55					60				
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val
65					70				75					80	
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala
				85					90					95	
Ser	Arg	Pro	Gln	Lys	Asp	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His
		100						105					110		
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg
	115						120					125			
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg
	130					135					140				
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg
145					150				155					160	
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val
			165					170						175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr

```

      180      185      190
Asp Arg Gly Leu Tyr Thr Ile Ala Gln Cys Cys Pro Glu Leu Arg Arg
      195      200      205
Leu Glu Val Ser Gly Cys Tyr Asn Ile Ser Asn Glu Ala Val Phe Asp
      210      215      220
Val Val Ser Leu Cys Pro Asn Leu Glu His Leu Asp Val Ser Gly Cys
225      230      235      240
Ser Lys Val Thr Cys Ile Ser Leu Thr Arg Glu Ala Ser Ile Lys Leu
      245      250      255
Ser Pro Leu His Gly Lys Gln Ile Ser Ile Arg Tyr Leu Asp Met Thr
      260      265      270
Asp Cys Phe Val Leu Glu Asp Glu Gly Leu His Thr Ile Ala Ala His
      275      280      285
Cys Thr Gln Leu Thr His Leu Tyr Leu Arg Arg Cys Val Arg Leu Thr
      290      295      300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu
305      310      315      320
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu
      325      330      335
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys
      340      345      350
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser
      355      360      365
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His
      370      375      380
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp
385      390      395      400
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala
      405      410      415
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser
      420      425      430
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu
      435      440      445
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg
      450      455      460
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro
465      470      475      480
Ala Phe Phe

```

<210> 777

<211> 705

<212> DNA

<213> Homo sapiens

<400> 777

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gggtaccatcg tttttaaac taattaagat attactcatt cttgttggtg cccaattcca
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caccaatctg ctctttaatg ccagactgat ggctctaaca atccttatta actccttttt
120
gtggcttcaa ggaaaaaaaa aaacctcttc tctcattcac cacctctagg ccaggagaaa
180
ttattttttg ttcaggcttt cacagtgggg gtctgaaagt gaccagtcta gaaaaggatg
240

```

actcagcaaa aggagagctc tgaaggtccc tgaggcggca cgggccagca ttattaggtc
 300
 acatgggtatg acctgaaaca aatacgttct tcccaaagt ggcaggaccg ggagagcttc
 360
 tcaccaggag ggaaccgccc caatgaccgc cggacgtcca gcaacacttg ttggtagtcc
 420
 ttgtcatct gccgtagggt cttccctgat ataggagggtg ggtcattggc attgacattg
 480
 aggagcttgg gccacacttt tcgtctgatc tcatcagtca ggagccctcc ttcactgata
 540
 gccatgcgtc taagggcagc cacatcagtg ggatcactgt tcagagcctg gtgtatctct
 600
 aacactttct ttttctttt ggcgtaaag tctgccttct ccgcgccgcc gtcccagtgg
 660
 ccggagggtgg gccgtcccct gcgcactccg gaggccatcc ccggg
 705

<210> 778
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 778
 Met Ala Ser Gly Val Arg Arg Gly Arg Pro Thr Ser Gly His Trp Asp
 1 5 10 15
 Gly Gly Ala Glu Lys Ala Asp Phe Asn Ala Lys Arg Lys Lys Lys Val
 20 25 30
 Leu Glu Ile His Gln Ala Leu Asn Ser Asp Pro Thr Asp Val Ala Ala
 35 40 45
 Leu Arg Arg Met Ala Ile Ser Glu Gly Gly Leu Leu Thr Asp Glu Ile
 50 55 60
 Arg Arg Lys Val Trp Pro Lys Leu Leu Asn Val Asn Ala Asn Asp Pro
 65 70 75 80
 Pro Pro Ile Ser Gly Lys Asn Leu Arg Gln Met Ser Lys Asp Tyr Gln
 85 90 95
 Gln Val Leu Leu Asp Val Arg Arg Ser Leu Arg Arg Phe Pro Pro Gly
 100 105 110
 Glu Lys Leu Ser Arg Ser Cys His Ile Trp Glu Glu Arg Ile Cys Phe
 115 120 125
 Arg Ser Tyr His Val Thr
 130

<210> 779
 <211> 322
 <212> DNA
 <213> Homo sapiens

<400> 779
 tccggacatg tgcaaacaat tcaatgatgt ggtgcgtcga catggtgtgc atcactctgt
 60
 gactgtgagt gattctgagg ataccgttgc gccgtcccag ctggttcgat cccctcgtaa
 120
 cgccttgcct ttgaaggaac ccagtgggaa ggctagacca agtaaatatg aatcaccaaa
 180

cgccagcaac ttcacgtca ggcattgtggc aactggcaaa gagggcactg atgatgagta
 240
 tgctaactca aactactact actcgatgtc tgccaatcga ctaggagacg aggaaacgga
 300
 ggaaatgata ggtttggcta cc
 322

<210> 780
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 780
 Met Cys Lys Gln Phe Asn Asp Val Val Arg Arg His Gly Val His His
 1 5 10 15
 Ser Val Thr Val Ser Asp Ser Glu Asp Thr Val Ala Pro Ser Gln Leu
 20 25 30
 Val Arg Ser Pro Arg Asn Ala Leu Pro Leu Lys Glu Pro Ser Gly Lys
 35 40 45
 Ala Arg Pro Ser Lys Tyr Glu Ser Pro Asn Ala Ser Asn Phe Ile Val
 50 55 60
 Arg His Val Ala Thr Gly Lys Glu Gly Thr Asp Asp Glu Tyr Ala Asn
 65 70 75 80
 Ser Asn Tyr Tyr Tyr Ser Met Ser Ala Asn Arg Leu Gly Asp Glu Glu
 85 90 95
 Thr Glu Glu Met Ile Gly Leu Ala Thr
 100 105

<210> 781
 <211> 297
 <212> DNA
 <213> Homo sapiens

<400> 781
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 60
 gtgtgtatgn gaatatgtgt gtgtatngga atgtgtgtgt gtgtttggaa tgtgtgtatg
 120
 gaatgtgtgt ctgtgtatgg aatatgtgtg agtatnggaa tgtgtgtgtg tgtttggaat
 180
 gtatcgaatg tgtgtctgtg tgtaaggaat gtgtgtgtat ggaatgtgtt tacgtgcatg
 240
 tgtctggaat gtgtgtgtat ggaatgtgtg tgtatgtgta tngaatgtg tgtgtgt
 297

<210> 782
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 782
 Xaa Arg Val Pro Gly Met Cys Val Cys Val Cys Val Cys Met Tyr Val
 1 5 10 15
 Cys Met Glu Cys Val Cys Met Xaa Ile Cys Val Cys Met Xaa Met Cys

```

      20      25      30
Val Cys Val Trp Asn Val Cys Met Glu Cys Val Ser Val Tyr Gly Ile
      35      40      45
Cys Val Ser Met Xaa Met Cys Val Cys Val Trp Asn Val Ser Asn Val
      50      55      60
Cys Leu Cys Val Arg Asn Val Cys Val Trp Asn Val Phe Thr Cys Met
65      70      75      80
Cys Leu Glu Cys Val Cys Met Glu Cys Val Cys Met Cys Met Xaa Met
      85      90      95
Cys Val Cys

```

<210> 783
 <211> 612
 <212> DNA
 <213> Homo sapiens

```

<400> 783
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60
caccgggtcg agtgagctgc ccagcagcaa gcccaccaca tcggtgacca gaccgatcac
120
tttgttgagc acgtcgatga cgggcaactt caaggaaatc caggtgcgga cttgcgcggt
180
ccgcacaaaa atcggctggg tgcgatcaa ctgcgggttg ccaatcgag aatttgcgcg
240
gttcgatgac acgtgtcttc accgtgatat tcagcagccc cagtacgtcc accggcaact
300
cgacggccac cgcgtgggt ttgttgga gctgcacaaa gccctgaatc aggttgaaca
360
gttgacaggtt gacgtccagg gcgctcttgt ccgtgccgtt ttgtatattg atcaggtcgc
420
ccaggtgcag gatctgcgtg cctggggcaa tcagcttgat tgcttcgagg ttattgatca
480
ccacctggac cgcattaccg cccagcttga gcacatcgat ggcggcctgg atcaactggc
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600
tgcccgacgc gt
612

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<210> 784
 <211> 190
 <212> PRT
 <213> Homo sapiens

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<400> 784
Met Ser Ile Cys Val Pro Gly Thr Gly Ser Ser Glu Leu Pro Ser Ser
1      5      10      15
Lys Pro Thr Thr Ser Val Thr Arg Pro Ile Thr Leu Leu Ser Thr Ser
      20      25      30
Met Thr Gly Asn Phe Lys Glu Ile Gln Val Arg Thr Cys Ala Val Arg
      35      40      45
Thr Lys Ile Gly Trp Val Ser Ile Asn Cys Gly Leu Pro Ile Ala Glu

```

```

      50              55              60
Phe Ala Arg Phe Asp Asp Thr Cys Leu His Arg Asp Ile Gln Gln Pro
65              70              75              80
Gln Tyr Val His Arg Gln Leu Asp Gly His Arg Ala Gly Phe Val Gly
      85              90              95
Gln Leu His Lys Ala Leu Asn Gln Val Glu Gln Leu Gln Val Asp Val
      100             105             110
Gln Gly Ala Leu Val Arg Ala Val Leu Tyr Ile Asp Gln Val Ala Gln
      115             120             125
Val Gln Asp Leu Arg Ala Trp Gly Asn Gln Leu Asp Cys Phe Glu Val
      130             135             140
Ile Asp His His Leu Asp Arg Ile Thr Ala Gln Leu Glu His Ile Asp
145             150             155             160
Gly Gly Leu Asp Gln Leu Ala Asp Gly Arg Val Gly Leu Glu Gln Leu
      165             170             175
Val Val Val Ala Gly Ala Asp Val Glu Ala Asp Gly Arg Arg
      180             185             190

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<210> 785
 <211> 408
 <212> DNA
 <213> Homo sapiens

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<400> 785
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cttcaggccg cccacgctcg tggctctgtca gtactgctcg acgggggtggt caaccacgtc
120
tcgcgtcgca accgcatcgt gcaggatgcg cagagtgtctg ggccagattc agacgccggc
180
cgtatggttc gctgggtgtga ggggcgcctc gacgttttcg aggggtcatag tgacctggtc
240
gcactcaacc acgacaaccc cgcagtgcgg gaacatgtca cccggatcat gaactattgg
300
tgcggtcgcg gtgttgacgg ctggcggctg gacgccgcta ttccgtcaat cctgagttct
360
gggctgcggg gctgcctccg gtgcgagaga agcgccctga cgtgagga
408

```

<210> 786
 <211> 134
 <212> PRT
 <213> Homo sapiens

```

<400> 786
Thr Leu Asp Tyr Phe Thr Ile Asp Pro Arg Leu Gly Asp Asp Asp Asp
1      5      10      15
Phe Asp His Leu Leu Gln Ala Ala His Ala Arg Gly Leu Ser Val Leu
      20      25      30
Leu Asp Gly Val Val Asn His Val Ser Arg Arg Asn Arg Ile Val Gln
      35      40      45
Asp Ala Gln Ser Ala Gly Pro Asp Ser Asp Ala Gly Arg Met Val Arg
      50      55      60
Trp Cys Glu Gly Arg Leu Asp Val Phe Glu Gly His Ser Asp Leu Val

```

```

65              70              75              80
Ala Leu Asn His Asp Asn Pro Ala Val Arg Glu His Val Thr Arg Ile
              85              90              95
Met Asn Tyr Trp Cys Gly Arg Gly Val Asp Gly Trp Arg Leu Asp Ala
              100              105              110
Ala Ile Pro Ser Ile Leu Ser Ser Gly Leu Arg Cys Cys Leu Arg Cys
              115              120              125
Glu Arg Ser Ala Leu Thr
              130

```

<210> 787
 <211> 310
 <212> DNA
 <213> Homo sapiens

```

<400> 787
acgcgtgaag ggggaatgaaa gggttttttcc tggatcaaaa tgatgcttgt ggcagacaca
60
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ccttggtctc tcctcattgc tgccgtcact gtgtgctggg catgccctgc agttacccca
180
aagctttatg tcacaacatt gaggctggcg gagaaagacc ggcccccttca cccacctta
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310

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<210> 788
 <211> 90
 <212> PRT
 <213> Homo sapiens

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<400> 788
Met Met Leu Val Ala Asp Thr Val Gly Thr Thr Asp Asp Ala Thr Leu
1              5              10              15
Val Ser Ala Val Arg His Trp Pro Thr Trp Arg Pro Trp Ser Leu Leu
              20              25              30
Ile Ala Ala Val Thr Val Cys Trp Ala Cys Pro Ala Val Thr Pro Lys
              35              40              45
Leu Tyr Val Thr Thr Leu Arg Leu Ala Glu Lys Asp Arg Pro Leu His
              50              55              60
Pro Thr Leu Asp Phe Leu Glu Gly Pro Pro Gly Ser Thr Thr Trp Pro
65              70              75              80
Val Asn Ser Leu Gly Ser Cys Trp Gly Arg
              85              90

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<210> 789
 <211> 369
 <212> DNA
 <213> Homo sapiens

<400> 789

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120
gcacgaggtg ttccaaagtg caaacaagct gctgttaaata aattattccc aaacgccaaa
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gcccttgctg gtttgcttgc ttgctttttt ctttttttgc ctgcacaga tatcgctagg
240
gcagagtatt gacatttcgt tttctttttg ttatgggtga taaagcacgg tgtttcttgt
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cccattttc
369

<210> 790
<211> 114
<212> PRT
<213> Homo sapiens

<400> 790
Met Asp Trp Gln Ser Ala Leu Gln Gly Asn Thr Gly Ile His Ser Gln
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Glu Thr Pro Cys Phe Ile Thr His Asn Lys Lys Lys Thr Lys Cys Gln
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Tyr Ser Ala Leu Ala Ile Ser Val Arg Gly Lys Lys Arg Lys Lys Gln
35 40 45
Ala Ser Lys Pro Ala Arg Ala Leu Ala Phe Gly Asn Asn Tyr Leu Thr
50 55 60
Ala Ala Cys Leu His Phe Gly Thr Pro Arg Ala Ser Arg Ala Gly Pro
65 70 75 80
Ser Cys Trp Gly Gly Glu Arg Ser Gln Arg Cys Cys Leu Ala Asp Leu
85 90 95
Gly Phe Gly Gly His Gln Lys Arg Gly Arg Leu Leu Ala Ala Ala Thr
100 105 110
Ser Arg

<210> 791
<211> 420
<212> DNA
<213> Homo sapiens

<400> 791
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120
agaatcaaaa tggaaagagt gggtaatgtg tgttcactgg aaatttctaa cattcaaaaa
180
ggagaagggg gagagtacat gtgtcatgct gtaaacaatca taggggaagc aaagagcttt
240
gcaaatgtag acataatgcc ccaggaagaa agagtgggtg cactaccacc tccagtaaca
300

catcagcatg tcatggagtt tgatttggaa cacaccacat catcaagaac accttctcct
 360
 caagaaattg tcctggaagt tgaattaagt gaaaaagacg ttaaagaatt tgagaagcag
 420

<210> 792
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 792
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 20 25 30
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 35 40 45
 Cys Ser Leu Glu Ile Ser Asn Ile Gln Lys Gly Glu Gly Gly Glu Tyr
 50 55 60
 Met Cys His Ala Val Asn Ile Ile Gly Glu Ala Lys Ser Phe Ala Asn
 65 70 75 80
 Val Asp Ile Met Pro Gln Glu Glu Arg Val Val Ala Leu Pro Pro Pro
 85 90 95
 Val Thr His Gln His Val Met Glu Phe Asp Leu Glu His Thr Thr Ser
 100 105 110
 Ser Arg Thr Pro Ser Pro Gln Glu Ile Val Leu Glu Val Glu Leu Ser
 115 120 125
 Glu Lys Asp Val Lys Glu Phe Glu Lys Gln
 130 135

<210> 793
 <211> 479
 <212> DNA
 <213> Homo sapiens

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 120
 aagccaaagt ctacaggtca ctggggcaga ggccgcccga aaccagcttc ccctcccggc
 180
 ctaggcgcg caggtccccg ccagccggg gcgatccttt ggtcggacag tgaggttggg
 240
 agcccaccgc acccaagtcc gccgcatcca cccggcgag gcgacccccg acgggcagcc
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 gctcaccttc tcctggcccc ggcttcagga aaactgcctg gaggtggccg gggttcccta
 360
 gcggaggctg ggcgggcggc ttgcgcctg cctcagtctc cccatccgtg gcccggggga
 420
 tggagcccgc tgcgcgcaga ggctgcggca ggtcccagcc aggtgccctg gaacgtgga
 479

<210> 794

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 794
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 20 25 30
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 35 40 45
 Gly Arg Gly Arg Pro Lys Pro Ala Ser Pro Pro Gly Leu Gly Ala Pro
 50 55 60
 Gly Pro Arg Pro Ala Gly Ala Ile Leu Trp Ser Asp Ser Glu Val Gly
 65 70 75 80
 Ser Pro Pro His Pro Ser Pro Pro His Pro Pro Gly Ala Gly Asp Pro
 85 90 95
 Arg Arg Ala Ala Ala His Leu Leu Leu Ala Pro Ala Ser Gly Lys Leu
 100 105 110
 Pro Gly Gly Gly Arg Gly Ser Leu Ala Glu Ala Gly Arg Arg Ala Ser
 115 120 125
 Arg Leu Pro Gln Ser Pro His Pro Trp Pro Gly Gly Trp Ser Pro Leu
 130 135 140
 Arg Ala Glu Ala Ala Ala Gly Pro Ser Gln Val Pro Trp Asn Val
 145 150 155

<210> 795
 <211> 1418
 <212> DNA
 <213> Homo sapiens

<400> 795
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 120
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 240
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 420
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accagctga ccatgaacgt tcctttccaa gccattcact tcatgaccta tgaattcctg
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<210> 796

<211> 176

<212> PRT

<213> Homo sapiens

<400> 796

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Tyr	His	Arg	Val	Thr	Asp	Cys	Val	Arg	Ala	Val	Trp	Gln	Asn	Glu	Gly
		20						25					30		
Ala	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr	Gln	Leu	Thr	Met	Asn	Val
		35					40					45			
Pro	Phe	Gln	Ala	Ile	His	Phe	Met	Thr	Tyr	Glu	Phe	Leu	Gln	Glu	His
	50					55					60				
Phe	Asn	Pro	Gln	Arg	Arg	Tyr	Asn	Pro	Ser	Ser	His	Val	Leu	Ser	Gly
65				70						75				80	
Ala	Cys	Ala	Gly	Ala	Val	Ala	Ala	Ala	Ala	Thr	Thr	Pro	Leu	Asp	Val
			85					90						95	
Cys	Lys	Thr	Leu	Leu	Asn	Thr	Gln	Glu	Ser	Leu	Ala	Leu	Asn	Ser	His
		100					105						110		
Ile	Thr	Gly	His	Ile	Thr	Gly	Met	Ala	Ser	Ala	Phe	Arg	Thr	Val	Tyr
	115					120					125				
Gln	Val	Gly	Gly	Val	Thr	Ala	Tyr	Phe	Arg	Gly	Val	Gln	Ala	Arg	Val
	130					135					140				
Ile	Tyr	Gln	Ile	Pro	Ser	Thr	Ala	Ile	Ala	Trp	Ser	Val	Tyr	Glu	Phe
145				150						155				160	
Phe	Lys	Tyr	Leu	Ile	Thr	Lys	Arg	Gln	Glu	Glu	Trp	Arg	Ala	Gly	Lys

165

170

175

<210> 797
 <211> 585
 <212> DNA
 <213> Homo sapiens

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 180
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 240
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 300
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 360
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<210> 798
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 798
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 20 25 30
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 35 40 45
 Ser Ser Glu Ile Tyr Gly Arg Thr Lys Ser Gly Ile Ala Ile Gly Gly
 50 55 60
 Ile Ala Gly Asp Gln Gln Ala Ala Leu Phe Gly Gln Met Cys Val Glu
 65 70 75 80
 Ala Gly Gln Ala Lys Asn Thr Tyr Gly Thr Gly Cys Phe Leu Leu Met
 85 90 95
 Asn Thr Gly Asp Lys Ala Val Lys Ser Lys His Gly Met Leu Thr Thr
 100 105 110
 Ile Ala Cys Gly Pro Arg Gly Glu Val Ala Tyr Ala Leu Glu Gly Ala
 115 120 125
 Val Phe Asn Gly Gly Ser Pro Val Gln Trp Leu Arg Asp Glu Leu Lys
 130 135 140
 Ile Ile Ala Asp Ala Thr Asp Thr Glu Tyr Phe Ala Gly Lys Val Lys

145		150		155		160
Asp Ser Asn Gly Val	Tyr Leu Val Pro Ala Phe Thr Gly Leu Gly Ala					
	165		170		175	
Pro Tyr Trp Asp Pro Tyr Ala Arg Gly Ala Leu Phe Gly Leu Thr Arg						
	180		185		190	
Gly Val Arg						
	195					

<210> 799
 <211> 2152
 <212> DNA
 <213> Homo sapiens

<400> 799
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 420
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 480
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 720
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<210> 800
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 800
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 Ala Gln Leu Thr Pro Val Ile Pro Ala Leu Trp Glu Ala Glu Ala Gly
 35 40 45
 Gly Ser Arg Asn Pro Ser Thr Leu Arg Gly Arg Gly Gly Gln Ile Met
 50 55 60
 Arg Ser Arg Asp Gln Asp His Pro Gly Gln Asn Gly Glu Thr Pro Ser
 65 70 75 80
 Leu Leu Lys Ile Gln Lys Leu Ala Glu Leu Ser Gly Thr His Leu
 85 90 95

<210> 801
 <211> 424

<212> DNA

<213> Homo sapiens

<400> 801

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gtaacatttc ctaccaataa aataacagcc ataattggac cgaatggatg tggtaagtct
180
accctactta gccatctata tcgacttcat tcaacaaaaa acaaaatcac attaaacgga
240
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300
tctagagacg ctatgattga tgattttctc gtaaaagata tcgttctcat gggacgggat
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420
atgn
424

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<210> 802

<211> 122

<212> PRT

<213> Homo sapiens

<400> 802

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Leu Lys Asn Ile Ser Val Thr Phe Pro Thr Asn Lys Ile Thr Ala Ile
20     25     30
Ile Gly Pro Asn Gly Cys Gly Lys Ser Thr Leu Leu Ser His Leu Tyr
35     40     45
Arg Leu His Ser Thr Lys Asn Lys Ile Thr Leu Asn Gly Lys Pro Leu
50     55     60
Glu Ser Tyr Lys Gly Arg Glu Phe Ala Gln Leu Val Ala Val Leu Thr
65     70     75     80
Gln Ser Arg Asp Ala Met Ile Asp Asp Phe Leu Val Lys Asp Ile Val
85     90     95
Leu Met Gly Arg Asp Pro Tyr Lys Gln His Phe Gly Thr Tyr Ser Ser
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Glu Asp Val Lys Ile Ala Glu His Tyr Met
115    120

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<210> 803

<211> 6863

<212> DNA

<213> Homo sapiens

<400> 803

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120

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<211> 1400

<212> PRT

<213> Homo sapiens

<400> 804

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 Arg Thr Leu Val Phe Arg Val Gln Phe His Thr Cys Thr Ile His Gly
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 <213> Homo sapiens

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 Arg Phe His Thr Gln Arg Glu Asp Ser Pro Thr Gln Thr Leu Lys Arg
 65 70 75 80
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<210> 809
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 <212> DNA
 <213> Homo sapiens

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<210> 810
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35      40      45
Arg Arg Ser Val Pro Pro Leu Pro His Asp Pro Asp Gly Pro Glu Ile
50      55      60
Pro Asp Asp Val Thr Thr Leu Ala Gln Gln Val Met Gly Leu Pro Arg
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His Leu Gly Ile His Ser Ala Gly Met Val Leu Thr Arg Glu Pro Val
85      90      95
Gly Arg Ile Cys Pro Ile Glu Pro Ala Arg Met Phe Gly Arg Thr Gly
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<210> 812
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 <213> Homo sapiens

<400> 812
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 Ala His Pro Glu Val Leu Glu Ser Phe Leu Gln Glu Leu Arg Pro Lys
 35 40 45
 Ala Ser Arg Lys Glu Arg Xaa Thr Thr Asn Leu Ile Phe Thr Pro Phe
 50 55 60
 Pro Cys His Leu Val Phe Pro Val Ile Phe Asn Pro Ile Leu Cys Ala
 65 70 75 80
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 85 90 95
 Val Thr Gly Ser Ser Ala Leu Tyr His Ser
 100 105

<210> 813
 <211> 558

<212> DNA

<213> Homo sapiens

<400> 813

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<210> 814

<211> 151

<212> PRT

<213> Homo sapiens

<400> 814

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20           25           30
Ala Phe Gly Pro Leu Ala Phe Gly Gln Arg Ala Ala Gln Phe Gly Val
35           40           45
Glu Asp Asp Pro Arg Pro Phe Asp Leu Asp His Asp Leu Gln Leu Pro
50           55           60
Ala Ile Val Phe Ala Ala Asp Ile Gln Arg Ala Ala Ala His Gln Arg
65           70           75           80
Leu Ala Gly Asp Gln Gly Glu Val Gln His His Leu Gln Arg Gly Leu
85           90           95
Gly Gln Arg Leu Arg Phe His Pro Pro Val Glu Leu Arg Ala Leu Ile
100          105          110
Val Gly Asn Gln Pro Leu Val Arg Gly Phe Arg Phe Ala Arg Val Asp
115          120          125
Leu Phe Ala Glu Pro Ala Gly Gly Ala Glu Gly Glu Ala Glu Glu Phe
130          135          140
Glu Leu Val Gly Gly Tyr Ala
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<210> 815

<211> 315

<212> DNA

<213> Homo sapiens

<400> 815

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<210> 816

<211> 90

<212> PRT

<213> Homo sapiens

<400> 816

Met	Pro	Ser	Asp	Leu	Pro	Lys	Val	Asp	Asp	Glu	Lys	Ala	His	Asp	Ala
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Pro	His	Thr	Asp	Gly	Ser	Glu	Pro	Gly	Gln	Ala	Ser	Ala	Gly	Glu	Ser
			20					25					30		
Arg	Asp	Leu	Thr	Ser	Glu	Ala	Asp	Ser	Ala	Ser	Ala	Gln	Pro	Ser	Thr
		35					40					45			
His	Ala	Glu	Val	Ser	Ser	Glu	Val	Thr	Ala	Thr	Ser	Ser	Ile	Asp	Glu
	50					55					60				
Gln	Val	Asp	Leu	Ile	Ala	Ala	Pro	Leu	Ser	Glu	Glu	Ser	Asn	Val	Ser
65					70					75				80	
Lys	Leu	Gly	Pro	Ser	Pro	Glu	Ala	Asp	Thr						
			85					90							

<210> 817

<211> 321

<212> DNA

<213> Homo sapiens

<400> 817

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120
aatacacttt tctcaaagct tcaaattaat caatccatta tattctgcaa ctctgttaat
180
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300
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321

<210> 818
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 818
 Glu Phe Lys Glu Lys Tyr Leu Pro Arg Pro Tyr Val Ile Asn Leu Met
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 20 25 30
 Glu Gly Gln Lys Val His Cys Leu Asn Thr Leu Phe Ser Lys Leu Gln
 35 40 45
 Ile Asn Gln Ser Ile Ile Phe Cys Asn Ser Val Asn Ser Val Glu Leu
 50 55 60
 Leu Ala Lys Lys Ile Thr Glu Leu Gly Tyr Ser Cys Phe Tyr Ile His
 65 70 75 80
 Ala Lys Met Leu Gln Asp His Arg Asn Arg Val Phe His Asp Cys Arg
 85 90 95
 Asn Gly Ala Cys Arg Asn Leu Val Cys Thr Asp
 100 105

<210> 819
 <211> 3422
 <212> DNA
 <213> Homo sapiens

<400> 819
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 420
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 3422

<210> 820

<211> 494

<212> PRT

<213> Homo sapiens

<400> 820

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Phe	Thr	Ser	Pro	Glu	Ala	Leu	Gln	Pro	Gly	Gly	Thr	Ala	Leu	Ala	Pro
			20					25					30		
Lys	Lys	Arg	Ser	Arg	Lys	Gly	Arg	Ala	Gly	Ala	His	Gly	Leu	Ser	Lys
		35				40					45				
Gly	Pro	Leu	Glu	Lys	Arg	Pro	Tyr	Leu	Gly	Pro	Ala	Leu	Pro	Leu	Thr
	50				55					60					
Pro	Arg	Asp	Arg	Ala	Ser	Gly	Thr	Gln	Gly	Ala	Ser	Glu	Asp	Asn	Ser
65					70				75					80	
Gly	Gly	Gly	Gly	Lys	Lys	Pro	Lys	Met	Glu	Glu	Leu	Gly	Leu	Ala	Ser

				85					90					95		
His	Pro	Pro	Glu	Gly	Arg	Pro	Cys	Gln	Pro	Gln	Thr	Arg	Ala	Gln	Lys	
			100					105					110			
Gln	Pro	Gly	His	Thr	Asn	Tyr	Ser	Ser	Tyr	Ser	Lys	Arg	Lys	Arg	Leu	
		115					120					125				
Thr	Arg	Gly	Arg	Ala	Lys	Asn	Thr	Thr	Ser	Ser	Pro	Cys	Lys	Gly	Arg	
	130					135					140					
Ala	Lys	Arg	Arg	Arg	Gln	Gln	Gln	Val	Leu	Pro	Leu	Asp	Pro	Ala	Glu	
145					150					155					160	
Pro	Glu	Ile	Arg	Leu	Lys	Tyr	Ile	Ser	Ser	Cys	Lys	Arg	Leu	Arg	Ser	
				165					170						175	
Asp	Ser	Arg	Thr	Pro	Ala	Phe	Ser	Pro	Phe	Val	Arg	Val	Glu	Lys	Arg	
			180					185					190			
Asp	Ala	Phe	Thr	Thr	Ile	Cys	Thr	Val	Val	Asn	Ser	Pro	Gly	Asp	Ala	
		195					200					205				
Pro	Lys	Pro	His	Arg	Lys	Pro	Ser	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser	
	210					215					220					
Ser	Ser	Ser	Phe	Ser	Leu	Asp	Ala	Ala	Gly	Ala	Ser	Leu	Ala	Thr	Leu	
225					230					235					240	
Pro	Gly	Gly	Ser	Ile	Leu	Gln	Pro	Arg	Pro	Ser	Leu	Pro	Leu	Ser	Ser	
				245					250					255		
Thr	Met	His	Leu	Gly	Pro	Val	Val	Ser	Lys	Ala	Leu	Ser	Thr	Ser	Cys	
			260					265					270			
Leu	Val	Cys	Cys	Leu	Cys	Gln	Asn	Pro	Ala	Asn	Phe	Lys	Asp	Leu	Gly	
		275					280					285				
Asp	Leu	Cys	Gly	Pro	Tyr	Tyr	Pro	Glu	His	Cys	Leu	Pro	Lys	Lys	Lys	
	290					295					300					
Pro	Lys	Leu	Lys	Glu	Lys	Val	Arg	Pro	Glu	Gly	Thr	Cys	Glu	Glu	Ala	
305					310					315					320	
Ser	Leu	Pro	Leu	Glu	Arg	Thr	Leu	Lys	Gly	Pro	Glu	Cys	Ala	Ala	Ala	
				325					330					335		
Ala	Thr	Ala	Gly	Lys	Pro	Pro	Arg	Pro	Asp	Gly	Pro	Ala	Asp	Pro	Ala	
			340					345					350			
Lys	Gln	Gly	Pro	Leu	Arg	Thr	Ser	Ala	Arg	Gly	Leu	Ser	Arg	Arg	Leu	
		355					360					365				
Gln	Ser	Cys	Tyr	Cys	Cys	Asp	Gly	Arg	Glu	Asp	Gly	Gly	Glu	Glu	Ala	
	370					375					380					
Ala	Pro	Ala	Asp	Lys	Gly	Arg	Lys	His	Glu	Cys	Ser	Lys	Glu	Ala	Pro	
385				390						395					400	
Ala	Glu	Pro	Gly	Gly	Glu	Ala	Gln	Glu	His	Trp	Val	His	Glu	Ala	Cys	
			405						410					415		
Ala	Val	Trp	Thr	Gly	Gly	Val	Tyr	Leu	Val	Ala	Gly	Lys	Leu	Phe	Gly	
			420					425					430			
Leu	Gln	Glu	Ala	Met	Lys	Val	Ala	Val	Asp	Met	Met	Cys	Ser	Ser	Cys	
		435					440									

<210> 821

<211> 420

<212> DNA

<213> Homo sapiens

<400> 821

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300
gaagactatc cctggacgat ggggcagttt gtctggacgg gcttcgacta cctcggtgaa
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<210> 822

<211> 133

<212> PRT

<213> Homo sapiens

<400> 822

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Met Asp Gln Val Ser Cys Val Leu Asp Asn Gly Phe Ala Ala Ile Met
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Asp Val Pro Gly Phe Asn Tyr Arg Ala His Arg Tyr Thr Glu Ala Tyr
 20           25           30
Arg Arg Leu Pro Gln Asn Val Val Leu Gly Ser Glu Thr Thr Ser Thr
 35           40           45
Val Ser Ser Arg Gly Val Tyr Lys Phe Pro Val Val Leu Lys Ser Asp
 50           55           60
Ala Ile Tyr Pro Asp His Gln Ser Ser Gly Tyr Asp Thr Glu Tyr Cys
 65           70           75           80
Ser Trp Ser Asn Thr Pro Asp Val Asp Phe Ala Leu Ala Glu Asp Tyr
 85           90           95
Pro Trp Thr Met Gly Gln Phe Val Trp Thr Gly Phe Asp Tyr Leu Gly
100          105          110
Glu Pro Ser Pro Tyr Asp Thr Asp Ala Trp Pro Ser His Ala Ser Leu
115          120          125
Phe Gly Ile Val Asp
130

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<210> 823

<211> 550

<212> DNA

<213> Homo sapiens

<400> 823

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120

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<210> 824
 <211> 161
 <212> PRT
 <213> Homo sapiens

<400> 824
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 Ala Leu Leu Asn Lys Arg Ile Ser Thr Gln Pro Gly Leu Thr Ala Leu
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 Pro Glu Asn Pro Asn Thr Thr Leu Pro Pro Phe Gln Asp Thr Pro Cys
 35 40 45
 Glu Leu Gln Pro Arg Ile Asp Pro Ser Leu Gly Gln Gln Val Lys Asp
 50 55 60
 Gly Leu Val Val Gly Gly Pro Gly Asp Ala Ser Val Asp Ala Ile Tyr
 65 70 75 80
 Lys Ala Val Val Asp Ala Ala Ser Lys Gly Met Gln Val Val Ile Thr
 85 90 95
 Thr Ala Val Asn Ser Thr Thr Gln Ile Ser Pro Ile Pro Ala Leu Ser
 100 105 110
 Ala Met Ser Ala Phe Thr Ala Ser Ile Gly Asp Pro Leu Asn Leu Ser
 115 120 125
 Ser Ala Val Ser Ala Val Ile His Gly Arg Asn Met Gly Gly Val Asp
 130 135 140
 His Asp Gly Arg Leu Arg Asn Ser Arg Gly Ala Arg Leu Pro Lys Asn
 145 150 155 160
 Leu

<210> 825
 <211> 327
 <212> DNA
 <213> Homo sapiens

<400> 825
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 aaccgcgata tcctcacctc ttcggtggcg gcgggtatcg cctccatcat cggtacgatt
 180
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 327

<210> 826
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 826
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 Glu Gly Ile Leu Gln Leu Leu Asp Glu Arg Glu Met Arg Gly Val Leu
 20 25 30
 Gly His Glu Leu Met His Val Tyr Asn Arg Asp Ile Leu Thr Ser Ser
 35 40 45
 Val Ala Ala Gly Ile Ala Ser Ile Ile Gly Thr Ile Ala Gln Ile Leu
 50 55 60
 Ser Phe Gly Ala Met Phe Gly Gly Ser Asn Arg Asp Gly Glu Arg Ser
 65 70 75 80
 Asn Pro Leu Ala Met Phe Val Val Ala Met Leu Ala Pro Ile Ala Thr
 85 90 95
 Gln Val Ile Gln Met Ala Ile Ser Arg Thr Arg Glu Phe
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<210> 827
 <211> 534
 <212> DNA
 <213> Homo sapiens

<400> 827
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534

<210> 828
<211> 174
<212> PRT
<213> Homo sapiens

<400> 828
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20 25 30
Thr Gly Arg Trp Arg Pro Val Leu Pro Asp Pro Ser Ile Thr Asp Pro
35 40 45
Thr Ala Val Thr Arg Ile Ile Leu Cys Ser Gly Lys Ala Arg Trp Glu
50 55 60
Leu Val Lys Gln Arg Lys Ala Ala Ser Leu Asp Gly Gln Leu Ala Ile
65 70 75 80
Ile Pro Met Glu Arg Leu Tyr Pro Leu Pro Val Asp Glu Leu Ala Glu
85 90 95
Val Phe Ala Pro Tyr Thr Asn Val Thr Asp Val Arg Trp Val Gln Glu
100 105 110
Glu Pro Glu Asn Gln Gly Ala Trp Tyr Tyr Met Leu Thr His Leu Pro
115 120 125
Gln Ala Met Ser Glu Lys Leu Pro Gly Phe Phe Asp Gly Leu Val Gly
130 135 140
Ile Thr Arg Pro Pro Ser Ser Ala Pro Ser Val Gly Gln His Ser Val
145 150 155 160
His Ile Arg Glu Glu Gln Glu Leu Leu Glu Lys Ala Ile Ala
165 170

<210> 829
<211> 492
<212> DNA
<213> Homo sapiens

<400> 829
nagtggccgg gtggccggcg ggtgccagcc gccatggagg ccgtgccccg catgccccatg
60
atctggctgg acctgaagga ggccggtgac tttcacttcc agccagctgt gaagaagttt
120
gtcctgaaga attatggaga gaaccagaa gcctacaatg aagaactgaa gaagctggag
180
ttgctcagac agaatgctgt ccgtgtccca cgagactttg agggctgtag tgtcctccgc
240
aagtacctcg gccagcttca ttacctgcag agtcgggtcc ccatgggctc gggccaggag
300
gccgctgtcc ctgtcacatg gacagagatc ttctcaggca agtctgtggc ccatgaggac
360
atcaagtacg agcaggcctg tattttctcc aacnttggag cgctgcactc catgctgggg
420
gccatggaca agcgggtgtc tgaggagggc atgaaggtct cctgtacca tttccagtgc
480

gcagccggcg cc
492

<210> 830

<211> 164

<212> PRT

<213> Homo sapiens

<400> 830

```

Xaa Trp Pro Gly Gly Arg Arg Val Pro Ala Ala Met Glu Ala Val Pro
 1           5           10           15
Arg Met Pro Met Ile Trp Leu Asp Leu Lys Glu Ala Gly Asp Phe His
      20           25           30
Phe Gln Pro Ala Val Lys Lys Phe Val Leu Lys Asn Tyr Gly Glu Asn
      35           40           45
Pro Glu Ala Tyr Asn Glu Glu Leu Lys Lys Leu Glu Leu Leu Arg Gln
      50           55           60
Asn Ala Val Arg Val Pro Arg Asp Phe Glu Gly Cys Ser Val Leu Arg
      65           70           75           80
Lys Tyr Leu Gly Gln Leu His Tyr Leu Gln Ser Arg Val Pro Met Gly
      85           90           95
Ser Gly Gln Glu Ala Ala Val Pro Val Thr Trp Thr Glu Ile Phe Ser
      100          105          110
Gly Lys Ser Val Ala His Glu Asp Ile Lys Tyr Glu Gln Ala Cys Ile
      115          120          125
Phe Ser Asn Xaa Gly Ala Leu His Ser Met Leu Gly Ala Met Asp Lys
      130          135          140
Arg Val Ser Glu Glu Gly Met Lys Val Ser Cys Thr His Phe Gln Cys
      145          150          155          160
Ala Ala Gly Ala

```

<210> 831

<211> 303

<212> DNA

<213> Homo sapiens

<400> 831

```

gcgttgctgc ggcgtggcga gaccatgacg gcggagaatc agcgtgccaa tgtgcgcac
60
gccgcaaacc acatcaagga ggttgcggtc gatcacgagg tcgttgtagc ccatggtaat
120
ggccccccagg taggtctggt ggctctgcaa tcgacagcct acgaggaagt cggatatctat
180
ccgctggatg tcctgggcgc agagtcacag gccatgatcg gctacatgat cgagcaggaa
240
ctcggcaatg tgatgcctca ggatcagcag atcgtcacca tgatcacgat gacagtcgtc
300
gac
303

```

<210> 832

<211> 101

<212> PRT

<213> Homo sapiens

<400> 832

```

Ala Leu Leu Arg Arg Gly Glu Thr Met Thr Ala Glu Asn Gln Arg Ala
 1           5           10           15
Asn Val Arg Ile Ala Ala Asn His Ile Lys Glu Val Ala Val Asp His
          20           25           30
Glu Val Val Val Ala His Gly Asn Gly Pro Gln Val Gly Leu Leu Ala
          35           40           45
Leu Gln Ser Thr Ala Tyr Glu Glu Val Gly Ile Tyr Pro Leu Asp Val
          50           55           60
Leu Gly Ala Glu Ser Gln Ala Met Ile Gly Tyr Met Ile Glu Gln Glu
65           70           75           80
Leu Gly Asn Val Met Pro Gln Asp Gln Gln Ile Val Thr Met Ile Thr
          85           90           95
Met Thr Val Val Asp
          100

```

<210> 833

<211> 466

<212> DNA

<213> Homo sapiens

<400> 833

```

nngatccgcg cgatcgacga ggcgggtgcg tgatgttgac agcgaaaatg cgcagccggc
60
catttgacga gggctgaaaa cgtcttctac cggctctgctg tgccgcctgg tgtcagcaaa
120
cgacgccatg atcgctccagt gggatatcgat ttgttctgcg gcgctggggg attcagttgc
180
ggattccacc aggccgggtg gcatgttgcg gcggcggttg agcacgacgt gtcggcgctct
240
ctgacctatg tcatgaatct cgctcggccc ggcgtcaaga ttcacatcga ccccgagcac
300
ccggagctgg gcccaagacc accgcgaacc aagaagaaga gcggcgggcg agtgccgttc
360
gatgcgcatg tcggaactgg gtggatcgcc agcgagcccg ccgacgatcc cggctgcgaa
420
cacttctacg tgtacgacgt caagaacctc agcggcgagc ggatcc
466

```

<210> 834

<211> 142

<212> PRT

<213> Homo sapiens

<400> 834

```

Gln Arg Lys Cys Ala Ala Gly His Leu Thr Arg Ala Glu Asn Val Phe
 1           5           10           15
Tyr Arg Ser Ala Val Pro Pro Gly Val Ser Lys Arg Arg His Asp Arg
          20           25           30
Pro Val Gly Ile Asp Leu Phe Cys Gly Ala Gly Gly Phe Ser Cys Gly
          35           40           45
Phe His Gln Ala Gly Trp His Val Ala Ala Ala Val Glu His Asp Val

```

50	55	60
Ser Ala Ser Leu Thr Tyr Val Met Asn Leu Ala Arg Pro Gly Val Lys		
65	70	75
Ile His Ile Asp Pro Glu His Pro Glu Leu Gly Pro Arg Pro Pro Arg		80
	85	90
Thr Lys Lys Lys Ser Gly Gly Ala Val Pro Phe Asp Ala His Val Gly		95
	100	105
Thr Gly Trp Ile Ala Ser Glu Pro Ala Asp Asp Pro Gly Cys Glu His		110
	115	120
Phe Tyr Val Tyr Asp Val Lys Asn Leu Ser Gly Glu Arg Ile		125
130	135	140

<210> 835

<211> 482

<212> DNA

<213> Homo sapiens

<400> 835

acgcgtgaag ggattttgat caccagaac aaccacctgt ctttttagat caagaagcag
60
aagctcagag caaagaacat cacaccacgt ccctcagtga ttgaagcagt gattgagtca
120
cagaataaat ctggaactca ggtcttctga tctttgctcc agatgttaga gacaaaacta
180
aaagtaaaat accaagtga atcaaagcat cacgattgag ccagaacat gaaaaagaac
240
ttcctggccc acttgagaaa ctgttaaacc ggacatacct ttggggactt cttcccttct
300
ctggaataag attgatgttt ccatgctgtg aaagacgatg atgttccttc tcccagattc
360
ctgctgtctt caaaaggcct agcaaaaacc actgctgctg ggtgcagttg agaaagggaa
420
tgaagaacaa tcccatggcc atgcaggcac tcctcccttc cacctctctg cccttcacgc
480
gt
482

<210> 836

<211> 120

<212> PRT

<213> Homo sapiens

<400> 836

Met Ala Met Gly Leu Phe Phe Ile Pro Phe Leu Asn Cys Thr Gln Gln		
1	5	10
Gln Trp Phe Leu Leu Gly Leu Leu Lys Thr Ala Gly Ile Trp Glu Lys		15
	20	25
Glu His His Arg Leu Ser Gln His Gly Asn Ile Asn Leu Ile Pro Glu		30
	35	40
Lys Gly Arg Ser Pro Gln Arg Tyr Val Arg Phe Asn Ser Phe Ser Ser		45
	50	55
Gly Pro Gly Ser Ser Phe Ser Cys Ser Gly Leu Asn Arg Asp Ala Leu		60
65	70	75
Ile Ser Leu Gly Ile Leu Leu Leu Val Leu Ser Leu Thr Ser Gly Ala		80


```

      85              90              95
Lys Ile Arg Arg Pro Glu Phe Gln Ile Tyr Ser Val Thr Gln Ser Leu
      100              105              110
Leu Gln Ser Leu Arg Asp Val Val
      115              120

```

<210> 837
 <211> 509
 <212> DNA
 <213> Homo sapiens

```

<400> 837
acgcgtggac ccccgcttctg cccgcctttg cagtcacgc cctccctgaa gtcaccgctg
60
cagaaatacg caggcactga cctgggggta cagccaggca agggagagac gaggggctca
120
ctctgcacca gccaaaggcct gtgtcctggc atggctcccc caggaagcga ggatggcggt
180
gcctggcggt cgagcccttc ttatcctggg gaatgctggg gggcgcttct gagcagacct
240
gcctgctgcc cctgctggct ggcactgcc ctccccggg gaaagggttg gtggtcccc
300
caggggaact caaagcagg gagcccttg aggccccaag tccctggaat atcttggcgc
360
tcagatggcc cccctcgaac accctcacac gggggggccg cgcggtggga ggtgaccag
420
cagccactct tacttggcga agacttttct cccaatgcga gcgcgggttg tatcagcctg
480
agccttcagg ttggtgaggc tgggggtacc
509

```

<210> 838
 <211> 119
 <212> PRT
 <213> Homo sapiens

```

<400> 838
Met Ala Pro Pro Gly Ser Glu Asp Gly Gly Ala Trp Arg Ser Ser Pro
1      5      10      15
Ser Tyr Pro Gly Glu Cys Trp Gly Ala Phe Leu Ser Arg Pro Ala Cys
      20      25      30
Cys Pro Cys Trp Leu Ala Leu Pro Leu Pro Arg Gly Lys Val Gly Trp
      35      40      45
Ser Pro Gln Gly Asn Ser Lys Gln Gly Ser Pro Trp Arg Pro Gln Val
      50      55      60
Pro Gly Ile Ser Trp Arg Ser Asp Gly Pro Pro Arg Thr Pro Ser His
65      70      75      80
Gly Gly Ala Ala Arg Trp Glu Val Thr Gln Gln Pro Leu Leu Leu Gly
      85      90      95
Glu Asp Phe Ser Pro Asn Ala Ser Ala Gly Gly Ile Ser Leu Ser Leu
      100      105      110
Gln Val Gly Glu Ala Gly Val
      115

```

<210> 839
 <211> 347
 <212> DNA
 <213> Homo sapiens

<400> 839
 acgcgtctcg tgttcgtgcg gcacggcagg acggcggtca atgtggaggg tcgggtccag
 60
 ggccgtctcg acatgccgtt ggatgagggtg gggcgccgtc aggcactcac agtgggtcaa
 120
 gtcacgccc agatggaacc tgacgcgatc atggcctctc cgctacaacg tgcgcgcgac
 180
 acagctcagg caatcgggtgc ttgtgctgga ttgggcgtac agctggatga tcgactcatc
 240
 gagatcgatg tcggacgttg gtcgggacaa cgggctgcgg acctgcgtcg caacgatcct
 300
 gagtacgcag caagtgtggt cagccctatc gattaccggg tcggagn
 347

<210> 840
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 840
 Thr Arg Leu Val Phe Val Arg His Gly Arg Thr Ala Phe Asn Val Glu
 1 5 10 15
 Gly Arg Leu Gln Gly Arg Leu Asp Met Pro Leu Asp Glu Val Gly Arg
 20 25 30
 Arg Gln Ala Leu Thr Val Ala Gln Val Ile Ala Glu Met Glu Pro Asp
 35 40 45
 Ala Ile Met Ala Ser Pro Leu Gln Arg Ala Arg Asp Thr Ala Gln Ala
 50 55 60
 Ile Gly Ala Cys Ala Gly Leu Gly Val Gln Leu Asp Asp Arg Leu Ile
 65 70 75 80
 Glu Ile Asp Val Gly Arg Trp Ser Gly Gln Arg Ala Ala Asp Leu Arg
 85 90 95
 Arg Asn Asp Pro Glu Tyr Ala Ala Ser Val Val Ser Pro Ile Asp Tyr
 100 105 110
 Arg Val Gly
 115

<210> 841
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 841
 tccggaactc accccgacgc cgtcattatg gacgtcatga tgccgcgtct agatggcttg
 60
 gaagccaccc ggatgctgcg cagcaatggc aacgacgtcc cgatcctcgt cctcaccgcc
 120
 cgcgatgctg tcgacgatcg cgttgacggc ctcgacgctg gcgcgatga ctacatggtc
 180

aagcccttcg ccctcgacga actcctcgtt cgcctacgcg ccctcactcg tcgttcccgt
 240
 cccgagccag agcaaaacga ggcccttgaa caactctcct tcgctgacct cacccttgat
 300
 ccaggcaccc gcgagatcac ccgcgggaac cgctcgcatca gtttgacgcg t
 351

<210> 842
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 842
 Ser Gly Thr His Pro Asp Ala Val Ile Met Asp Val Met Met Pro Arg
 1 5 10 15
 Leu Asp Gly Leu Glu Ala Thr Arg Met Leu Arg Ser Asn Gly Asn Asp
 20 25 30
 Val Pro Ile Leu Val Leu Thr Ala Arg Asp Ala Val Asp Asp Arg Val
 35 40 45
 Asp Gly Leu Asp Ala Gly Ala Asp Asp Tyr Met Val Lys Pro Phe Ala
 50 55 60
 Leu Asp Glu Leu Leu Ala Arg Leu Arg Ala Leu Thr Arg Arg Ser Arg
 65 70 75 80
 Pro Glu Pro Glu Gln Asn Glu Ala Pro Glu Gln Leu Ser Phe Ala Asp
 85 90 95
 Leu Thr Leu Asp Pro Gly Thr Arg Glu Ile Thr Arg Gly Asn Arg Arg
 100 105 110
 Ile Ser Leu Thr Arg
 115

<210> 843
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 843
 ctagcccagg ctctcggtcca cgaggggctg cgcgctgtgg cctctggggc aaaccgggtc
 60
 ggcctcaagc gcggtatcga gaaggctgtc gacgccgttg tggaggagct ccgctctatc
 120
 tcgcgcgcca tcgacaccac ctccgacatg gccagcgttg ccaccatctc cagccgtgac
 180
 gagaccatcg gcgccctcat cgctgaggcc ttcgacaagg ttggttaagga cgggggttatc
 240
 accgtcgacg agtcgcagac cttcggcact gagcttgact tcaccgaggg catgcagttc
 300
 gacaagggtt acctgtcgcc ctacatggtc accgaccagg ttcgcatgga ggctgtgate
 360
 gaggatcctt acatcctcat tcactcccgc aag
 393

<210> 844
 <211> 131
 <212> PRT

<213> Homo sapiens

<400> 844

```

Leu Ala Gln Ala Leu Val His Glu Gly Leu Arg Ala Val Ala Ser Gly
 1           5           10           15
Ala Asn Pro Val Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Ala
      20           25           30
Val Val Glu Glu Leu Arg Ser Ile Ser Arg Ala Ile Asp Thr Thr Ser
      35           40           45
Asp Met Ala Ser Val Ala Thr Ile Ser Ser Arg Asp Glu Thr Ile Gly
      50           55           60
Ala Leu Ile Ala Glu Ala Phe Asp Lys Val Gly Lys Asp Gly Val Ile
      65           70           75           80
Thr Val Asp Glu Ser Gln Thr Phe Gly Thr Glu Leu Asp Phe Thr Glu
      85           90           95
Gly Met Gln Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Met Val Thr Asp
      100           105           110
Gln Val Arg Met Glu Ala Val Ile Glu Asp Pro Tyr Ile Leu Ile His
      115           120           125
Ser Arg Lys
      130

```

<210> 845

<211> 505

<212> DNA

<213> Homo sapiens

<400> 845

```

gccacctgcc caaggctgga tgacgggcct agggcacatc taaggaacaa ggacaggaca
60
gaagcaaagc cacagctgct ggggcagggt gggggccggt atgtctggcc agcagcatca
120
cccctgcccc cggcggggct ccaggaccgg gagactcatc agccggaagc tcttggagga
180
ggcggctgcc gtgaagacag gcacccttgc tcctgagagg ggcacccaga gaaccaagac
240
tcagcagagg gaacacaggg ctacgcccag gccccaggcc tgatatccag agtctaaatc
300
ccacctcagc ccagggggga gccttgagag gagctatgtc cctcatggac cccagtttcc
360
tctgcatacg ggctccgagc cctgcactgc ctccagggta gttcccaagg tcttttccca
420
ttacctccta cgtgagcact cagtaaacca atacacatac acaagggtga cattaattcc
480
agccacagaa tcccaggcca cgcgt
505

```

<210> 846

<211> 130

<212> PRT

<213> Homo sapiens

<400> 846

```

Met Gly Lys Asp Leu Gly Asn Tyr Pro Gly Gly Ser Ala Gly Leu Gly

```

```

      1             5             10             15
Ala Arg Met Gln Arg Lys Leu Gly Ser Met Arg Asp Ile Ala Pro Leu
      20             25             30
Lys Ala Pro Pro Trp Ala Glu Val Gly Phe Arg Leu Trp Ile Ser Gly
      35             40             45
Leu Gly Pro Gly Arg Ser Pro Val Phe Pro Leu Leu Ser Leu Gly Ser
      50             55             60
Leu Gly Ala Pro Leu Arg Ser Lys Gly Ala Cys Leu His Gly Ser Arg
      65             70             75             80
Leu Leu Gln Glu Leu Pro Ala Asp Glu Ser Pro Gly Pro Gly Ala Pro
      85             90             95
Pro Gly Ala Gly Val Met Leu Leu Ala Arg His Thr Gly Pro His Pro
      100            105            110
Ala Pro Ala Ala Val Ala Leu Leu Ser Cys Pro Cys Ser Leu Asp
      115            120            125
Val Pro
      130

```

<210> 847
 <211> 448
 <212> DNA
 <213> Homo sapiens

```

<400> 847
aagcttttaa aggagcaaga aaacatgaaa gagctagtag tcaaccttct ccgcatgact
60
caaatcaaaa ttgatgaaaa ggaacaaaag tccaaggatt tcctgaaagc tcagcaaaaa
120
tacaccaaca ttgttaaaga aatgaaagca aaggatcttg aaatcaggat acacaagaag
180
aaaaaatgtg aaatttatcg gagactgaga gagcttgcta aactgtatga caccattcga
240
aatgaaagaa acaaatttgt taacttactc cacaaagctc atcagaaagt aaatgaaata
300
aaagaaaggc ataaaatgtc attaaatgaa cttgaaattc tgagaaatag tgccgtagt
360
caagaaagaa agctacaaaa ttccatgctg aaacacgcca acaatgttac catcagagag
420
agcatgcaaa acgatgtgcg caaaattt
448

```

<210> 848
 <211> 149
 <212> PRT
 <213> Homo sapiens

```

<400> 848
Lys Leu Leu Lys Glu Gln Glu Asn Met Lys Glu Leu Val Val Asn Leu
      1             5             10             15
Leu Arg Met Thr Gln Ile Lys Ile Asp Glu Lys Glu Gln Lys Ser Lys
      20             25             30
Asp Phe Leu Lys Ala Gln Gln Lys Tyr Thr Asn Ile Val Lys Glu Met
      35             40             45
Lys Ala Lys Asp Leu Glu Ile Arg Ile His Lys Lys Lys Lys Cys Glu

```

```

      50              55              60
Ile Tyr Arg Arg Leu Arg Glu Leu Ala Lys Leu Tyr Asp Thr Ile Arg
65              70              75              80
Asn Glu Arg Asn Lys Phe Val Asn Leu Leu His Lys Ala His Gln Lys
      85              90              95
Val Asn Glu Ile Lys Glu Arg His Lys Met Ser Leu Asn Glu Leu Glu
      100             105             110
Ile Leu Arg Asn Ser Ala Val Ser Gln Glu Arg Lys Leu Gln Asn Ser
      115             120             125
Met Leu Lys His Ala Asn Asn Val Thr Ile Arg Glu Ser Met Gln Asn
      130             135             140
Asp Val Arg Lys Ile
145

```

```

<210> 849
<211> 463
<212> DNA
<213> Homo sapiens

```

```

<400> 849
nnacgcgtga ttgttggggc caaggaatgc catgtggaga gtgcaggtga agtgataagt
60
cttttggaga tggggaatgc agccagacat acaggtacca ctcaaataaa tgagcactcc
120
agcagatcac atgcaatttt tacaatcagc atttgtcaag ttcataaaaa tatggaggca
180
gctgaagatg gatcatggta ttcccctcgg catattgtct caaagttcca ctttgtggat
240
ttggcaggat cagaaagagt aacaaaaacg ggggaatactg gtgaacggtt caaagaatcc
300
attcaaatca atagtggatt gctggcttta ggaaatgtaa taagcgctct tggggaccca
360
cgcaggaaga gttcacatat tccatatagg gatgctaaaa ttacccgggt tctgaaagat
420
tctctgggag gcagtgctaa gactgtcatg atcacatgtg tca
463

```

```

<210> 850
<211> 154
<212> PRT
<213> Homo sapiens

```

```

<400> 850
Xaa Arg Val Ile Val Gly Ala Lys Glu Cys His Val Glu Ser Ala Gly
1              5              10              15
Glu Val Ile Ser Leu Leu Glu Met Gly Asn Ala Ala Arg His Thr Gly
      20              25              30
Thr Thr Gln Met Asn Glu His Ser Ser Arg Ser His Ala Ile Phe Thr
      35              40              45
Ile Ser Ile Cys Gln Val His Lys Asn Met Glu Ala Ala Glu Asp Gly
      50              55              60
Ser Trp Tyr Ser Pro Arg His Ile Val Ser Lys Phe His Phe Val Asp
65              70              75              80
Leu Ala Gly Ser Glu Arg Val Thr Lys Thr Gly Asn Thr Gly Glu Arg

```

```

      85              90              95
Phe Lys Glu Ser Ile Gln Ile Asn Ser Gly Leu Leu Ala Leu Gly Asn
      100              105              110
Val Ile Ser Ala Leu Gly Asp Pro Arg Arg Lys Ser Ser His Ile Pro
      115              120              125
Tyr Arg Asp Ala Lys Ile Thr Arg Leu Leu Lys Asp Ser Leu Gly Gly
      130              135              140
Ser Ala Lys Thr Val Met Ile Thr Cys Val
145              150

```

<210> 851
 <211> 372
 <212> DNA
 <213> Homo sapiens

```

<400> 851
aaatttcctg tttctgatcg acgaaataaa gtttagcgtg atgagtgagc tgcttatgca
60
gttcctccat tcgcttataa acagttttat ttctcatttc gaaaactctc gatgcagaat
120
aaaggctaga gtctggggac caagtcccca gctccgttta cgcgacttcc ttgaccttgt
180
ttgttatgct gataagggtta ttcagcttga cgatttggtc gtggtctttc aaccgttttg
240
cagctgggtcg acgatattcc tggtaggaac tacgatagaa gaccagcatc ggaagaactt
300
tgtagatgct gaacaaacac ccaccgatca cttcagcctc gaagtaaggg ttatactgtc
360
taaccacgcg gt
372

```

<210> 852
 <211> 110
 <212> PRT
 <213> Homo sapiens

```

<400> 852
Met Ser Glu Leu Leu Met Gln Phe Leu His Ser Leu Ile Asn Ser Phe
1      5      10      15
Ile Ser His Phe Glu Asn Ser Arg Cys Arg Ile Lys Ala Arg Val Trp
      20      25      30
Gly Pro Ser Pro Gln Leu Arg Leu Arg Asp Phe Leu Asp Leu Val Cys
      35      40      45
Tyr Ala Asp Lys Val Ile Gln Leu Asp Asp Leu Phe Val Val Phe Gln
      50      55      60
Pro Phe Cys Ser Trp Ser Thr Ile Phe Leu Val Gly Thr Thr Ile Glu
65      70      75      80
Asp Gln His Arg Lys Asn Phe Val Asp Ala Glu Gln Thr Pro Thr Asp
      85      90      95
His Phe Ser Leu Glu Val Arg Val Ile Leu Ser Asn Pro Arg
      100      105      110

```

<210> 853
 <211> 423

<212> DNA

<213> Homo sapiens

<400> 853

acgcgttcag aaacttatgg tgaaatggcc gaactagaaa acctagtcga cgaatattac
60
caagctatgg gcatggatgt gcgtcgagaa acctggctgc gcgagcagat actcaagaaa
120
gtccaagaaa cgcatttggt agaagagctt gcaggcatag aatcagggtga tgatggcgca
180
gtgggtggaag agagcgtatt agaaggcctc gatacctatt tatgtgagat aaaagaagca
240
cagattcgtc atggattgca tcgtcttgga gaattaccag aagacgataa attggccgat
300
accttggctg ccttattgcg tttaccccggt ggcagtgaca ttaccagcaa gggaattttg
360
catgccttaa tggcagattt agagttagaa caagacgatt ttgacccaat gcaaagcacg
420
cgt
423

<210> 854

<211> 141

<212> PRT

<213> Homo sapiens

<400> 854

Thr	Arg	Ser	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Glu	Leu	Glu	Asn	Leu	Val
1				5					10					15	
Asp	Glu	Tyr	Tyr	Gln	Ala	Met	Gly	Met	Asp	Val	Arg	Arg	Glu	Thr	Trp
			20					25					30		
Leu	Arg	Glu	Gln	Ile	Leu	Lys	Lys	Val	Gln	Glu	Thr	His	Leu	Leu	Glu
		35					40					45			
Glu	Leu	Ala	Gly	Ile	Glu	Ser	Gly	Asp	Asp	Gly	Ala	Val	Val	Glu	Glu
		50				55				60					
Ser	Val	Leu	Glu	Gly	Leu	Asp	Thr	Tyr	Leu	Cys	Glu	Ile	Lys	Glu	Ala
65					70					75				80	
Gln	Ile	Arg	His	Gly	Leu	His	Arg	Leu	Gly	Glu	Leu	Pro	Glu	Asp	Asp
			85					90					95		
Lys	Leu	Ala	Asp	Thr	Leu	Val	Ala	Leu	Leu	Arg	Leu	Pro	Arg	Gly	Ser
			100					105					110		
Asp	Ile	Thr	Ser	Lys	Gly	Ile	Leu	His	Ala	Leu	Met	Ala	Asp	Leu	Glu
		115					120						125		
Leu	Glu	Gln	Asp	Asp	Phe	Asp	Pro	Met	Gln	Ser	Thr	Arg			
		130				135						140			

<210> 855

<211> 338

<212> DNA

<213> Homo sapiens

<400> 855

acgcgtgaag ggggagctca aagtagatgg acctctgact agatggagct ctgagtaaga
60

tgaatgtctg tgcggatggt gctcacagca agatagtgtc tggagcgtt ggcacttcga
 120
 acaagatgga gcatggagca gatggagctc tgagcaagat ggagcgtgga gtagatagag
 180
 cttggagcaa gaaggagctc caagcaagat ggagcttgca gcaggtgctt ctcagtgtaa
 240
 gatggagctc agagaagatg atgctcagag taagattgag ctcggtgatt ggcactccaa
 300
 acattgtctc gagcccattg gagnctctga gcagaaag
 338

<210> 856
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 856
 Met Asn Val Cys Ala Asp Val Ala His Ser Lys Ile Val Leu Gly Ala
 1 5 10 15
 Ile Gly Thr Ser Asn Lys Met Glu His Gly Ala Asp Gly Ala Leu Ser
 20 25 30
 Lys Met Glu Arg Gly Val Asp Arg Ala Trp Ser Lys Lys Glu Leu Gln
 35 40 45
 Ala Arg Trp Ser Leu Gln Gln Val Leu Leu Ser Val Arg Trp Ser Ser
 50 55 60
 Glu Lys Met Met Leu Arg Val Arg Leu Ser Ser Val Ile Gly Thr Pro
 65 70 75 80
 Asn Ile Ala Leu Ser Pro Leu Glu Xaa Leu Ser Arg Lys
 85 90

<210> 857
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 857
 ccggacagtg ggccaccagt gtttgccccc agcaatcatg tcagtgaagc ccaacctcgg
 60
 gagacacccc ggcccctcat gcctcctacc aagcctttcc tagcacctga gaccaccagc
 120
 cctggtgaca ggggtggagac ccctgtgggg gagagagccc caaccctgt ctcagcaagc
 180
 tctgaggtct cccctgagag ccaagaggac tcagagaccc cagcagagga ggacagtggc
 240
 tctgagcagc ctcccaacag cgtcctgcct gacaaactga aggtgagctg ggagaacccc
 300
 agccccagg agggccctgc tgcagagagt gcagaaccgt cccaggcacc ctgttctgag
 360
 acttctgagg ctgccccag ggagggtggg aagcccccta cccccacc caagatctta
 420
 tcagagaaac tgaaa
 435

<210> 858

<211> 145
 <212> PRT
 <213> Homo sapiens

<400> 858
 Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser Glu
 1 5 10 15
 Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys Pro
 20 25 30
 Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr Pro
 35 40 45
 Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val Ser
 50 55 60
 Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser Gly
 65 70 75 80
 Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val Ser
 85 90 95
 Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Ala Glu Ser Ala Glu
 100 105 110
 Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg Glu
 115 120 125
 Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Lys Leu
 130 135 140
 Lys
 145

<210> 859
 <211> 561
 <212> DNA
 <213> Homo sapiens

<400> 859
 nacgcgtggt gtggtaatcc ggtttctggt ggcgacggct gccacccctc gtggcaagac
 60
 atgccgttgc gtgccgatat gccatacgaa gcttggccta gtgcgaaaag ctcgctggaa
 120
 ccctcgaaga ggcagggtcg gcaggttacc gtggctcggtg tacgcatcgt ttcgacgatg
 180
 aaccccatc tgggagcaga tatgacgacg taccagtacc tcattgtcgg tggcgggatg
 240
 gccgctgatt ctgccgcccg cggtatccgc gacatcgaca agaaagggtc gatcgccatc
 300
 ctcagcgctg acgtcgacgc cccgtatcct cggccagcgc tgagcaagaa gctgtggact
 360
 gaccctgagt tcacctggga ccaggctgac cttgctactg tcgctgacac cggcgcggaa
 420
 ttgcggctcg gcactgaggt gctcagcatt gaccgtgacg gcaagaccgt cctgaccgct
 480
 tccggccagg tattcggcta ccagaagttg ctgctcgta cgggccttac cccgtcgcgc
 540
 attgacgacg acggcgatgc c
 561

<210> 860

<211> 187
 <212> PRT
 <213> Homo sapiens

<400> 860
 Xaa Ala Trp Cys Gly Asn Pro Val Ser Gly Gly Asp Gly Cys His Pro
 1 5 10 15
 Ser Trp Gln Asp Met Pro Leu Arg Ala Asp Met Pro Tyr Glu Ala Trp
 20 25 30
 Pro Ser Ala Lys Ser Ser Leu Glu Pro Ser Lys Arg Gln Gly Arg Gln
 35 40 45
 Val Thr Val Val Gly Val Arg Ile Val Ser Thr Met Asn Pro Ile Leu
 50 55 60
 Gly Ala Asp Met Thr Thr Tyr Gln Tyr Leu Ile Val Gly Gly Gly Met
 65 70 75 80
 Ala Ala Asp Ser Ala Ala Arg Gly Ile Arg Asp Ile Asp Lys Lys Gly
 85 90 95
 Ser Ile Ala Ile Leu Ser Ala Asp Val Asp Ala Pro Tyr Pro Arg Pro
 100 105 110
 Ala Leu Ser Lys Lys Leu Trp Thr Asp Pro Glu Phe Thr Trp Asp Gln
 115 120 125
 Val Asp Leu Ala Thr Val Ala Asp Thr Gly Ala Glu Leu Arg Leu Gly
 130 135 140
 Thr Glu Val Leu Ser Ile Asp Arg Asp Gly Lys Thr Val Leu Thr Ala
 145 150 155 160
 Ser Gly Gln Val Phe Gly Tyr Gln Lys Leu Leu Leu Val Thr Gly Leu
 165 170 175
 Thr Pro Ser Arg Ile Asp Asp Asp Gly Asp Ala
 180 185

<210> 861
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 861
 ccattgggttt ctatgctctg aggtttcatc tgtggggaac agtattgact tacttacaaa
 60
 gagataatgg tcatacccta tggtcactca ccatagtctg gcggtacatg gacttctcag
 120
 cccagtaag atctgtatcc acaggacact taaagtcacc ttacagaggg ctatcccagt
 180
 gcctgaggcc tattagaggg gtctcttttc agccatcagt gttagaggcc atctgcatgg
 240
 gatcccagag cctgcctcgg gaatggcaga agctggctgg tgcttggcgt gggctttgcc
 300
 tgtttcactg ctttcagggg ggcctgccac aggggagaaa ctgggggggg ga
 352

<210> 862
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 862

```

Met Gly Phe Tyr  Ala Leu Arg Phe His Leu Trp Gly Thr Val Leu Thr
 1          5          10          15
Tyr Leu Gln Arg  Asp Asn Gly His  Thr Leu Trp Ser Leu Thr Ile Val
          20          25          30
Trp Arg Tyr Met  Asp Phe Ser Ala Pro Val Arg Ser Val Ser Thr Gly
          35          40          45
His Leu Lys Ser  Pro Tyr Arg Gly Leu Ser Gln Cys Leu Arg Pro Ile
          50          55          60
Arg Gly Val Ser  Phe Gln Pro Ser Val Leu Glu Ala Ile Cys Met Gly
65          70          75          80
Ser Gln Ser Leu  Pro Arg Glu Trp Gln Lys Leu Ala Gly Ala Trp Arg
          85          90          95
Gly Leu Cys Leu  Phe His Cys Phe Gln Gly Gly Leu Pro Gln Gly Arg
          100          105          110
Asn Trp Gly Gly
          115

```

<210> 863

<211> 327

<212> DNA

<213> Homo sapiens

<400> 863

```

tccggatcga cccggacgaa ttccacgggc cagccattga cttccaaatg ctctttgaca
60
tacgccgtga catgttcaat gtccaactta cgcattgtcca cccgctcacc ggtctcattg
120
agtttgagct gcgagtagac gttgcggttag ttctcgttga ccgactgctc atacgagatg
180
tgcagaagca tcggtttgcg gccatcctcg gacggcattg gcttggttgta catggccgct
240
tggcggaaca tgttcagggt aaagcccgac ttgaagttgt gcgacagggc agaaacacac
300
agcatttctg accggcgatg acccatn
327

```

<210> 864

<211> 108

<212> PRT

<213> Homo sapiens

<400> 864

```

Met Gly His Arg  Arg Ser Glu Met Leu Cys Val Ser Ala Leu Ser His
 1          5          10          15
Asn Phe Lys Ser  Gly Phe Thr Leu Asn Met Phe Arg Gln Ala Ala Met
          20          25          30
Tyr Asn Lys Pro Met Pro Ser Glu Asp Gly Arg Lys Pro Met Leu Leu
          35          40          45
His Ile Ser Tyr Glu Gln Ser Val Asn Glu Asn Tyr Arg Asn Val Tyr
          50          55          60
Ser Gln Leu Lys Leu Asn Glu Thr Gly Glu Arg Val Asp Met Arg Lys
65          70          75          80
Leu Asp Ile Glu His Val Thr Ala Tyr Val Lys Glu His Leu Glu Val

```

85 90 95
 Asn Gly Trp Thr Val Glu Phe Val Arg Val Asp Pro
 100 105

<210> 865
 <211> 729
 <212> DNA
 <213> Homo sapiens

<400> 865
 acgcgtcatc ctcattcaag aggccccagga ggagcaccac cctccgcata ttgcgcgtgc
 60
 agctctcgtt ctgggtctctg agcatgccca cggcgctctg cacacagctt ctcagcagcc
 120
 tgggtggtgtc caggatcgac acatcactgc ctccgagttc agaggtttcc tttcccacct
 180
 tctcagaact ttctgtttcc atggcctcct ctgccacctc tgccacctcc cctgatgtgc
 240
 tggcctccgt ctccatcgcc tctcatggc cgtcttccgc ccggtgttcc aagcccagct
 300
 caggcaagtc tccgggcgcg aacagctggc tgatggtgac atgctgcagc ctggtcacat
 360
 cagaaacat gaggggtgat ctccggaggt catcgatgtg gacagactgc cacagccctc
 420
 cgtggaagcc cacataggct gttcctcttc ccacccggga cagttttgtg atgaaataga
 480
 cgaagatacg gtccctcattt tctcgtattt tggtgatttc atttataaca gaatacttag
 540
 ctgaggcaat gagctgggcg ctacggattc catcttcaaa atctgtctga aaaatgagga
 600
 ttttacattt ggctgtattc gttaaacagt ttcggacttc tttgaggaat gagtactcgg
 660
 tgtcaaactg ctgcagccac aggagtgtgg gtttcggagc cctgcctgtg acctctgatt
 720
 ctaaaaattt
 729

<210> 866
 <211> 83
 <212> PRT
 <213> Homo sapiens

<400> 866
 Ala Cys Pro Arg Arg Ser Ala His Ser Phe Ser Ala Ala Trp Trp Cys
 1 5 10 15
 Pro Gly Ser Thr His His Cys Leu Arg Val Gln Arg Phe Pro Phe Pro
 20 25 30
 Pro Ser Gln Asn Phe Leu Phe Pro Trp Pro Pro Leu Pro Pro Leu Pro
 35 40 45
 Pro Pro Leu Met Cys Trp Pro Pro Ser Pro Ser Pro Pro His Gly Arg
 50 55 60
 Leu Pro Pro Gly Val Pro Ser Pro Ala Gln Ala Ser Leu Arg Ala Arg
 65 70 75 80
 Thr Ala Gly

<210> 867
 <211> 640
 <212> DNA
 <213> Homo sapiens

<400> 867
 nntccggaac atcaagatcc aggcgcagaa gaccgtcaga agctgcactg gccacctcct
 60
 tcaggtggac tctcgttggt ggccggcgctc gctggccccc tcgcacccgg tcccgtgtca
 120
 catgctccag ggcgcagctc ttgtccacct ttacctcatc gaaagccttg tttttgcctc
 180
 ggtaaatccc ttcattgagg gctttgatcc aggattcctt ctctccccc gtgggtgcct
 240
 ggaatttgat gtcgctgacc ttgttccttg gggatcgag caggataaag cgggtgttttc
 300
 gcttgaggag ggcacgaagg tccctggcact tctcatagct gcccagctcc acagtctcca
 360
 cacacttctg atcatcctca ttctcataga ccagcagctg ggccctggcag aggagcagat
 420
 atcgggtcttt ccagaaaccc aggaggcccc cactgctctt cttgatccag ccagccttgt
 480
 ccaccatctg tgctccccga ggcttctcac cggcttctct cacaccctcc tctccatgg
 540
 cgagtccgcc gaggtcccg cgcctccgcca ctcgcttcca gcgcgcgcgc ggctctgcc
 600
 ccgcgtctac gcccgccag gcggcgactc tccgcgttct
 640

<210> 868
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 868
 Gly Gly His Glu Gly Pro Gly Thr Ser His Ser Cys Pro Ala Pro Gln
 1 5 10 15
 Ser Pro His Thr Ser Asp His Pro His Ser His Arg Pro Ala Ala Gly
 20 25 30
 Pro Gly Arg Gly Ala Asp Ile Gly Leu Ser Arg Asn Pro Gly Gly Pro
 35 40 45
 His Cys Ser Ser
 50

<210> 869
 <211> 321
 <212> DNA
 <213> Homo sapiens

<400> 869
 ngggtgatgc tgctcgcggc attgagcatc tttgtgtcga gcgcgctgtt tatcgacaac
 60

ttcctgtcgc cgctgaatat gcgcgggctg ggcctggcga tttcgacggg gggcatcgct
 120
 gcgtgcacca tgctgttctg cctggcgctg gggcatttcg acttgctcggg gggctcgggtg
 180
 atcgccctgtg ccggtgtggg cgcggggatt gtgattcgtg acaccgatag cgtggcactc
 240
 ggcgtgtccg ctgcgttggc catgggcctg gtagtggggc tgatcaacgg catcgtgac
 300
 gccaaagctgc gcatcaacgc g
 321

<210> 870

<211> 107

<212> PRT

<213> Homo sapiens

<400> 870

Xaa	Val	Met	Leu	Leu	Ala	Ala	Leu	Ser	Ile	Phe	Val	Leu	Ser	Ala	Leu
1			5					10					15		
Phe	Ile	Asp	Asn	Phe	Leu	Ser	Pro	Leu	Asn	Met	Arg	Gly	Leu	Gly	Leu
		20					25					30			
Ala	Ile	Ser	Thr	Val	Gly	Ile	Ala	Ala	Cys	Thr	Met	Leu	Phe	Cys	Leu
		35				40					45				
Ala	Ser	Gly	His	Phe	Asp	Leu	Ser	Val	Gly	Ser	Val	Ile	Ala	Cys	Ala
	50				55				60						
Gly	Val	Val	Ala	Gly	Ile	Val	Ile	Arg	Asp	Thr	Asp	Ser	Val	Ala	Leu
65			70					75					80		
Gly	Val	Ser	Ala	Ala	Leu	Ala	Met	Gly	Leu	Val	Val	Gly	Leu	Ile	Asn
			85				90					95			
Gly	Ile	Val	Ile	Ala	Lys	Leu	Arg	Ile	Asn	Ala					
		100					105								

<210> 871

<211> 320

<212> DNA

<213> Homo sapiens

<400> 871

agatcttcag agtcctcgtc ttttaaattgg gggtaacagc agcaagtcct cagaggtgtc
 60
 ctgagcctca aaacacatcc tggtttgtaa cgtcgcgagc ctcagcaggg gctaggcaca
 120
 gaacaagcat tcaggacctg gaaggtacca gcgacacctg gtctctccctt cccaggcaca
 180
 aggcagcccc tctccattca agctctgccc cagcccagca aagagagggg tctcagcca
 240
 ctgccccac cactaccaca atcatactca cctctcctgg tccatacgtg acaaaggacc
 300
 tgccacggcc agggagacaa
 320

<210> 872

<211> 98

<212> PRT

<213> Homo sapiens

<400> 872

```

Met Gly Val Thr Ala Ala Ser Pro Gln Arg Cys Pro Glu Pro Gln Asn
 1             5             10             15
Thr Ser Trp Phe Val Thr Ser Ala Ala Ser Ala Gly Ala Arg His Arg
      20             25             30
Thr Ser Ile Gln Asp Leu Glu Gly Thr Ser Asp Thr Trp Ser Ser Leu
      35             40             45
Pro Arg His Lys Ala Ala Pro Leu His Ser Ser Ser Ala Pro Ala Gln
      50             55             60
Gln Arg Glu Gly Ser Ser Ala Thr Ala Pro Thr Thr Thr Thr Ile Ile
65             70             75             80
Leu Thr Ser Pro Gly Pro Tyr Val Thr Lys Asp Leu Pro Arg Pro Gly
      85             90             95
Arg Gln

```

<210> 873

<211> 363

<212> DNA

<213> Homo sapiens

<400> 873

```

nttgtttagc atcggtttttt acgggtgtat cagcgcgttt agcagcgttt ttagcggatg
60
catcagcatg ttttgcgtca cgtttttacaa ctgtgctacc gtgttttagca tcatttttga
120
cggaggtatc aatacgttta gcatcgtttt taacagatgt atcaacacgg ggttcatccg
180
cttttagcaga atccccagct ctagtagcca ctttagatac ttcagatttt atatgagtcg
240
cagttgtttc agcgtgagcc atgctgaatg tagaaccaag ggccaatgta attgctaaag
300
acaaagataa tttatttagt ttcattgttcg gagagaagtg tgcgaattcg gcgatacagt
360
cag
363

```

<210> 874

<211> 108

<212> PRT

<213> Homo sapiens

<400> 874

```

Met Lys Leu Asn Lys Leu Ser Leu Ser Leu Ala Ile Thr Leu Ala Leu
 1             5             10             15
Gly Ser Thr Phe Ser Met Ala His Ala Glu Thr Thr Ala Thr His Ile
      20             25             30
Lys Ser Glu Val Ser Lys Val Ala Thr Arg Ala Gly Asp Ser Ala Lys
      35             40             45
Ala Asp Glu Pro Arg Val Asp Thr Ser Val Lys Asn Asp Ala Lys Arg
      50             55             60
Ile Asp Thr Ser Val Lys Asn Asp Ala Lys His Gly Ser Thr Val Val

```



```

65          70          75          80
Lys Arg Asp Ala Lys His Ala Asp Ala Ser Ala Lys Asn Ala Ala Lys
          85          90          95
Arg Ala Asp Thr Pro Val Lys Asn Asp Ala Lys Gln
          100          105

```

<210> 875
 <211> 355
 <212> DNA
 <213> Homo sapiens

```

<400> 875
acgcgtgaag gggaccctaa ctcgtctggg ctgtaggatg cgggcgaggc ttccacaaac
60
tcactgtctg ggggagaaga aaagcagaaa acaactcgaa tcgctaccat tcaggacgaa
120
cccgccaaagc accagctcaa gcgcaggtcc ccgggaaaaa gcgcgggctt ctctctccca
180
gcgctcagaa tccttgagcc ggaggccccg cgggattcag accgccagat ccccaggag
240
tgacaaatcg ccgcagaaac ttgggggaca actcggccct ggcaccgcgc ggcttccagg
300
cgcgggcagg cgcgcgccaa ctttccccgc gtgccacccc gcggtcccc cgcn
355

```

<210> 876
 <211> 106
 <212> PRT
 <213> Homo sapiens

```

<400> 876
Met Arg Ala Arg Leu Pro Gln Thr His Cys Leu Gly Glu Lys Lys Ser
1          5          10          15
Arg Lys Gln Leu Glu Ser Leu Pro Phe Arg Thr Asn Pro Pro Ser Thr
          20          25          30
Ser Ser Ser Ala Gly Pro Arg Glu Lys Ala Arg Ala Ser Leu Ser Gln
          35          40          45
Arg Ser Glu Ser Leu Ser Arg Arg Pro Arg Gly Ile Gln Thr Ala Arg
          50          55          60
Ser Pro Gly Ser Asp Lys Ser Pro Gln Lys Leu Gly Gly Gln Leu Gly
65          70          75          80
Pro Gly Thr Ala Arg Leu Pro Gly Ala Gly Arg Arg Ala Pro Thr Phe
          85          90          95
Pro Ala Cys His Pro Ala Ala Pro Pro Ala
          100          105

```

<210> 877
 <211> 487
 <212> DNA
 <213> Homo sapiens

```

<400> 877
acgcgtactt tgggtaatga actgacgacc gctgagatcg actgccttta tctgtgttac
60

```

caatccacct atgctaaacg tggtcagcaa gggtatctca cagagaatt ctttggtttg
 120
 ttggccaata ccatgggaga tcaaatacctt ttagtacagg cgtacagaga aggcgaagcg
 180
 atcgccgcgt cgtggtgttt ctttgatgat cattcactat atgggcggtta ttggggctgt
 240
 atggaagaag tggattgcct gcattttgaa gcttgttatt accaaggaat cgagttttgt
 300
 ctcgaaaaag ggttacagca tttcgatccg ggtacacaag gggaacacaa gattgcgcgc
 360
 ggctttgaac ctgttttttag ccacagcgtg cattacattg ctcataagg ttttcgtgaa
 420
 gcgattggga atttctgtga ggaagaagcg caagctgtgc gcgagtatca tcaagatacc
 480
 cacgcgt
 487

<210> 878

<211> 162

<212> PRT

<213> Homo sapiens

<400> 878

Thr	Arg	Thr	Leu	Gly	Asn	Glu	Leu	Thr	Thr	Ala	Glu	Ile	Asp	Cys	Leu
1				5					10					15	
Tyr	Leu	Cys	Tyr	Gln	Ser	Thr	Tyr	Ala	Lys	Arg	Gly	Gln	Gln	Gly	Tyr
			20					25					30		
Leu	Thr	Arg	Glu	Phe	Phe	Gly	Leu	Leu	Ala	Asn	Thr	Met	Gly	Asp	Gln
			35				40					45			
Ile	Leu	Leu	Val	Gln	Ala	Tyr	Arg	Glu	Gly	Glu	Ala	Ile	Ala	Ala	Ser
			50				55				60				
Trp	Cys	Phe	Phe	Asp	Asp	His	Ser	Leu	Tyr	Gly	Arg	Tyr	Trp	Gly	Cys
65					70					75				80	
Met	Glu	Glu	Val	Asp	Cys	Leu	His	Phe	Glu	Ala	Cys	Tyr	Tyr	Gln	Gly
				85					90					95	
Ile	Glu	Phe	Cys	Leu	Glu	Lys	Gly	Leu	Gln	His	Phe	Asp	Pro	Gly	Thr
			100					105					110		
Gln	Gly	Glu	His	Lys	Ile	Ala	Arg	Gly	Phe	Glu	Pro	Val	Phe	Ser	His
			115				120					125			
Ser	Val	His	Tyr	Ile	Ala	His	Gln	Gly	Phe	Arg	Glu	Ala	Ile	Gly	Asn
			130				135				140				
Phe	Cys	Glu	Glu	Glu	Ala	Gln	Ala	Val	Arg	Glu	Tyr	His	Gln	Asp	Thr
145						150				155				160	
His	Ala														

<210> 879

<211> 993

<212> DNA

<213> Homo sapiens

<400> 879

nncttagcat ttaagccaac gaggcagcta atgtcctctg aacagcaaag gaaattcagc
 60

agccagtcca gtagggctct gacccctcct tcctacagta ctgctaaaaa ttcattggga
 120
 tcaagatcca gtgaatcctt tgggaagtac acatcgccag taatgagtga gcatggggac
 180
 gagcacaggc agctcctctc tcacccaatg caaggccctg gactccgtgc agctacctca
 240
 tccaaccact ctgtggacga gcaactgaag aatactgaca cgcacctcat cgacctggta
 300
 accaatgaga ttatcaccca aggacctcca gtggactgga atgacattgc tgggtctcgac
 360
 ctgggtgaagg ctgtcattaa agaggagggtt ttatggccag tgttgagggtc agacgcgttc
 420
 agtgggactga cggccttacc tcggagcatc cttttatttg gacctcgggg gacaggcaaa
 480
 acattattgg gcagatgcat cgctagtcag ctggggggcca catttttcaa aattgccggt
 540
 tctggactag tcgccaaggg gttaggagaa gcagagaaaa ttatccatgc ctcttttctt
 600
 gtggccaggt gtcgccagcc ctcgggtgatt tttgttagtg acattgacat gcttctctcc
 660
 tctcaagtga atgaggaaca tagtccagtc agtcggatga gaaccgaatt tctgatgcaa
 720
 ctggacactg tactaacttc ggctgaggac caaatcgtag taatttgtgc caccagtaaa
 780
 ccagaagaaa tagatgaatc ccttcggagg tacttcatga aacgactttt aatcccactt
 840
 cctgacagca cagcgaggca ccagataata gtacaactgc tctcacagca caattactgt
 900
 ctcaatgaca aggagtttgc actgctcgtc cagcgcacag aaggcttttc tggactagat
 960
 gtgggtcatt tgtgtcagga agcagtgggtg ggc
 993

<210> 880

<211> 331

<212> PRT

<213> Homo sapiens

<400> 880

Xaa	Leu	Ala	Phe	Lys	Pro	Thr	Arg	Gln	Leu	Met	Ser	Ser	Glu	Gln	Gln
1				5				10					15		
Arg	Lys	Phe	Ser	Ser	Gln	Ser	Ser	Arg	Ala	Leu	Thr	Pro	Pro	Ser	Tyr
			20					25				30			
Ser	Thr	Ala	Lys	Asn	Ser	Leu	Gly	Ser	Arg	Ser	Ser	Glu	Ser	Phe	Gly
			35				40					45			
Lys	Tyr	Thr	Ser	Pro	Val	Met	Ser	Glu	His	Gly	Asp	Glu	His	Arg	Gln
			50			55					60				
Leu	Leu	Ser	His	Pro	Met	Gln	Gly	Pro	Gly	Leu	Arg	Ala	Ala	Thr	Ser
65					70					75				80	
Ser	Asn	His	Ser	Val	Asp	Glu	Gln	Leu	Lys	Asn	Thr	Asp	Thr	His	Leu
			85					90						95	
Ile	Asp	Leu	Val	Thr	Asn	Glu	Ile	Ile	Thr	Gln	Gly	Pro	Pro	Val	Asp
			100				105					110			
Trp	Asn	Asp	Ile	Ala	Gly	Leu	Asp	Leu	Val	Lys	Ala	Val	Ile	Lys	Glu

115 120 125
 Glu Val Leu Trp Pro Val Leu Arg Ser Asp Ala Phe Ser Gly Leu Thr
 130 135 140
 Ala Leu Pro Arg Ser Ile Leu Leu Phe Gly Pro Arg Gly Thr Gly Lys
 145 150 155 160
 Thr Leu Leu Gly Arg Cys Ile Ala Ser Gln Leu Gly Ala Thr Phe Phe
 165 170 175
 Lys Ile Ala Gly Ser Gly Leu Val Ala Lys Gly Leu Gly Glu Ala Glu
 180 185 190
 Lys Ile Ile His Ala Ser Phe Leu Val Ala Arg Cys Arg Gln Pro Ser
 195 200 205
 Val Ile Phe Val Ser Asp Ile Asp Met Leu Leu Ser Ser. Gln Val Asn
 210 215 220
 Glu Glu His Ser Pro Val Ser Arg Met Arg Thr Glu Phe Leu Met Gln
 225 230 235 240
 Leu Asp Thr Val Leu Thr Ser Ala Glu Asp Gln Ile Val Val Ile Cys
 245 250 255
 Ala Thr Ser Lys Pro Glu Glu Ile Asp Glu Ser Leu Arg Arg Tyr Phe
 260 265 270
 Met Lys Arg Leu Leu Ile Pro Leu Pro Asp Ser Thr Ala Arg His Gln
 275 280 285
 Ile Ile Val Gln Leu Leu Ser Gln His Asn Tyr Cys Leu Asn Asp Lys
 290 295 300
 Glu Phe Ala Leu Leu Val Gln Arg Thr Glu Gly Phe Ser Gly Leu Asp
 305 310 315 320
 Val Ala His Leu Cys Gln Glu Ala Val Val Gly
 325 330

<210> 881

<211> 313

<212> DNA

<213> Homo sapiens

<400> 881

cgcgtgagcg tcgacaatgc tccaggaacc ggtgtgtatg aggccgggga ttctaccggt
 60

cgtgggttgc agggcatgcg tgagcgcgcc cgtatccatg gcggcaccgc gcgctggggc
 120

gactcgcagt attatgaagg cggtttcaac gtcacggtgg agattccaac atgagcggcc
 180

aaaggatgaa catggacacg acgcgccccca atcacggtcg gggcttgccg acgatcagcc
 240

ggctgggtgc gcaccggttt tgccatggtg ctggattcgc aggacgacat cacggtggcc
 300

tggcaagccg acn
 313

<210> 882

<211> 57

<212> PRT

<213> Homo sapiens

<400> 882

Arg Val Ser Val Asp Asn Ala Pro Gly Thr Gly Val Tyr Glu Ala Gly

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      1           5           10           15
Asp Ser Thr Gly Arg Gly Leu Gln Gly Met Arg Glu Arg Ala Arg Ile
      20           25           30
His Gly Gly Thr Ala Arg Trp Gly Asp Ser Gln Tyr Tyr Glu Gly Gly
      35           40           45
Phe Asn Val Thr Val Glu Ile Pro Thr
      50           55

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<210> 883
 <211> 576
 <212> DNA
 <213> Homo sapiens

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<400> 883
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tcctcactga ccaaggcaag ccatgcttct gagtgcttga ggccaccgaa atgaacaaat
120
ggaaaacact cccatctttt tcaagcctac ctttttagcag aagaggcaga tacacaagcc
180
ctaaagatgt aacatcaggc tgagtggagg aaggctgaga agaaaaataa agcaggctca
240
ggaggagaga gtgatgtcag gatgcccttg tgcttactcc agcctccttg tgaaaaccca
300
gctctcctgt ctcccagtga agacttggat ggcagccatc aggggaaggct ggggtcccagc
360
tgggagtatg ggtgtgagct ctatagacca tccctctctg caatcaataa acacttgctt
420
gtgaaagagg cccaagccac catccgcattg gacaccagtg caagtggccc caccgcctg
480
gtcctcagtg actgtgccac cagccatggg agcctgcgca tccaactgct gcataagctc
540
tccttcctgg tgaacgcctt agctaagcag gtcattg
576

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<210> 884
 <211> 105
 <212> PRT
 <213> Homo sapiens

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<400> 884
Met Pro Leu Cys Leu Leu Gln Pro Pro Cys Glu Asn Pro Ala Leu Leu
      1           5           10           15
Ser Pro Ser Glu Asp Leu Asp Gly Ser His Gln Gly Arg Leu Gly Pro
      20           25           30
Ser Trp Glu Tyr Gly Cys Glu Leu Tyr Arg Pro Ser Leu Ser Ala Ile
      35           40           45
Asn Lys His Leu Pro Val Lys Glu Ala Gln Ala Thr Ile Arg Met Asp
      50           55           60
Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys Ala Thr
      65           70           75           80
Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser Phe Leu
      85           90           95
Val Asn Ala Leu Ala Lys Gln Val Met

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100

105

<210> 885
 <211> 370
 <212> DNA
 <213> Homo sapiens

<400> 885
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 ggtgaggcga tgctgacgaa cgacacaccg gtgacttggg atggcgggaa agtacggggc
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 aggcggtgt cgcgctcgg tgcgatcgag ttgtcgtcga ccccggtccg cccagatccg
 180
 gtacgggctc gccacgtggc gctggaagca gtgaggtctg ggggacttga cgtagcgagc
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 ctgacgaaga acggtgaatc tttgcgacgc cgtcttgccc tggcccatcg ggtgtttggt
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 370

<210> 886
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 886
 Thr Ser Gly Ala Leu Ile Arg Ala Ala Val Pro Leu Ser Glu Ser Ala
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 Ala Leu Glu Ser Gly Glu Ala Met Leu Thr Asn Asp Thr Pro Val Thr
 20 25 30
 Trp Asp Gly Gly Lys Val Arg Gly Arg Arg Val Ser Arg Leu Gly Ala
 35 40 45
 Ile Glu Leu Ser Ser Thr Pro Val Arg Pro Asp Pro Val Arg Ala Arg
 50 55 60
 His Val Ala Leu Glu Ala Val Arg Ser Gly Gly Leu Asp Val Ala Ser
 65 70 75 80
 Leu Thr Lys Asn Gly Glu Ser Leu Arg Arg Arg Leu Ala Leu Ala His
 85 90 95
 Arg Val Phe Gly Asp Pro Trp Pro Asp Val Ser Asp Glu Ala Leu Leu
 100 105 110
 Ala Cys Ala Glu Glu Trp Leu Asp Leu Asp Ala
 115 120

<210> 887
 <211> 447
 <212> DNA
 <213> Homo sapiens

<400> 887
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attatctccg gctgcctgaa ccagcttggt aaacgctatc cgcatctgac cggcgaaggc
 120
 caactgatgc caaacctgac taatgctgat accacggctt cccaaccggc gttctccggt
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 aaagcggacg tgaccacat tgcctccggc gcgttgctgg ccgtgctgct ttacatggtg
 240
 ggtaggttgg ttcacaagtt gattggcctg cctgctccgg ttggcatgtt gtttgtggcg
 300
 gtgctggtca aactgtgcaa cggcgcttct ccccgctgac tcgaaggctc gcaggtgggt
 360
 tacaaattct tccagacctc cgtaacctat ccgattctgt tcgccgttgg cgtggcgatt
 420
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 447

<210> 888
 <211> 149
 <212> PRT
 <213> Homo sapiens

<400> 888
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 20 25 30
 Tyr Pro His Leu Thr Gly Glu Gly Gln Leu Met Pro Asn Arg Ala Asn
 35 40 45
 Ala Asp Thr Thr Ala Ser Gln Pro Ala Phe Ser Gly Lys Ala Asp Val
 50 55 60
 Thr Thr Ile Ala Ser Gly Ala Leu Leu Ala Val Leu Leu Tyr Met Val
 65 70 75 80
 Gly Arg Leu Val His Lys Leu Ile Gly Leu Pro Ala Pro Val Gly Met
 85 90 95
 Leu Phe Val Ala Val Leu Val Lys Leu Cys Asn Gly Ala Ser Pro Arg
 100 105 110
 Leu Leu Glu Gly Ser Gln Val Val Tyr Lys Phe Phe Gln Thr Ser Val
 115 120 125
 Thr Tyr Pro Ile Leu Phe Ala Val Gly Val Ala Ile Thr Pro Trp Gln
 130 135 140
 Glu Leu Val Asn Ala
 145

<210> 889
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 889
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 atctcccctc agtaaaattc aggatgcccc gtgaagtttg aatgtcagat aaacaatttg
 120
 ttagtataag gatgtaccta gcattgaaat gatgccttgt aatttactaa atctgcaact
 180

atgcagcctt atttcatggc gggcagtggc ggtgatccca ggtttcaggg gcggggaagg
 240
 gtgctgggga gacctgagg tcaggaaccc gtacacctct gcttctgccc tctcttccct
 300
 gtgccggcca caaggcaatg actcctgtgt ggggtgcagag gcagaaatgg gtctggaagg
 360
 ggattcccag tgtctggcaa gttctggtaa attctgcatt ggaggttctc tctgtagtaa
 420
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 450

<210> 890

<211> 100

<212> PRT

<213> Homo sapiens

<400> 890

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Trp	Arg	Ala	Val	Ala	Val	Ile	Pro	Gly	Phe	Arg	Gly	Gly	Glu	Gly	Cys
			20					25					30		
Trp	Gly	Asp	Pro	Glu	Val	Arg	Asn	Pro	Tyr	Thr	Ser	Ala	Ser	Ala	Leu
		35					40					45			
Ser	Ser	Leu	Cys	Arg	Pro	Gln	Gly	Asn	Asp	Ser	Cys	Val	Gly	Ala	Glu
	50					55					60				
Ala	Glu	Met	Gly	Leu	Glu	Gly	Asp	Ser	Gln	Cys	Leu	Ala	Ser	Ser	Gly
65				70					75					80	
Lys	Phe	Cys	Ile	Gly	Gly	Ser	Leu	Cys	Ser	Lys	Gly	Ser	Trp	Pro	Gly
			85					90						95	
Arg	Pro	Ser	Arg												
			100												

<210> 891

<211> 318

<212> DNA

<213> Homo sapiens

<400> 891

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 120
 actaacggcc cggctgatag cgggactggc acccactctg agcagggaaa ctccgacata
 180
 tctagccccg tcagctctag tgacgtgctt aacaccaccg acagcactgc tggcaatacc
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 300
 ccctatgcaa gcaccggt
 318

<210> 892

<211> 106

<212> PRT

<213> Homo sapiens

<400> 892

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Xaa Thr Val Pro Val Leu Asp Pro Arg Glu Asp Phe Ala Asp Cys Met
 1           5           10           15
His Ile Asp Val Leu Asp Pro Phe His Thr Asp Asn Thr Ser Glu His
 20           25           30
Ser Asp Leu Ala Thr Asp Gly Gln Thr Asn Gly Pro Ala Asp Ser Gly
 35           40           45
Thr Gly Thr His Ser Glu Gln Gly Asn Ser Asp Ile Ser Ser Pro Val
 50           55           60
Ser Ser Ser Asp Ala Ala Asn Thr Thr Asp Ser Thr Ala Gly Asn Thr
 65           70           75           80
Gly Glu Gly Thr Ala Ala Asn Met Pro Gly Asp Met Ala His Ser Ser
 85           90           95
Thr Ala Thr His Pro Tyr Ala Ser Thr Gly
 100           105

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<210> 893

<211> 510

<212> DNA

<213> Homo sapiens

<400> 893

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nnggataccta tccctgaatc taagggttggt gacacatgtg tttgggatag caaggtagag
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 120
gcaatcagca aagccaagag tacagcaa ataaagacag aacaggaagg tgaggcatct
 180
gagaagagct tgcattctgag cccacagcat atcacacacc agactatgcc tataggacag
 240
agaggcagtg agcaaggcaa acgtgtggag aacattaatg gaacctccta ccctagtcta
 300
cagcagaaaa ccaatgctgt taagaaatta cataaatgtg atgaatgtgg gaaatccttc
 360
aaatataatt cccgccttgt tcaacataaa attatgcaca ctggggaaaa gcgctatgaa
 420
tgtgatgact gtggagggac tttccggagc agctcgagcc ttcgggtcca caaacggatc
 480
cacactgggt acggagagaa gacaacgcgt
 510

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<210> 894

<211> 170

<212> PRT

<213> Homo sapiens

<400> 894

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Xaa Asp Pro Ile Pro Glu Ser Lys Val Gly Asp Thr Cys Val Trp Asp
 1           5           10           15
Ser Lys Val Glu Lys Ser Gln Lys Lys Pro Val Glu Asn Arg Met Lys
 20           25           30
Glu Asp Lys Ser Ser Ile Arg Glu Ala Ile Ser Lys Ala Lys Ser Thr

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<400> 895
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120
ccgcaccgga atcgggcttt tcctggggct gccttcctaa atgcggtgtc ctcttgtcg
180
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240
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300
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420
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480
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540
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720
acgcttaccg ccttggtagc cgatccccgt cacgaggtag ctgccgtcct gacgcgtccg
780
gatgcagcag taggacggca ccgtactcca cgtccatgcc cggtcgccaa ggctgccgag
840
gaactcggtg tccccgccat taaggcgacc agcgtgaagt ccggcgaggg tcacgatgcc
900

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gtcacttccc tcgatgtcga cgtagccgtc gtcgtagcct acggaggtct cattccccgc
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 1020
 tggcgcggcg ctgctcccat acaacgggccc atcatggcgg gggatgagga gacgggcgct
 1080
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 1119

<210> 896
 <211> 147
 <212> PRT
 <213> Homo sapiens

<400> 896
 Val Arg Leu Leu Phe Ala Gly Thr Pro Asp Val Ala Val Pro Thr Leu
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 Thr Ala Leu Val Ala Asp Pro Arg His Glu Val Ala Ala Val Leu Thr
 20 25 30
 Arg Pro Asp Ala Ala Val Gly Arg His Arg Thr Pro Arg Pro Cys Pro
 35 40 45
 Val Ala Lys Ala Ala Glu Glu Leu Gly Ile Pro Ala Ile Lys Ala Thr
 50 55 60
 Ser Val Lys Ser Gly Glu Gly His Asp Ala Val Thr Ser Leu Asp Val
 65 70 75 80
 Asp Val Ala Val Val Val Ala Tyr Gly Gly Leu Ile Pro Ala Asp Leu
 85 90 95
 Leu Ala Val Pro Arg His Gly Trp Ile Asn Leu His Phe Ser Leu Leu
 100 105 110
 Pro Arg Trp Arg Gly Ala Ala Pro Ile Gln Arg Ala Ile Met Ala Gly
 115 120 125
 Asp Glu Glu Thr Gly Ala Cys Val Phe Gln Leu Val Glu Ser Leu Asp
 130 135 140
 Ala Gly Pro
 145

<210> 897
 <211> 384
 <212> DNA
 <213> Homo sapiens

<400> 897
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 gacgactacc tcgtccagct gtcgaaggaa gggctcgaga cccgtctcgc gcagctgtat
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 ccggtcgaag cccgacgcga cgcgcagcgc gacacctact acaagcgcct cgaattcgag
 180
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 aactgggcaa agaacaacgg cgtgccggtc ggcccgggccc gcggctcggg cgccgggttcg
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 360

gagcgccttcc tgaacccgga acgc
384

<210> 898

<211> 128

<212> PRT

<213> Homo sapiens

<400> 898

Glu	Leu	Glu	Ala	Gly	Lys	Pro	Glu	Val	Pro	Leu	Phe	Pro	Thr	Pro	Asp
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Gly	Met	Ser	Leu	Asp	Asp	Tyr	Leu	Val	Gln	Leu	Ser	Lys	Glu	Gly	Leu
			20					25					30		
Glu	Thr	Arg	Leu	Ala	Gln	Leu	Tyr	Pro	Val	Glu	Ala	Arg	Arg	Asp	Ala
		35					40					45			
Gln	Arg	Asp	Thr	Tyr	Tyr	Lys	Arg	Leu	Glu	Phe	Glu	Cys	Gly	Thr	Ile
	50					55					60				
Thr	Lys	Met	Gly	Phe	Pro	Gly	Tyr	Phe	Leu	Ile	Val	Ala	Asp	Phe	Ile
65					70					75					80
Asn	Trp	Ala	Lys	Asn	Asn	Gly	Val	Pro	Val	Gly	Pro	Gly	Arg	Gly	Ser
			85						90					95	
Gly	Ala	Gly	Ser	Leu	Val	Ala	Tyr	Ala	Leu	Gly	Ile	Thr	Asp	Leu	Glu
			100					105					110		
Val	Leu	Arg	Tyr	Asp	Leu	Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg
		115					120						125		

<210> 899

<211> 6171

<212> DNA

<213> Homo sapiens

<400> 899

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aatctcctga cggatcagtg catacctgtc ctggtagggc acctgcacct gcgaatcttg
180
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3360
ccttgacaaa tatgatacct gctaggtatt tcccaggga atttagggat tggcctcttt
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<210> 900

<211> 734

<212> PRT

<213> Homo sapiens

<400> 900

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Leu	Glu	Ser	Leu	Pro	Ser	Ala	Cys	Thr	Gly	Glu	Glu	Ser	Leu	Ser	Met
			20					25					30		
Leu	Gln	Leu	Leu	Tyr	Leu	Thr	Asn	Asn	Leu	Leu	Thr	Asp	Gln	Cys	Ile
		35					40					45			
Pro	Val	Leu	Val	Gly	His	Leu	His	Leu	Arg	Ile	Leu	His	Leu	Ala	Asn
		50				55					60				
Asn	Gln	Leu	Gln	Thr	Phe	Pro	Ala	Ser	Lys	Leu	Asn	Lys	Leu	Glu	Gln
65				70						75				80	
Leu	Glu	Glu	Leu	Asn	Leu	Ser	Gly	Asn	Lys	Leu	Lys	Thr	Ile	Pro	Thr
			85					90						95	
Thr	Ile	Ala	Asn	Cys	Lys	Arg	Leu	His	Thr	Leu	Val	Ala	His	Ser	Asn
			100					105					110		
Asn	Ile	Ser	Ile	Phe	Pro	Glu	Ile	Leu	Gln	Leu	Pro	Gln	Ile	Gln	Phe
		115					120					125			
Val	Asp	Leu	Ser	Cys	Asn	Asp	Leu	Thr	Glu	Ile	Leu	Ile	Pro	Glu	Ala
		130				135					140				
Leu	Pro	Ala	Thr	Leu	Gln	Asp	Leu	Asp	Leu	Thr	Gly	Asn	Thr	Asn	Leu
145				150						155				160	
Val	Leu	Glu	His	Lys	Thr	Leu	Asp	Ile	Phe	Ser	His	Ile	Thr	Thr	Leu
			165						170					175	
Lys	Ile	Asp	Gln	Lys	Pro	Leu	Pro	Thr	Thr	Asp	Ser	Thr	Val	Thr	Ser
			180					185						190	
Thr	Phe	Trp	Ser	His	Gly	Leu	Ala	Glu	Met	Ala	Gly	Gln	Arg	Asn	Lys

		195					200					205			
Leu	Cys	Val	Ser	Ala	Leu	Ala	Met	Asp	Ser	Phe	Ala	Glu	Gly	Val	Gly
	210					215					220				
Ala	Val	Tyr	Gly	Met	Phe	Asp	Gly	Asp	Arg	Asn	Glu	Glu	Leu	Pro	Arg
225					230					235					240
Leu	Leu	Gln	Cys	Thr	Met	Ala	Asp	Val	Leu	Leu	Glu	Glu	Val	Gln	Gln
				245					250					255	
Ser	Thr	Asn	Asp	Thr	Val	Phe	Met	Ala	Asn	Thr	Phe	Leu	Val	Ser	His
			260					265					270		
Arg	Lys	Leu	Gly	Met	Ala	Gly	Gln	Lys	Leu	Gly	Ser	Ser	Ala	Leu	Leu
		275					280					285			
Cys	Tyr	Ile	Arg	Pro	Asp	Thr	Ala	Asp	Pro	Ala	Ser	Ser	Phe	Ser	Leu
	290					295					300				
Thr	Val	Ala	Asn	Val	Gly	Thr	Cys	Gln	Ala	Val	Leu	Cys	Arg	Gly	Gly
305					310					315					320
Lys	Pro	Val	Pro	Leu	Ser	Lys	Val	Phe	Ser	Leu	Glu	Gln	Asp	Pro	Glu
				325					330					335	
Glu	Ala	Gln	Arg	Val	Lys	Asp	Gln	Lys	Ala	Ile	Ile	Thr	Glu	Asp	Asn
			340					345					350		
Lys	Val	Asn	Gly	Val	Thr	Cys	Cys	Thr	Arg	Met	Leu	Gly	Cys	Thr	Tyr
		355					360					365			
Leu	Tyr	Pro	Trp	Ile	Leu	Pro	Lys	Pro	His	Ile	Ser	Ser	Thr	Pro	Leu
	370					375					380				
Thr	Ile	Gln	Asp	Glu	Leu	Leu	Ile	Leu	Gly	Asn	Lys	Ala	Leu	Trp	Glu
385					390					395					400
His	Leu	Ser	Tyr	Thr	Glu	Ala	Val	Asn	Ala	Val	Arg	His	Val	Gln	Asp
				405					410					415	
Pro	Leu	Ala	Ala	Ala	Lys	Lys	Leu	Cys	Thr	Leu	Ala	Gln	Ser	Tyr	Gly
		420						425					430		
Cys	Gln	Asp	Ser	Val	Gly	Ala	Met	Val	Val	Tyr	Leu	Asn	Ile	Gly	Glu
		435					440					445			
Glu	Gly	Cys	Thr	Cys	Glu	Met	Asn	Gly	Leu	Thr	Leu	Pro	Gly	Pro	Val
	450					455					460				
Gly	Phe	Ala	Ser	Thr	Thr	Thr	Ile	Lys	Asp	Ala	Pro	Lys	Pro	Ala	Thr
465					470					475					480
Pro	Ser	Ser	Ser	Ser	Gly	Ile	Ala	Ser	Glu	Phe	Ser	Ser	Glu	Met	Ser
				485					490					495	
Thr	Ser	Glu	Val	Ser	Ser	Glu	Val	Gly	Ser	Thr	Ala	Ser	Asp	Glu	His
			500					505					510		
Asn	Ala	Gly	Gly	Leu	Asp	Thr	Ala	Leu	Leu	Pro	Arg	Pro	Glu	Arg	Arg
		515					520					525			
Cys	Ser	Leu	His	Pro	Thr	Pro	Thr	Ser	Gly	Leu	Phe	Gln	Arg	Gln	Pro
	530					535					540				
Ser	Ser	Ala	Thr	Phe	Ser	Ser	Asn	Gln	Ser	Asp	Asn	Gly	Leu	Asp	Ser
545					550										

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625          630          635          640
Pro Ser Thr Ser Cys Leu Tyr Gly Lys Lys Leu Ser Asn Gly Ser Ile
          645          650          655
Val Pro Leu Glu Asp Ser Leu Asn Leu Ile Glu Val Ala Thr Glu Val
          660          665          670
Pro Lys Arg Lys Thr Gly Tyr Phe Ala Ala Pro Thr Gln Met Glu Pro
          675          680          685
Glu Asp Gln Phe Val Val Pro His Asp Leu Glu Glu Glu Val Lys Glu
          690          695          700
Gln Met Lys Gln His Gln Asp Ser Arg Leu Glu Pro Glu Pro His Glu
705          710          715          720
Glu Asp Arg Thr Glu Pro Pro Glu Glu Phe Asp Thr Ala Leu
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<210> 901
<211> 309
<212> DNA
<213> Homo sapiens

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<400> 901
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120
tggttaagtag tgatggacac ttatggagtt ttcagagact tatgcattgg gtaacaaggc
180
actgcaagag accccagata gcacagcatc atctcacatt tacaccacat cacatcaaca
240
tcgatgctag gaggtctaaa gctgatgcc acttcagagc tgcaagtatc caaaagactc
300
cactcatga
309

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<210> 902
<211> 102
<212> PRT
<213> Homo sapiens

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<400> 902
Met Ile His Leu Pro Arg Pro Pro Lys Val Leu Gly Leu His Thr Asp
1          5          10          15
Gly Lys Leu His Phe Leu Phe Leu Leu Met Gln Gln Gly His Pro Lys
20          25          30
Ile Arg Leu Pro Ser Val Ser Val Val Ser Ser Asp Gly His Leu Trp
35          40          45
Ser Phe Gln Arg Leu Met His Trp Val Thr Arg His Cys Lys Arg Pro
50          55          60
Gln Ile Ala Gln His His Leu Thr Phe Thr Pro His His Ile Asn Ile
65          70          75          80
Asp Ala Arg Arg Ser Lys Ala Asp Ala Thr Phe Arg Ala Ala Ser Ile
85          90          95
Gln Lys Thr Pro Leu Met
100

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<210> 903
 <211> 349
 <212> DNA
 <213> Homo sapiens

<400> 903
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 taagggtctt gatggcctca tgggttgaca ggaacagaag acaaagacta gggcccaccc
 120
 aaggtgtgaa gtctaataagg aaaccttttc tccataaggc tacaatgggt ctacaaaaaa
 180
 taaaaccatg ccaccccagg gactgcagcc caattttata tcaccatgag gtccaaaaaa
 240
 ttccaagctg tgaatttagt ttcaaattggc cttgggtctcc agtatcccta gccatgtggc
 300
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 349

<210> 904
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 904
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 1 5 10 15
 Arg Asn Arg Arg Gln Arg Leu Gly Pro Thr Gln Gly Val Lys Ser Asn
 20 25 30
 Arg Lys Pro Phe Leu His Lys Ala Thr Met Gly Leu Pro Lys Ile Lys
 35 40 45
 Pro Cys His Pro Arg Asp Cys Ser Pro Ile Leu Tyr His His Glu Val
 50 55 60
 Gln Lys Ile Pro Ser Cys Glu Phe Ser Phe Lys Trp Pro Trp Ser Pro
 65 70 75 80
 Val Ser Leu Ala Met Trp Gln Lys Gln Thr Ile Leu Phe Gly Gly Tyr
 85 90 95
 Ile Phe Ile Leu Arg Leu
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<210> 905
 <211> 377
 <212> DNA
 <213> Homo sapiens

<400> 905
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 ctcaacgaag acatcattat cgcgggtgac cgggcagacg cggtgattag cgtatcccag
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 gggctctgcg acaggctggc tggacatggc gtgacctcaa cggtggttcc caacatcggt
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 gacgtcgagc tgtttgaccg tcttgatcga cgacatgagg ggacgatcgt cgtcagcgtc
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gccaccctca acccgggaaa gggcatgatt gagttagctc aggctgttga gcgtcttccc
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 gaggttcagt tgagaatcat cggagatgga ccgcagcggc accaactgga ggccattgcc
 360
 gctgataatc cacgcgt
 377

<210> 906
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 906
 Xaa Pro Glu Pro Val Val Trp Thr Glu His Asp Ser His Leu Ala His
 1 5 10 15
 Pro Asp Gln Arg Leu Asn Glu Asp Ile Ile Ile Ala Gly Asp Arg Ala
 20 25 30
 Asp Ala Val Ile Ser Val Ser Gln Gly Leu Cys Asp Arg Leu Ala Gly
 35 40 45
 His Gly Val Thr Ser Thr Val Val Pro Asn Ile Val Asp Val Glu Leu
 50 55 60
 Phe Asp Arg Pro Asp Arg Arg His Glu Gly Thr Ile Val Val Ser Val
 65 70 75 80
 Ala Thr Leu Asn Pro Gly Lys Gly Met Ile Glu Leu Ala Gln Ala Val
 85 90 95
 Glu Arg Leu Pro Glu Val Gln Leu Arg Ile Ile Gly Asp Gly Pro Gln
 100 105 110
 Arg His Gln Leu Glu Ala Ile Ala Ala Asp Asn Pro Arg
 115 120 125

<210> 907
 <211> 332
 <212> DNA
 <213> Homo sapiens

<400> 907
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 gaccagttct tcaacggcga ggttcaactg aaccttgtgc cgcagggtac attcgccgag
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 180
 gccgtgcaga aggggtgagct tgttcttaag tatgaaaaga aggacggtaa ggctgtgcca
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 gtcattgacgt ccaagccgcg tgaagtgcgc tcgtttgacg gccgtgacta tataatagaa
 300
 gaggttatta aggatgaata ggatatggtg aa
 332

<210> 908
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 908

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Thr Arg Arg Met Met Lys Ser Val Thr Gly Ser Phe Leu Gly Gly Asn
 1           5           10           15
Arg Glu Val Gly Asp Gln Phe Phe Asn Gly Glu Val Gln Leu Asn Leu
          20          25          30
Val Pro Gln Gly Thr Phe Ala Glu Arg Ile Arg Ala Gly Ala Ala Gly
        35          40          45
Ile Ala Ala Phe Phe Thr Pro Thr Gly Tyr Gly Thr Ala Val Gln Lys
       50          55          60
Gly Glu Leu Val Leu Lys Tyr Glu Lys Lys Asp Gly Lys Ala Val Pro
65          70          75          80
Val Met Thr Ser Lys Pro Arg Glu Val Arg Ser Phe Asp Gly Arg Asp
          85          90          95
Tyr Ile Ile Glu Glu Val Ile Lys Asp Glu
        100          105

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<210> 909

<211> 318

<212> DNA

<213> Homo sapiens

<400> 909

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tgccgcaggg gcaccgacgc tgtcgccatc aaaagagccg cctcgcgccc gcagcgcctc
120
ccagggacgg cgactcacgt ggctcgacac gcgcgcgcga gtcgcgtggg tgtgtcacgc
180
cccttttttt cccaccccaa caccgaaccg gcgggccatg gctgaggatt cgcaccccat
240
tcgctccggc ttgcgcatgc tcaagcgctc ctggagctcg aatgagaatg taccgccgcc
300
acaaagctcg ccgccggc
318

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<210> 910

<211> 102

<212> PRT

<213> Homo sapiens

<400> 910

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Met Ala Ala Val Gln Ile Tyr Arg Val Ser Arg Ala Tyr Ala His Met
 1           5           10           15
Met Pro Gln Gly His Arg Arg Cys Arg His Gln Lys Ser Arg Leu Ala
          20          25          30
Pro Ala Ala Pro Pro Arg Asp Gly Asp Ser Arg Gly Ser Thr Arg Ala
          35          40          45
Arg Glu Ser Arg Gly Cys Val Thr Pro Leu Phe Phe Pro Pro Gln His
          50          55          60
Arg Thr Gly Gly Pro Trp Leu Arg Ile Arg Thr Pro Phe Ala Pro Ala
65          70          75          80
Cys Ala Cys Ser Ser Ala Pro Gly Ala Arg Met Arg Met Tyr Arg Arg
          85          90          95
His Lys Ala Arg Arg Arg

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100

<210> 911
 <211> 506
 <212> DNA
 <213> Homo sapiens

<400> 911
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 aggctgcatg cgaggttggt gtgaaatgca tatctggctt tgtagctggt cggtcacct
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 240
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 300
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 360
 aaaaaaaaa atccagtgtt ctcaggtcag ccttccacca gccaggattc atcgtctgat
 420
 ctgtttgggg agagagcatg gagtgggtgga gatgggttg gcccagtgt tttctgatta
 480
 actgcagtt cacctgaaac attttg
 506

<210> 912
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 912
 Met Phe Gln Val Asn Cys Glu Leu Ile Arg Lys His Trp Gly Pro Thr
 1 5 10 15
 His Leu His His Ser Met Leu Ser Pro Gln Thr Asp Gln Thr Met Asn
 20 25 30
 Pro Gly Trp Trp Lys Ala Asp Leu Arg Thr Leu Asp Phe Phe Phe
 35 40 45
 Leu Ala Leu His His Leu Gln Gly Ser Glu Met Ala Gly Leu Gly Gly
 50 55 60
 Gly Gln Gly Val Pro Gln Gly Leu Leu Gln Arg Pro Gly Cys Ser Val
 65 70 75 80
 Val Pro Gly Pro Ser Arg Leu Arg Phe His Pro Leu Ala His Ser Ser
 85 90 95
 His Gly Arg Thr Pro Ala Pro Val Pro Thr Pro Glu Val Ser Arg Pro
 100 105 110
 Ala Thr Lys Pro Asp Met His Phe Thr Pro Thr Ser His Ala Ala Ser
 115 120 125
 Arg

<210> 913
 <211> 339

<212> DNA

<213> Homo sapiens

<400> 913

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 ctggggcgcca cggacctgct tttcgccctc gactcgattc cggcgtccta tggtttcacc
 180
 aacgaggggt accttaccct taccgctaac gtctttgctc tcatgggctt gcgtcagttg
 240
 tatttcctta ttggaagcct gttggaacgt ctgggtgtact tgtcgtggg actggtcgtg
 300
 attttgggct ttatcgccct caagctcatt ggccacgcg
 339

<210> 914

<211> 113

<212> PRT

<213> Homo sapiens

<400> 914

Arg	Phe	Met	Ala	Trp	Phe	Arg	Arg	Thr	Val	Pro	Ala	Thr	Gly	Asp	Tyr
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Arg	Gly	Thr	Lys	Phe	Phe	Val	Arg	Glu	Asn	Gly	Lys	Thr	Leu	Ala	Thr
			20					25					30		
Ser	Met	Phe	Met	Val	Cys	Val	Ala	Leu	Gly	Ala	Thr	Asp	Leu	Leu	Phe
		35					40					45			
Ala	Leu	Asp	Ser	Ile	Pro	Ala	Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Gly	Tyr
	50					55					60				
Leu	Ile	Leu	Thr	Ala	Asn	Val	Phe	Ala	Leu	Met	Gly	Leu	Arg	Gln	Leu
65					70				75					80	
Tyr	Phe	Leu	Ile	Gly	Ser	Leu	Leu	Glu	Arg	Leu	Val	Tyr	Leu	Ser	Leu
			85					90					95		
Gly	Leu	Val	Val	Ile	Leu	Gly	Phe	Ile	Ala	Leu	Lys	Leu	Ile	Gly	His
			100					105					110		

Ala

<210> 915

<211> 663

<212> DNA

<213> Homo sapiens

<400> 915

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 120
 ttaaccaagg gagagacttg catgaatcct caggatttta agccaggagc aatgggtctg
 180
 gaggagaatg gaaaatcggg acacactttg actgggtgatg gtctcaatgg accatcagat
 240

gcaagtgagc agagagtatc catggcatcg tcaggcagct cccagcctga actagtgact
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 360
 cagaaggtga aaatgatact ggatagtcag tgggtgtcaag gccttcagaa aggagatata
 420
 attaaggaaa tataccatca aaatgtgcag aatttaacac atctccaagt ggtagagggtg
 480
 ctaaagcagt ttccagtagg tgctgatgta ccattgctta tcttaagagg aggtccccct
 540
 tcaccaacca aaagtgccaa aatgaaaaca gataaaaagg aaaatgcagg aagtttggag
 600
 gccataaatg agcctattcc tcagcctatg ccttttccac cgagcattat caggtcagga
 660
 tcc
 663

<210> 916

<211> 221

<212> PRT

<213> Homo sapiens

<400> 916

Xaa	Val	Pro	Val	Asn	Gln	Tyr	Val	Asn	Leu	Thr	Leu	Cys	Arg	Gly	Tyr
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Pro	Leu	Pro	Asp	Asp	Ser	Glu	Asp	Pro	Val	Val	Asp	Ile	Val	Ala	Ala
			20					25					30		
Thr	Pro	Val	Ile	Asn	Gly	Gln	Ser	Leu	Thr	Lys	Gly	Glu	Thr	Cys	Met
			35				40					45			
Asn	Pro	Gln	Asp	Phe	Lys	Pro	Gly	Ala	Met	Val	Leu	Glu	Gln	Asn	Gly
	50					55					60				
Lys	Ser	Gly	His	Thr	Leu	Thr	Gly	Asp	Gly	Leu	Asn	Gly	Pro	Ser	Asp
65					70					75				80	
Ala	Ser	Glu	Gln	Arg	Val	Ser	Met	Ala	Ser	Ser	Gly	Ser	Ser	Gln	Pro
				85					90					95	
Glu	Leu	Val	Thr	Ile	Pro	Leu	Ile	Lys	Gly	Pro	Lys	Gly	Phe	Gly	Phe
			100					105					110		
Ala	Ile	Ala	Asp	Ser	Pro	Thr	Gly	Gln	Lys	Val	Lys	Met	Ile	Leu	Asp
		115					120					125			
Ser	Gln	Trp	Cys	Gln	Gly	Leu	Gln	Lys	Gly	Asp	Ile	Ile	Lys	Glu	Ile
	130					135					140				
Tyr	His	Gln	Asn	Val	Gln	Asn	Leu	Thr	His	Leu	Gln	Val	Val	Glu	Val
145					150					155				160	
Leu	Lys	Gln	Phe	Pro	Val	Gly	Ala	Asp	Val	Pro	Leu	Leu	Ile	Leu	Arg
			165					170						175	
Gly	Gly	Pro	Pro	Ser	Pro	Thr	Lys	Ser	Ala	Lys	Met	Lys	Thr	Asp	Lys
		180					185					190			
Lys	Glu	Asn	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Asn	Glu	Pro	Ile	Pro	Gln
	195					200						205			
Pro	Met	Pro	Phe	Pro	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Ser			
	210					215					220				

<210> 917

<211> 615

<212> DNA

<213> Homo sapiens

<400> 917

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atcgtggacc agaagttccc tgagtgtggc ttctacggcc tttacgacaa gatcctgctt
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ttcaaacaatg accccacgtc ggccaacctc ctgcagctgg tgcgctcgtc cggagacatc
120
caggagggcg acctggtgga ggtggtgctg tcggcctcgg ccaccttcga ggacttccag
180
atccgcccgc acgccctcac ggtgcactcc tatcgggcgc ctgccttctg tgatcactgc
240
ggggagatgc tcttcggcct agtgcgccag ggcctcaagt gcgatggctg cgggctgaac
300
taccacaagc gctgtgcctt cagcatcccc aacaactgta gtggggccccg caaacggcgc
360
ctgtcatcca cgtctctggc cagtggccac tcggtgcgcc tcggcacctc cgagtccctg
420
ccctgcacgg ctgaagagga gccgtagcac caccgaactc ctgcctcgcc gtccccgtca
480
tcctcttctt cctcttctgc ctcatcgat acggggccgcc ccattgagct ggacaagatg
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gtttgccagg cttgc
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<210> 918

<211> 148

<212> PRT

<213> Homo sapiens

<400> 918

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Ile Val Asp Gln Lys Phe Pro Glu Cys Gly Phe Tyr Gly Leu Tyr Asp
1           5           10           15
Lys Ile Leu Leu Phe Lys His Asp Pro Thr Ser Ala Asn Leu Leu Gln
20          25          30
Leu Val Arg Ser Ser Gly Asp Ile Gln Glu Gly Asp Leu Val Glu Val
35          40          45
Val Leu Ser Ala Ser Ala Thr Phe Glu Asp Phe Gln Ile Arg Pro His
50          55          60
Ala Leu Thr Val His Ser Tyr Arg Ala Pro Ala Phe Cys Asp His Cys
65          70          75          80
Gly Glu Met Leu Phe Gly Leu Val Arg Gln Gly Leu Lys Cys Asp Gly
85          90          95
Cys Gly Leu Asn Tyr His Lys Arg Cys Ala Phe Ser Ile Pro Asn Asn
100         105         110
Cys Ser Gly Ala Arg Lys Arg Arg Leu Ser Ser Thr Ser Leu Ala Ser
115         120         125
Gly His Ser Val Arg Leu Gly Thr Ser Glu Ser Leu Pro Cys Thr Ala
130         135         140
Glu Glu Glu Pro
145

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<210> 919
 <211> 294
 <212> DNA
 <213> Homo sapiens

<400> 919
 accggtatgc gtccgctggc tgtgctcggc gacaacatca ccaccgacca tctatcgccg
 60
 acaaatgcga tcctgctcga tagcgagcgc ggtgagtacc tcgccaagat gggcccgcgcg
 120
 gaagaagact tcatttcgaa cgcgacccat cgtggcgatc acctgaccgc acagcgcgcc
 180
 accttcgcca acccgacctt gctcaacgag atggccgtag tcgatggtga agtgaagaaa
 240
 ggctcgcttg cccgcgtgga accggaaggc catgtgatgc gcatgtggga agcc
 294

<210> 920
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 920
 Thr Gly Met Arg Pro Leu Ala Val Leu Gly Asp Asn Ile Thr Thr Asp
 1 5 10 15
 His Leu Ser Pro Thr Asn Ala Ile Leu Leu Asp Ser Ala Ala Gly Glu
 20 25 30
 Tyr Leu Ala Lys Met Gly Pro Pro Glu Glu Asp Phe Ile Ser Asn Ala
 35 40 45
 Thr His Arg Gly Asp His Leu Thr Ala Gln Arg Ala Thr Phe Ala Asn
 50 55 60
 Pro Thr Leu Leu Asn Glu Met Ala Val Val Asp Gly Glu Val Lys Lys
 65 70 75 80
 Gly Ser Leu Ala Arg Val Glu Pro Glu Gly His Val Met Arg Met Trp
 85 90 95
 Glu Ala

<210> 921
 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 921
 acgcgtttgc gcatcgcttt gaccggtctg acgatggctg agtacttccg cgatgttcag
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 aaccaggacg tgctgttggt catcgacaac atcttccggt tctcccaggc tggttctgag
 120
 gtttcaaccc tgctaggtcg tatgccctcg gcggtgggct accagcccaa cttggccgac
 180
 gagatgggccc aattgcagga gcgaatcacc tcgaccctg gtcactccat cacctcgatg
 240
 caggccgtct acgtccccgc tgacgattac accgaccggt ctccggcgac gaccttcgcc
 300

cacctggatg ccaccacgga gctttctcgt gagattgcct ctcgtaggect gtacccggcc
 360
 gtggatccgc tggcgctcg
 378

<210> 922
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 922
 Thr Arg Leu Arg Ile Ala Leu Thr Gly Leu Thr Met Ala Glu Tyr Phe
 1 5 10 15
 Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn Ile Phe
 20 25 30
 Arg Phe Ser Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly Arg Met
 35 40 45
 Pro Ser Ala Val Gly Tyr Gln Pro Asn Leu Ala Asp Glu Met Gly Gln
 50 55 60
 Leu Gln Glu Arg Ile Thr Ser Thr Arg Gly His Ser Ile Thr Ser Met
 65 70 75 80
 Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala
 85 90 95
 Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Ser Arg Glu Ile
 100 105 110
 Ala Ser Arg Gly Leu Tyr Pro Ala Val Asp Pro Leu Ala Ser
 115 120 125

<210> 923
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 923
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 120
 caacgcaaga atgtcgaaga agaagacatc ttcgccgccc accttgcgct attggaagac
 180
 cccacgctgc tggacgccgc cactggtgcc atcgaacacg gcagcgccgc caccacgcc
 240
 tggcgcgatg caatccaggc gcaatgcgcc gtggttcttg ccctgggcaa accgctgttt
 300
 gccgagcgcg ccaacgacct gcgcgatctg caacagcgag tactgcgtgc gctgttgggg
 360
 gaagcctggc acttcgaatt gccggccggg ccgattttca ggnnggcat taacttacc
 420
 ccttcgcct tgttgcaact gaggcccaa aacgccgtgg gtatttgcac ggccgaaggc
 480
 ggcgctacgt ctacgctgc gattttggcc cgaggcaaag gcttgccgtg cgtggctcgcg
 540
 ctggggcgccg aagtgctcga cgtgcccga g
 571

<210> 924
 <211> 190
 <212> PRT
 <213> Homo sapiens

<400> 924
 Thr Gly Ile Glu Leu Pro Gln Asp Thr Gly Lys His Val Ala Asp Glu
 1 5 10 15
 Gln Leu Gln Arg Leu Asp Thr Ala Leu Glu His Val Arg Gly Glu Ile
 20 25 30
 Arg Ile Thr Leu Glu His Ala Arg Gln Arg Lys Asn Val Glu Glu Glu
 35 40 45
 Asp Ile Phe Ala Ala His Leu Ala Leu Leu Glu Asp Pro Thr Leu Leu
 50 55 60
 Asp Ala Ala Thr Gly Ala Ile Glu His Gly Ser Ala Ala Thr His Ala
 65 70 75 80
 Trp Arg Asp Ala Ile Gln Ala Gln Cys Ala Val Leu Leu Ala Leu Gly
 85 90 95
 Lys Pro Leu Phe Ala Glu Arg Ala Asn Asp Leu Arg Asp Leu Gln Gln
 100 105 110
 Arg Val Leu Arg Ala Leu Leu Gly Glu Ala Trp His Phe Glu Leu Pro
 115 120 125
 Ala Gly Pro Ile Phe Arg Xaa Ala Ile Asn Leu Pro Pro Ser Ala Leu
 130 135 140
 Leu Gln Leu Ser Ala Gln Asn Ala Val Gly Ile Cys Met Ala Glu Gly
 145 150 155 160
 Gly Ala Thr Ser His Val Ala Ile Leu Ala Arg Gly Lys Gly Leu Pro
 165 170 175
 Cys Val Val Ala Leu Gly Ala Glu Val Leu Asp Val Pro Gln
 180 185 190

<210> 925
 <211> 620
 <212> DNA
 <213> Homo sapiens

<400> 925
 acgcgtgcac tgtgtgtatg catggtaacg tacacgtgtg cactgtgtgt ggtgtgcatg
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 ncatgggtgtg tgcacgtgtg cnactgtgta tgcattggtaa tgtgcacgtg tgcactgtgt
 120
 gtgggtgtgta tgcattggtg gtgcacgtgt gcactgtgtg tgtgtgtatg catgtgtgtg
 180
 cacgtgtgcc tgtgtgtatg catggtaatg tgcgtgtgca ctgtgtggtg tgtatgcatg
 240
 tgtgtgcacg tgtgcactgt gtatgcatag tgtgtgcacg tgtgcactgt gtgtggatgc
 300
 atggtaatgt gcacgtgtgc actgtgtgtg gtgtgtatga tgggtgtgtgc acgtgtgcac
 360
 ggtgtgtggt gtgtatgcat gtgtgtgcac gtgtgcactg tgtggcaggg gtgtttggtg
 420
 tgtgtgcatg tatgcatggt gtgtgcatac gtgtgcagca gcacctggtc ccatctccag
 480

tgcccagcag catcacacgc acttttggtgc ttataaatg catggtcagt gaggctgcca
 540
 gcaccaagct gtccctttac cataacacct ggaatagtca cctgtgataa gctatcacat
 600
 aggaaacatt tttaaaattt
 620

<210> 926
 <211> 89
 <212> PRT
 <213> Homo sapiens

<400> 926
 Thr Arg Ala Leu Cys Val Cys Met Val Thr Tyr Thr Cys Ala Leu Cys
 1 5 10 15
 Val Val Cys Met Xaa Trp Cys Val His Val Cys Xaa Cys Val Cys Met
 20 25 30
 Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly Val Cys
 35 40 45
 Thr Cys Ala Leu Cys Val Cys Val Cys Met Cys Val His Val Cys Leu
 50 55 60
 Cys Val Cys Met Val Met Cys Val Cys Thr Val Trp Cys Val Cys Met
 65 70 75 80
 Cys Val His Val Cys Thr Val Tyr Ala
 85

<210> 927
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 927
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 60
 aagaggcatt tgggggtcctg ttcagatcat tccaacagca aaccgggcat ggagacccca
 120
 tctcaggtct gtgcttctct ggggggccacc cagccatcct gccaccagc tcagaggcag
 180
 ggacaaagcc ctccaagag gcagcaggca gcaagggtca gccagcgag tgggggacagg
 240
 caggtacaac ctggaaaccc caaaggaccc cagatggcaa tgtgacacgg cccatccacc
 300
 aagcacctgt aatgccggct tcccacagag gcgagccaga tcctggcact attctttaag
 360

<210> 928
 <211> 111
 <212> PRT
 <213> Homo sapiens

<400> 928
 Met Glu Leu Leu Glu Ile Val Arg His Asp Gln Arg Glu Glu Ala Phe
 1 5 10 15
 Gly Val Leu Phe Arg Ser Phe Gln Gln Gln Thr Gly His Gly Asp Pro

	20		25		30										
Ile	Ser	Gly	Leu	Cys	Phe	Ser	Gly	Gly	His	Pro	Ala	Ile	Leu	Pro	Thr
	35		40		45										
Ser	Ser	Glu	Ala	Gly	Thr	Lys	Pro	Ser	Gln	Glu	Ala	Ala	Gly	Ser	Lys
	50		55		60										
Gly	Gln	Pro	Ala	Gln	Trp	Gly	Gln	Ala	Gly	Thr	Thr	Trp	Lys	Pro	Gln
65			70		75									80	
Arg	Thr	Pro	Asp	Gly	Asn	Val	Thr	Arg	Pro	Ile	His	Gln	Ala	Pro	Val
			85		90									95	
Met	Pro	Ala	Ser	His	Arg	Gly	Glu	Pro	Asp	Pro	Gly	Thr	Ile	Leu	
			100		105									110	

<210> 929

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 929

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nnctccccag ggccgagtct tccggagtca gcagagagcc tggatggatc acaggaggat
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120
aacaacagcc ggctcaaggc caagggcgtg ggccagcacg acaacgcccc gaactttggt
180
aaccagagct ttgaggagct gcgagcagcc tgtctaagaa agggggagct cttcgaggac
240
cccttattcc ctgctgaacc cagctcactg ggcttcaagg acctgggccc caactccaaa
300
aatgtgcaga acatctcctg gcagcggccc aaggatatca taaacaaccc tctattcatc
360
atggatggga tttctccaac agacatctgc caggggatcc tcggggactg ctggctgctg
420
gctgccatcg gctcccttac cacctgcccc aaactgctat accgcgtggt gcccagagga
480
cagagcttca agaaaaacta tgctggcatc ttccattttc agatttgga gtttgacag
540
tgggtgaacg tggtggtaga tgaccggctg ccacaaaaga atgacaagct ggtgtttgtg
600
cactcaaccg aacgcagtga gttctggagt gccctgctgg agaaggcgta tgccaagctg
660
agtgggtcct atgaagcatt gtcagggggc agtaccatgg agggccttga ggacttcaca
720
ggaggcgtgg ccagagctt ccaactccag agggccctc agaacctgct caggctcctt
780
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840
gaactggaat ccatgactga caagatgctg gtgagagggc acgcttactc tgtgactggc
900
cttcaggatg tccactacag aggcaaaatg gaaacactga ttcgggtccg gaatccctgg
960
ggccggattg agtggaatgg agcttggagt gacagtgccg gggagtggga agaggtggcc
1020
tcagacatcc agatgcagct gctgcacaag acggaggagc gggagtcttg gatgtcctac
1080

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caagatttcc tgaacaactt cacgctcctg gagatctgca acctcacgcc tgatacactc
 1140
 tctggggact acaagagcta ctggcacacc accttctacg agggcagctg ggcagaggcc
 1200
 agctccgcag ggggctgcag gaaccaccct ggcacgttct ggaccaaccc ccagttaaag
 1260
 atctctcttc ctgaggggga tgaccagag gatgacgcag agggcaatgt tgtggctctgc
 1320
 acctgcctgg tggccctaata gcagaagaac tggcggcatg cacggcagca gggagcccag
 1380
 ctgcagacca ttggctttgt cctctacgcg gtcccaaaaag agtttcagaa cattcaggat
 1440
 gtccacttga agaaggaatt cttcacgaag tatcaggacc acggcttctc agagatcttc
 1500
 accaactcac gggaggtgag cagccaactc cggctgcctc cgggggaata tatcattatt
 1560
 ccctccacct ttgagccaca cagagatgct gacttcctgc ttcgggtctt caccgagaag
 1620
 cacagcgagt catgggaatt ggatgaagtc aactatgctg agcaactcca agaggaaaag
 1680
 gtctctgagg atgacatgga ccaggacttc ctacatttgt ttaagatagt ggcaggagag
 1740
 ggcaaggaga taggggtgta tgagctccag aggctgctca acaggatggc catcaaattc
 1800
 aaaagcttca agaccaaggg ctttggcctg gatgcttgcc gctgcatgat caacctcatg
 1860
 gataaagatg gctctggcaa gctggggctt ctagagttca agatcctgtg gaaaaaactc
 1920
 aagaaatgga tggacatctt cagagagtgt gaccaggacc attcaggcac cttgaactcc
 1980
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 2100
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 2160
 ggccatattt gcttgagcct ggaacagtgg ctgcagatga ccatgtgggg atagaggcgc
 2220
 tgtaggagcc tggatcatctc taccagcagc agcagcagcg aggttctagc ccaggagggt
 2280
 ggggtgcttc ttgtagccct cagctctcca gtctctgctg atgaaatggg atccagggtg
 2340

<210> 930
 <211> 702
 <212> PRT
 <213> Homo sapiens

<400> 930
 Met Val Ala His Ile Asn Asn Ser Arg Leu Lys Ala Lys Gly Val Gly
 1 5 10 15
 Gln His Asp Asn Ala Gln Asn Phe Gly Asn Gln Ser Phe Glu Glu Leu
 20 25 30
 Arg Ala Ala Cys Leu Arg Lys Gly Glu Leu Phe Glu Asp Pro Leu Phe

35 40 45
 Pro Ala Glu Pro Ser Ser Leu Gly Phe Lys Asp Leu Gly Pro Asn Ser
 50 55 60
 Lys Asn Val Gln Asn Ile Ser Trp Gln Arg Pro Lys Asp Ile Ile Asn
 65 70 75 80
 Asn Pro Leu Phe Ile Met Asp Gly Ile Ser Pro Thr Asp Ile Cys Gln
 85 90 95
 Gly Ile Leu Gly Asp Cys Trp Leu Leu Ala Ala Ile Gly Ser Leu Thr
 100 105 110
 Thr Cys Pro Lys Leu Leu Tyr Arg Val Val Pro Arg Gly Gln Ser Phe
 115 120 125
 Lys Lys Asn Tyr Ala Gly Ile Phe His Phe Gln Ile Trp Gln Phe Gly
 130 135 140
 Gln Trp Val Asn Val Val Val Asp Asp Arg Leu Pro Thr Lys Asn Asp
 145 150 155 160
 Lys Leu Val Phe Val His Ser Thr Glu Arg Ser Glu Phe Trp Ser Ala
 165 170 175
 Leu Leu Glu Lys Ala Tyr Ala Lys Leu Ser Gly Ser Tyr Glu Ala Leu
 180 185 190
 Ser Gly Gly Ser Thr Met Glu Gly Leu Glu Asp Phe Thr Gly Gly Val
 195 200 205
 Ala Gln Ser Phe Gln Leu Gln Arg Pro Pro Gln Asn Leu Leu Arg Leu
 210 215 220
 Leu Arg Lys Ala Val Glu Arg Ser Ser Leu Met Gly Cys Ser Ile Glu
 225 230 235 240
 Val Thr Ser Asp Ser Glu Leu Glu Ser Met Thr Asp Lys Met Leu Val
 245 250 255
 Arg Gly His Ala Tyr Ser Val Thr Gly Leu Gln Asp Val His Tyr Arg
 260 265 270
 Gly Lys Met Glu Thr Leu Ile Arg Val Arg Asn Pro Trp Gly Arg Ile
 275 280 285
 Glu Trp Asn Gly Ala Trp Ser Asp Ser Ala Arg Glu Trp Glu Glu Val
 290 295 300
 Ala Ser Asp Ile Gln Met Gln Leu Leu His Lys Thr Glu Asp Gly Glu
 305 310 315 320
 Phe Trp Met Ser Tyr Gln Asp Phe Leu Asn Asn Phe Thr Leu Leu Glu
 325 330 335
 Ile Cys Asn Leu Thr Pro Asp Thr Leu Ser Gly Asp Tyr Lys Ser Tyr
 340 345 350
 Trp His Thr Thr Phe Tyr Glu Gly Ser Trp Arg Arg Gly Ser Ser Ala
 355 360 365
 Gly Gly Cys Arg Asn His Pro Gly Thr Phe Trp Thr Asn Pro Gln Phe
 370 375 380
 Lys Ile Ser Leu Pro Glu Gly Asp Asp Pro Glu Asp Asp Ala Glu Gly
 385 390 395 400
 Asn Val Val Val Cys Thr Cys Leu Val Ala Leu Met Gln Lys Asn Trp
 405 410 415
 Arg His Ala Arg Gln Gln Gly Ala Gln Leu Gln Thr Ile Gly Phe Val
 420 425 430
 Leu Tyr Ala Val Pro Lys Glu Phe Gln Asn Ile Gln Asp Val His Leu
 435 440 445
 Lys Lys Glu Phe Phe Thr Lys Tyr Gln Asp His Gly Phe Ser Glu Ile
 450 455 460
 Phe Thr Asn Ser Arg Glu Val Ser Ser Gln Leu Arg Leu Pro Pro Gly


```

465          470          475          480
Glu Tyr Ile Ile Ile Pro Ser Thr Phe Glu Pro His Arg Asp Ala Asp
          485          490          495
Phe Leu Leu Arg Val Phe Thr Glu Lys His Ser Glu Ser Trp Glu Leu
          500          505          510
Asp Glu Val Asn Tyr Ala Glu Gln Leu Gln Glu Glu Lys Val Ser Glu
          515          520          525
Asp Asp Met Asp Gln Asp Phe Leu His Leu Phe Lys Ile Val Ala Gly
          530          535          540
Glu Gly Lys Glu Ile Gly Val Tyr Glu Leu Gln Arg Leu Leu Asn Arg
545          550          555          560
Met Ala Ile Lys Phe Lys Ser Phe Lys Thr Lys Gly Phe Gly Leu Asp
          565          570          575
Ala Cys Arg Cys Met Ile Asn Leu Met Asp Lys Asp Gly Ser Gly Lys
          580          585          590
Leu Gly Leu Leu Glu Phe Lys Ile Leu Trp Lys Lys Leu Lys Lys Trp
          595          600          605
Met Asp Ile Phe Arg Glu Cys Asp Gln Asp His Ser Gly Thr Leu Asn
610          615          620
Ser Tyr Glu Met Arg Leu Val Ile Glu Lys Ala Gly Ile Lys Leu Asn
625          630          635          640
Asn Lys Val Met Gln Val Leu Val Ala Arg Tyr Ala Asp Asp Gly Leu
          645          650          655
Ile Ile Asp Phe Asp Ser Phe Ile Ser Cys Phe Leu Arg Leu Lys Thr
          660          665          670
Met Phe Thr Phe Phe Leu Thr Met Asp Pro Lys Asn Thr Gly His Ile
675          680          685
Cys Leu Ser Leu Glu Gln Trp Leu Gln Met Thr Met Trp Gly
690          695          700

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<210> 931
 <211> 297
 <212> DNA
 <213> Homo sapiens

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<400> 931
tcgcgaaggg agcctgacat gggccagaaa atcaatcccc atggtttccg tctcgggtgtg
60
acgaccgatc acaagacccg ctggtacgcc gagaagcagt acgccgagct cgtgggtgag
120
gatgtcaaga tccgagagtg gctccacaag aatctggagc gcgccggtct ttcgtccatc
180
gagatcgagc gtcgctccga gcgcgtgacc attttctttt acgccgctcg cccgggcatc
240
gttatcgggc gcaatggccg ggaggccgag cgcgtgcgtn ntgagctcga aaagctt
297

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<210> 932
 <211> 93
 <212> PRT
 <213> Homo sapiens

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<400> 932
Met Gly Gln Lys Ile Asn Pro His Gly Phe Arg Leu Gly Val Thr Thr

```

```

      1           5           10           15
Asp His Lys Thr Arg Trp Tyr Ala Glu Lys Gln Tyr Ala Glu Leu Val
      20           25           30
Gly Glu Asp Val Lys Ile Arg Glu Trp Leu His Lys Asn Leu Glu Arg
      35           40           45
Ala Gly Leu Ser Ser Ile Glu Ile Glu Arg Arg Ser Glu Arg Val Thr
      50           55           60
Ile Phe Leu Tyr Ala Ala Arg Pro Gly Ile Val Ile Gly Arg Asn Gly
      65           70           75           80
Arg Glu Ala Glu Arg Val Arg Xaa Glu Leu Glu Lys Leu
      85           90

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<210> 933
 <211> 305
 <212> DNA
 <213> Homo sapiens

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<400> 933
nnacgcgtcg ccaagctggt gatggccgaa tacaaggggc tcaacgtcat cgtcaaaacc
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tccgccgatc cggcaagcca agccaatgcc gtgcaggatc tggcgggggc aggcacgcac
120
gcgctggcca tcttgccgac cgaccggat cagctgggtt cggcgatcca gcagggtcaag
180
gacgacggca agttcgtggc gctggtcgac cgtgcgcctt ccgtcaacga caacacgatc
240
cgcgatctct acgtggccgg caacaaccgg gcgctcggcg aagtggcggg caaattcatg
300
ggcga
305

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<210> 934
 <211> 101
 <212> PRT
 <213> Homo sapiens

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<400> 934
Xaa Arg Val Ala Lys Leu Leu Met Ala Glu Tyr Lys Gly Leu Asn Val
      1           5           10           15
Ile Val Lys Thr Ser Ala Asp Pro Ala Ser Gln Ala Asn Ala Val Gln
      20           25           30
Asp Leu Ala Gly Ala Gly Ile Asp Ala Leu Ala Ile Leu Pro Thr Asp
      35           40           45
Pro Asp Gln Leu Val Ser Ala Ile Gln Gln Val Lys Asp Asp Gly Lys
      50           55           60
Phe Val Ala Leu Val Asp Arg Ala Pro Ser Val Asn Asp Asn Thr Ile
      65           70           75           80
Arg Asp Leu Tyr Val Ala Gly Asn Asn Pro Ala Leu Gly Glu Val Ala
      85           90           95
Gly Lys Phe Met Gly
      100

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<210> 935
 <211> 333

<212> DNA

<213> Homo sapiens

<400> 935

acgcgtgaag ggctgatgag tgctatgaaa aagccagggg cccgaggaca ctgggggtgga
 60
 caggctcccc tggggaagtc ctcttagaac tgagggatca acactggagg agactgcaag
 120
 ggggtacggga taaatgttcc tgggtgaagga aacagcaggg gcaaaggccc tgcagcagaa
 180
 aggagcgagg ccctttggag taacagaaaag accatgggtga caggagctca gaaagaccac
 240
 tgggtgttaag actataagcc agtggaggcc agattggggga atgggatggg aggggtgctt
 300
 gaagaccatg gtgaggctct cttggtcttt act
 333

<210> 936

<211> 103

<212> PRT

<213> Homo sapiens

<400> 936

Met	Val	Phe	Lys	His	Pro	Ser	His	Pro	Ile	Pro	Gln	Ser	Gly	Leu	His
1			5						10					15	
Trp	Leu	Ile	Val	Leu	Thr	Pro	Val	Val	Phe	Leu	Ser	Ser	Cys	His	His
			20					25					30		
Gly	Leu	Ser	Val	Thr	Pro	Lys	Gly	Leu	Ala	Pro	Phe	Cys	Cys	Arg	Ala
		35					40					45			
Phe	Ala	Pro	Ala	Val	Ser	Phe	Thr	Arg	Asn	Ile	Tyr	Pro	Val	Pro	Leu
	50					55					60				
Ala	Val	Ser	Ser	Ser	Val	Asp	Pro	Ser	Val	Leu	Arg	Gly	Leu	Pro	Gln
65					70					75				80	
Gly	Ser	Leu	Ser	Thr	Pro	Val	Ser	Ser	Gly	Pro	Trp	Leu	Phe	His	Ser
				85					90					95	
Thr	His	Gln	Pro	Phe	Thr	Arg									
															100

<210> 937

<211> 464

<212> DNA

<213> Homo sapiens

<400> 937

nnnttatctg cggagggggg ggccaccctg cccacactca tgctgcaggc ctccaccgac
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 120
 gaccgtgccc tggcagggtt gcgtgccagt cacgtcatcg acgaagctcg cgccgaggtg
 180
 cagcggcgtg ccgatctcgc ccgtggccat ctcgccatcc ttcccgcagg cgatgcccg
 240
 acggcggttg agaccctgtg cgacgaggtg gggtcccggg cggcctgaac cccgaccctg
 300

ccagnctgcg tcccatctcc tggccgggac cgtccagcg tctgctctct gacagctcat
 360
 cgttcttccg acaccaagga gtttctcgtg gcccgctcgc tcgatctcat cggcattggg
 420
 cccggcaacc cggactggat caccctgggt gccgtcaagg ccan
 464

<210> 938
 <211> 95
 <212> PRT
 <213> Homo sapiens

<400> 938
 Xaa Leu Ser Ala Glu Gly Val Ala Thr Leu Pro Thr Leu Met Leu Gln
 1 5 10 15
 Ala Ser Thr Asp Pro Ala Asp Asp Glu Leu Lys Asp Leu Leu Thr Ala
 20 25 30
 Asp Leu Met Asp Gln His Asn Leu Asp Arg Ala Leu Ala Gly Leu Arg
 35 40 45
 Ala Ser His Val Ile Asp Glu Ala Arg Ala Glu Val Gln Arg Arg Ala
 50 55 60
 Asp Leu Ala Arg Gly His Leu Ala Ile Leu Pro Ala Gly Asp Ala Arg
 65 70 75 80
 Thr Ala Leu Glu Thr Leu Cys Asp Glu Val Gly Ser Arg Ala Ala
 85 90 95

<210> 939
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 939
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 120
 acatggcggg ggatcgaggt tggcggctat gaaatccatc acgggcgtct gtcgttcgct
 180
 gaggacgctg aagccttcct cgacggcgta cacgtcggtc cggtatgggg gacgatgtgg
 240
 cacggggcat tcgagcacga cgaattccgt cgcacgtggc tggctgacgc ggcccgtcac
 300
 gctggatcat cctggcgctc gcactccgac gagctggggt atcaggctcg acgcgaggcg
 360
 atgatcgaaa ccctcgccga cgcgt
 385

<210> 940
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 940
 Xaa Thr Ile Leu Asp Pro Asp Gly Gln Glu Thr Thr Pro Gly Ser Val

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      1           5           10           15
Ile Glu Gly Leu Gly Leu Leu Pro Val Glu Val Asp Phe Ala Ala Thr
      20           25           30
Lys Thr Leu Ala Leu Ser His Gly Thr Trp Arg Gly Ile Glu Val Gly
      35           40           45
Gly Tyr Glu Ile His His Gly Arg Leu Ser Phe Ala Glu Asp Ala Glu
      50           55           60
Ala Phe Leu Asp Gly Val His Val Gly Pro Val Trp Gly Thr Met Trp
      65           70           75           80
His Gly Ala Phe Glu His Asp Glu Phe Arg Arg Thr Trp Leu Ala Asp
      85           90           95
Ala Ala Arg His Ala Gly Ser Ser Trp Arg Pro His Ser Asp Glu Leu
      100          105          110
Gly Tyr Gln Ala Arg Arg Glu Ala Met Ile Glu Thr Leu Ala Asp Ala
      115          120          125

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<210> 941
 <211> 348
 <212> DNA
 <213> Homo sapiens

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<400> 941
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gaagccatgc aaaccatggt cgtgctggcc gggctgccgt tctcgggtggt gctgattttc
120
ttcatgttcg gtttgcacaa ggcgatgcgc caggacgtgg ccatggagca ggagcaggca
180
caattggctg aacgtggctg ccgtggtttc agcgagcgcc tgaccgcgct ggacctgcaa
240
ccgagccagg gcaccgtgca acgctttatg gacaaacatg tgacgccggc gttggaacaa
300
gcggcgactg cgttgctgta tcaagggctg gaagtgcaga ccctgctt
348

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<210> 942
 <211> 116
 <212> PRT
 <213> Homo sapiens

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<400> 942
Ile Phe Trp Ser Ala Val Ile Thr Leu Val Thr Ile Gly Leu Leu Phe
1           5           10           15
Ala Gly Asn Phe Glu Ala Met Gln Thr Met Val Val Leu Ala Gly Leu
      20           25           30
Pro Phe Ser Val Val Leu Ile Phe Phe Met Phe Gly Leu His Lys Ala
      35           40           45
Met Arg Gln Asp Val Ala Met Glu Gln Glu Gln Ala Gln Leu Ala Glu
      50           55           60
Arg Gly Arg Arg Gly Phe Ser Glu Arg Leu Thr Ala Leu Asp Leu Gln
      65           70           75           80
Pro Ser Gln Gly Thr Val Gln Arg Phe Met Asp Lys His Val Thr Pro
      85           90           95
Ala Leu Glu Gln Ala Ala Thr Ala Leu Arg Asp Gln Gly Leu Glu Val

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100
Gln Thr Leu Leu
115

105

110

<210> 943
<211> 439
<212> DNA
<213> Homo sapiens

<400> 943
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ctcctctaata gcatcctggg ctcttgctaa ccctgtggga aacaccgtct cttctctcct
120
ttgccctctt ctgtgatcac atcctcactt ctgagcctat ctgcccattc agtcaatccc
180
ccttggttct gggatgctat ttccctggcc gcctccctct aggagtgttt agaaccctca
240
ctgtgggcag aaggaggga agatggctga ggtacctgga aaggacgtg tggatccccg
300
ggcatggaag gaaggaggca ggagagctag aaaaagggat gagatctaata gttccctaag
360
gaacctggct tagtgctggc cttcacata ctgagacatg gaatccttac tactgttctc
420
tgaggaaaga ggctgttcc
439

<210> 944
<211> 118
<212> PRT
<213> Homo sapiens

<400> 944
Met Ala Gly Ala Glu Gln Ile Glu Gln Asp Leu Val Ser Phe Ser Leu
1 5 10 15
His Phe Val Pro Pro Leu Met His Pro Gly Leu Leu Leu Thr Leu Trp
20 25 30
Glu Thr Pro Ser Leu Leu Ser Phe Ala Leu Phe Cys Asp His Ile Leu
35 40 45
Thr Ser Glu Pro Ile Cys Pro Ser Ser Gln Ser Pro Leu Val Leu Gly
50 55 60
Cys Tyr Phe Pro Gly Arg Leu Pro Leu Gly Val Phe Arg Thr Leu Thr
65 70 75 80
Val Gly Arg Arg Glu Gly Arg Trp Leu Arg Tyr Leu Glu Arg Asp Val
85 90 95
Trp Ile Pro Gly His Gly Arg Lys Glu Ala Gly Glu Leu Glu Lys Gly
100 105 110
Met Arg Ser Asn Val Pro
115

<210> 945
<211> 339
<212> DNA
<213> Homo sapiens

<400> 945
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 gagatgggtga tatatatata tactcacaca catatatatg tgtgtgtgtg tatatatgta
 120
 tatatatata gcgtgtacaa caaaacatgc actgtttact cagcaccctcg tgtttgtctc
 180
 agcaatagct tttctaaaga actgctacta tttgaaatgg agggggaggg gggtcctgga
 240
 cagagtattg tgcaagttga aagtctctgg atggggctat gtatataccta ccagccaatt
 300
 tgggtgcaaa ttggatttga aggcctgcct ctgtccacn
 339

<210> 946
 <211> 113
 <212> PRT
 <213> Homo sapiens

<400> 946
 Xaa Ile Arg Glu Ala Phe His Ile Phe Phe Leu Leu Ile Ile Ser Ile
 1 5 10 15
 Ala Leu Tyr Val Glu Met Val Ile Tyr Ile Tyr Thr His Thr His Ile
 20 25 30
 Tyr Val Cys Val Cys Ile Tyr Val Tyr Ile Tyr Ser Val Tyr Asn Lys
 35 40 45
 Thr Cys Thr Val Tyr Ser Ala Pro Arg Val Cys Leu Ser Asn Ser Phe
 50 55 60
 Ser Lys Glu Leu Leu Leu Phe Glu Met Glu Gly Glu Gly Gly Pro Gly
 65 70 75 80
 Gln Ser Ile Val Gln Val Glu Ser Leu Trp Met Gly Leu Cys Ile Ser
 85 90 95
 Tyr Gln Pro Ile Trp Val Gln Ile Gly Phe Glu Gly Leu Pro Leu Ser
 100 105 110
 Thr

<210> 947
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 947
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 ctctggcat cacacctgtg cacgggggtg gggaaggagt ggacaggagt ggacaagtca
 120
 agtagtgctg ccggctcaag cgatgcctca gcctttctgc tgtgtgcgaa gctttgcaga
 180
 ggagatgatg cttcaaagtt gtccctgttg gggatgagca gccaggcctt tatacactgg
 240
 gacagtcagt catggatacg tggatactct ggaaaccctc atccctggag gtctgagccc
 300

ctggatacca tgcccttctt aggctggagt tgctgccctt gtccatttac cataaaaatt
 360
 ggacaagaga ataccaggac acacctgagt ttctcatcgt atgctaaacc tgttcttcca
 420
 cgtacatccc caatgtgtac agccctactt tttctgctg atcaagttca attacttctg
 480
 ctaagatggg gactattctt gcctgctggg ccttggatgc aaggacccca atgttcaggc
 540
 agccttttgg gccttctagc atacgaatca gagcattatc tttagggtgtg gaataagctg
 600
 ccccaaaacc tgttgaagcc agccaggcac tgtgctcct tcacgcgt
 648

<210> 948
 <211> 154
 <212> PRT
 <213> Homo sapiens

<400> 948
 Met Glu Met Ser Gly Gln Gln Val Tyr Gly Val Leu Val Ala Ser His
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 Leu Cys Thr Gly Val Gly Lys Glu Trp Thr Gly Val Asp Lys Ser Ser
 20 25 30
 Ser Ala Ala Gly Ser Ser Asp Ala Ser Ala Phe Leu Leu Cys Ala Lys
 35 40 45
 Leu Cys Arg Gly Asp Asp Ala Ser Lys Leu Ser Leu Leu Gly Met Ser
 50 55 60
 Ser Gln Ala Phe Ile His Trp Asp Ser Gln Ser Trp Ile Arg Gly Tyr
 65 70 75 80
 Ser Gly Asn Pro His Pro Trp Arg Ser Glu Pro Leu Asp Thr Met Pro
 85 90 95
 Phe Leu Gly Trp Ser Cys Cys Pro Cys Pro Phe Thr Ile Lys Ile Gly
 100 105 110
 Gln Glu Asn Thr Arg Thr His Leu Ser Phe Ser Ser Tyr Ala Lys Pro
 115 120 125
 Val Leu Pro Arg Thr Ser Pro Met Cys Thr Ala Leu Leu Phe Ser Ala
 130 135 140
 Asp Gln Val Gln Leu Leu Leu Arg Trp
 145 150

<210> 949
 <211> 661
 <212> DNA
 <213> Homo sapiens

<400> 949
 acgcgtactg gttggctcat tcactgaaaa tatgatgaca tttaaaggaa atgcaagaat
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 aagtaatgtg gaattttatc acagtgggtca agaaggcttc agggatagca cagatccaag
 120
 atatgctgta acgtttctta acctaggaca gattcaagaa catggctcat cttatattcg
 180
 aggctgtgct tttcaccatg gcttctctcc agcaattggg gtatttggga cagatggatt
 240

ggacatagat gacaacatca ttcactttac agtgggggaa ggcataagaa tatgggggaa
 300
 tgccaaccga gtccgagga atttgattgc actttcggtt tggccaggaa cctatcagaa
 360
 cagaaaagat ttaagttcaa ctctctggca tgcagcaatt gagataaata gagggaccaa
 420
 tacagtttta cagaataatg tagtggtctgg atttggaaga gcaggatacc gcattgatgg
 480
 tgaaccttgc ccaggccagt ttaatcctgt ggaaaagtgg tttgacaatg aagcccatgg
 540
 aggtttatat gggatctata tgaaccaaga tggccttcct ggatgttctc ttatacaagg
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 660
 C
 661

<210> 950
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 950
 Met Met Thr Phe Lys Gly Asn Ala Arg Ile Ser Asn Val Glu Phe Tyr
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 His Ser Gly Gln Glu Gly Phe Arg Asp Ser Thr Asp Pro Arg Tyr Ala
 20 25 30
 Val Thr Phe Leu Asn Leu Gly Gln Ile Glu His Gly Ser Ser Tyr
 35 40 45
 Ile Arg Gly Cys Ala Phe His His Gly Phe Ser Pro Ala Ile Gly Val
 50 55 60
 Phe Gly Thr Asp Gly Leu Asp Ile Asp Asp Asn Ile Ile His Phe Thr
 65 70 75 80
 Val Gly Glu Gly Ile Arg Ile Trp Gly Asn Ala Asn Arg Val Arg Gly
 85 90 95
 Asn Leu Ile Ala Leu Ser Val Trp Pro Gly Thr Tyr Gln Asn Arg Lys
 100 105 110
 Asp Leu Ser Ser Thr Leu Trp His Ala Ala Ile Glu Ile Asn Arg Gly
 115 120 125
 Thr Asn Thr Val Leu Gln Asn Asn Val Val Ala Gly Phe Gly Arg Ala
 130 135 140
 Gly Tyr Arg Ile Asp Gly Glu Pro Cys Pro Gly Gln Phe Asn Pro Val
 145 150 155 160
 Glu Lys Trp Phe Asp Asn Glu Ala His Gly Gly Leu Tyr Gly Ile Tyr
 165 170 175
 Met Asn Gln Asp Gly Leu Pro Gly Cys Ser Leu Ile Gln Gly Phe Thr
 180 185 190
 Ile Trp Thr Cys Trp Asp Tyr Gly Ile Tyr Phe Gln Thr Thr Glu Ser
 195 200 205
 Val His
 210

<210> 951
 <211> 2615

<212> DNA

<213> Homo sapiens

<400> 951

nntccagccc ccaccatgcc gtggcccttg ctgctgctgc tggccgtgag tggggcccag
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120
agcttcagcc tgactcgggt ggattgtagc ggcttgggcc cccacatcat gccggtgccc
180
atccctctgg acacagccca cttggacctg tctccaacc ggctggagat ggtgaatgag
240
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300
ctcaccagca tctcaccac tgccttctcc cgccttcgct acctggagtc gcttgacctc
360
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420
gtgaacctta gccacaacca gctccgggag gtctcagtgt ctgccttcac gacgcacagt
480
cagggccggg cactacacgt ggacctctcc cacaacctct caccgcctcg tgccccacce
540
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600
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660
ctagctgtca ttggtccggg tgccttcgcg gggctgggag gccttacaca cctgtctctg
720
gccagcctgc agaggctccc tgagctggcg cccagtggct tccgtgagct accgggcctg
780
caggtcctgg acctgtcggg caaccccaag cttaactggg caggagctga ggtgttttca
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900
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1080
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1320
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cttttctaac atagcccttt ctttgccatg aggccatgag gcccgttca tccttttcta
 1560
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 1620
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 1680
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 1860
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 1920
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 1980
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 2040
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 aaggttgcat ttgttcactt ttgtaatat gtcttgggccc tgtgttgggg tgttggggga
 2400
 agctgggcat cagtggccac atgggcatca ggggctggcc ccacagagac cccacagggc
 2460
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 2520
 aataaacact ataaaatgaa gactaaggaa acagcccagg gttcggaagc tgagatgcta
 2580
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 2615

<210> 952

<211> 357

<212> PRT

<213> Homo sapiens

<400> 952

Xaa	Pro	Ala	Pro	Thr	Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Leu	Ala	Val
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Ser	Gly	Ala	Gln	Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu
			20				25						30		
Val	Glu	Thr	Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp
		35				40					45				
Cys	Ser	Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
	50				55					60					
Thr	Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu

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65          70          75          80
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp Leu
      85          90          95
Ser His Asn Leu Leu Thr Ser Ile Ser Pro Thr Ala Phe Ser Arg Leu
      100         105         110
Arg Tyr Leu Glu Ser Leu Asp Leu Ser His Asn Gly Leu Thr Ala Leu
      115         120         125
Pro Ala Glu Ser Phe Thr Ser Ser Pro Leu Ser Asp Val Asn Leu Ser
      130         135         140
His Asn Gln Leu Arg Glu Val Ser Val Ser Ala Phe Thr Thr His Ser
145         150         155         160
Gln Gly Arg Ala Leu His Val Asp Leu Ser His Asn Leu Ser Pro Pro
      165         170         175
Arg Ala Pro Pro His Glu Gly Arg Pro Ala Cys Ala His His Ser Glu
      180         185         190
Pro Glu Pro Gly Leu Glu Pro Ala Pro Cys Arg Ala Gln Pro Arg Asp
      195         200         205
Leu Pro Leu Arg Tyr Leu Ser Leu Asp Gly Asn Pro Leu Ala Val Ile
      210         215         220
Gly Pro Gly Ala Phe Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu
225         230         235         240
Ala Ser Leu Gln Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu
      245         250         255
Leu Pro Gly Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn
      260         265         270
Trp Ala Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu
      275         280         285
Asp Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu
      290         295         300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg Cys
305         310         315         320
Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly Ser Ser
      325         330         335
Pro Lys Val Ala Leu His Cys Val Asp Thr Arg Glu Ser Ala Ala Arg
      340         345         350
Gly Pro Thr Ile Leu
      355

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<210> 953
 <211> 347
 <212> DNA
 <213> Homo sapiens

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<400> 953
acgcgtgaag ccacccctgt gcgcaggcca gtctcgcggg ggtcaccacg gagcgtgtgc
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accacacttt ccccatccct tgatccatca ttgggcgttg aggttttccc atgtcttgac
120
tggtgtacct ggcggctctg cggagtaacc gctgcggaca cacagtagga cgggagggag
180
aagccattgc gtttcaccct ttcattggccc ttcctttccc cttccaagtg agctctttga
240
ggtgagtcac ggagggcagt gtcctctctg atcctgtctg gggttgtcaa atatggccaa
300

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gtgggctcca tcggggcagc ggggtggggtg ggggggtgtct gtcagag
347

<210> 954
<211> 103
<212> PRT
<213> Homo sapiens

<400> 954
Met Glu Pro Thr Trp Pro Tyr Leu Thr Thr Pro Asp Arg Met Gln Arg
1 5 10 15
Asp Thr Ala Leu His Asp Ser Pro Gln Arg Ala His Leu Glu Gly Glu
20 25 30
Arg Lys Gly His Glu Arg Val Lys Arg Asn Gly Phe Ser Leu Pro Ser
35 40 45
Tyr Cys Val Ser Ala Ala Val Thr Pro Gln Ser Arg Gln Val Gln Gln
50 55 60
Ser Arg His Gly Lys Thr Ser Thr Pro Asn Asp Gly Ser Arg Asp Gly
65 70 75 80
Glu Ser Val Val His Thr Leu Arg Gly Asp Pro Arg Glu Thr Gly Leu
85 90 95
Arg Thr Gly Met Ala Ser Arg
100

<210> 955
<211> 634
<212> DNA
<213> Homo sapiens

<400> 955
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ctctgcagggt gaatggttct gcagggtgaag ggctctgcag gtgaacgggt ctgcagggtga
120
agggtctctgc aggtgaacgg ttctgcagggt gagcggctct gcaggtgagc ggctctgcat
180
gtgagtgcct ctgtgactgg ctcgcaagca gcatttgtgc acacttgact ggccacaaca
240
gaatgttctt ctctgttgtc agcactgagg aggaagctcc tgcctaagcg accacagcca
300
ggcaccgcgt ccatggagac attgctctct ccagactcca ttcagactca ggaaacctga
360
gtcctctggaa tgcaggctga ggcagctccc acacaaaagc tatctactct ggcagttatc
420
agaggcctcc gttgcacaaa tcacacacct actgtgcctg acgtggctgg gcctccagca
480
ggacccgctc ctgagaacac acgggtgcta gtccaagttc acagcacggc tcaagtcact
540
cccacaaacc tctctataca aacacacaaa gctctgggag gctaccctgc atccaagagt
600
caccatctca cacctggaac aagggttacg gccg
634

<210> 956

<211> 113
 <212> PRT
 <213> Homo sapiens

<400> 956
 Met Glu Ser Gly Glu Ser Asn Val Ser Met Glu Arg Val Pro Gly Cys
 1 5 10 15
 Gly Arg Leu Gly Arg Ser Phe Leu Leu Ser Ala Asp Asn Arg Glu Glu
 20 25 30
 His Ser Val Val Ala Ser Gln Val Cys Thr Asn Ala Ala Cys Glu Pro
 35 40 45
 Val Thr Glu Ala Leu Thr Cys Arg Ala Ala His Leu Gln Ser Arg Ser
 50 55 60
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Leu His Leu Gln Asn Arg Ser
 65 70 75 80
 Pro Ala Glu Pro Phe Thr Cys Arg Thr Ile His Leu Gln Ser Arg Ser
 85 90 95
 Pro Ala Glu Pro Phe Thr Cys Arg Ala Ala His Leu Gln Ser Pro Ser
 100 105 110
 Arg

<210> 957
 <211> 823
 <212> DNA
 <213> Homo sapiens

<400> 957
 acgcgtggcc tgaccaccgt gtcccgccca tctacaggtg cccgagatcg tgagcgtcct
 60
 gcgctccaag cttcaggagg cccagggaga gcacgtcctg ccggccaccc agcacagcgt
 120
 gtacctcctg gccaccacgc actgcgcagc cgtgggtgtcc agcctcctgg gcagcccctt
 180
 gcccttggac aggtaccacg ctcagactcc aggccttaggg gtccctctgg aatgatgctc
 240
 cccctggaat gatgctcccc gagccctcca cccggetctg caccocgact ttctgcatga
 300
 gttcccatgg ctgtaggcca cgtgggacag aaagtgcacat ggagccaggc cccagtctct
 360
 caggtaccca cggggacctc tcctctccag gcgttttggg atcctcactg gctccggtgg
 420
 gcctgcaca gcacccccac agggaagctg ctgtttctgc ctctctctaa ggtcccaaaa
 480
 ctgcctgggt gctctgttgg cccagggctc cagcacacac tggaggctgc ccctcaccct
 540
 gtgtcttgggt tccggctact ccaagccttg tcctctgcag ggcattcact gctgcctgtg
 600
 agcagacccc tgggaactgc ctgatctgag cccctcagg agcccaagga caaccttgtc
 660
 tgtaccatac atcactatgt ctcccaagc tcacacctcc cagctcccag caaagggcag
 720
 ggcgtgtcta ccacccacca gccactggg gtcccccttc ctgcgcgagg cctccggagc
 780

atgggtctgc tggcccttcc tttctttgcc tcttagtctg gaa
823

<210> 958
<211> 105
<212> PRT
<213> Homo sapiens

<400> 958
Met Ala Val Gly His Val Gly Gln Lys Val Thr Trp Ser Gln Ala Pro
1 5 10 15
Val Ser Gln Val Pro Thr Gly Thr Ser Pro Leu Gln Ala Phe Trp Asp
20 25 30
Pro His Trp Leu Arg Trp Ala Leu His Ser Thr Pro Thr Gly Lys Leu
35 40 45
Leu Phe Leu Pro Ser Ser Lys Val Pro Lys Leu Pro Gly Cys Ser Val
50 55 60
Gly Pro Arg Leu Gln His Thr Leu Glu Ala Ala Pro His Pro Val Ser
65 70 75 80
Trp Phe Arg Leu Leu Gln Ala Leu Ser Ser Ala Gly His Pro Leu Leu
85 90 95
Pro Val Ser Arg Pro Leu Gly Thr Ala
100 105

<210> 959
<211> 586
<212> DNA
<213> Homo sapiens

<400> 959
ngtcatgact gcatggccaa gcatgactcc aacaccatca ttaagtttgc cgacgacaca
60
acagtggtag gcctgatcac cgacaacgat gaggcagcct atagggagga ggtcagagac
120
ctggcagtgt ggtgccagga taacaacctc tccctcaacg tgatcaagac cacgaagatg
180
atcgtggact acaggaaaag gagggctcgag cacgccccca ttctcattga tggggctgta
240
tgggagccag ttgagagctt caagttcctt ggtgtccaca tcaccatcga actatcatgg
300
tccaaacaca ccaagacagt agtgaagagg gtgcgacaat gcctattcca cctcggtaga
360
caaaaaagat ttggaatgga tcctcagacc ctcaaaaagt ttgacatcta caccatcgag
420
agcatcatga ctggttgcac caccgcctgg tatggcaact gctcggcctc cgaccgcaag
480
gcactacaga gggtagtgcg tacggcccag tacatcactg gggctaagct tcctgccatc
540
caggacctct ataccaggcg gtgtcagcgg aagaccctga caattg
586

<210> 960
<211> 195
<212> PRT

<213> Homo sapiens

<400> 960

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Xaa His Asp Cys Met Ala Lys His Asp Ser Asn Thr Ile Ile Lys Phe
 1           5           10           15
Ala Asp Asp Thr Thr Val Val Gly Leu Ile Thr Asp Asn Asp Glu Ala
 20           25           30
Ala Tyr Arg Glu Glu Val Arg Asp Leu Ala Val Trp Cys Gln Asp Asn
 35           40           45
Asn Leu Ser Leu Asn Val Ile Lys Thr Thr Lys Met Ile Val Asp Tyr
 50           55           60
Arg Lys Arg Arg Val Glu His Ala Pro Ile Leu Ile Asp Gly Ala Val
 65           70           75           80
Trp Glu Pro Val Glu Ser Phe Lys Phe Leu Gly Val His Ile Thr Ile
 85           90           95
Glu Leu Ser Trp Ser Lys His Thr Lys Thr Val Val Lys Arg Val Arg
100           105           110
Gln Cys Leu Phe His Leu Gly Arg Gln Lys Arg Phe Gly Met Asp Pro
115           120           125
Gln Thr Leu Lys Lys Phe Asp Ile Tyr Thr Ile Glu Ser Ile Met Thr
130           135           140
Gly Cys Ile Thr Ala Trp Tyr Gly Asn Cys Ser Ala Ser Asp Arg Lys
145           150           155           160
Ala Leu Gln Arg Val Val Arg Thr Ala Gln Tyr Ile Thr Gly Ala Lys
165           170           175
Leu Pro Ala Ile Gln Asp Leu Tyr Thr Arg Arg Cys Gln Arg Lys Thr
180           185           190
Leu Thr Ile
195

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<210> 961

<211> 502

<212> DNA

<213> Homo sapiens

<400> 961

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acgcgttgtc gtctctccgt agaccattca gtttggcaaa acttccactg gagtctgtgc
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atgactggat ggtctctttg acagccctgt caaggaatac caacagaata ttgattctcc
120
taaaactgtat agtaacctgc taaccagtcg gaaagagcta ccaccaatg gagatactaa
180
atccatggta atggaccatc gagggcaacc tccagagttg gctgctcttc cactcctga
240
gtctacaccc gtgcttcacc agaagaccct gcaggccatg aagagccact cagaaaaggg
300
ccatggccat ggagcttcaa ggaaagaaac ccctcagttt tttccgtcta gtccgccacc
360
tcattcccca ataagtcatg ggcatatccc cagtgccatt gttcttccaa atgctaccca
420
tgactacaac acgtctttct caaactccaa tgctcacaaa gctgaaaaga agcttcaaaa
480
cattgatcac cccttcacgc gt
502

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<210> 962
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 962
 Met Val Met Asp His Arg Gly Gln Pro Pro Glu Leu Ala Ala Leu Pro
 1 5 10 15
 Thr Pro Glu Ser Thr Pro Val Leu His Gln Lys Thr Leu Gln Ala Met
 20 25 30
 Lys Ser His Ser Glu Lys Ala His Gly His Gly Ala Ser Arg Lys Glu
 35 40 45
 Thr Pro Gln Phe Phe Pro Ser Ser Pro Pro Pro His Ser Pro Ile Ser
 50 55 60
 His Gly His Ile Pro Ser Ala Ile Val Leu Pro Asn Ala Thr His Asp
 65 70 75 80
 Tyr Asn Thr Ser Phe Ser Asn Ser Asn Ala His Lys Ala Glu Lys Lys
 85 90 95
 Leu Gln Asn Ile Asp His Pro Phe Thr Arg
 100 105

<210> 963
 <211> 1298
 <212> DNA
 <213> Homo sapiens

<400> 963
 nntcgcgagc acactccagc ctctggggag caggccacag aacgcagggt gaaacccaag
 60
 gcgctctaga ggagatgaat tatggatccg ccctcccgga atcctggctc ggccctcccc
 120
 acgccacca gggccagtcg ggtctgctca cagcccagg aggcgcgctg tccagccgcg
 180
 ggcaagagac agagcaggtc cctgtgtatc caagtccctg agcccgtgac accggcccca
 240
 ggccctgtag agagccagca gccaccatgg cgaaggagga agatgaggag aagaaagcca
 300
 agaaagggaa gaaggggaag aaggcaccgg acccgagaa gcccaaacgg agcctgaagg
 360
 ggacgtcgcg ggtgttcatt ggcttccgcg accgaacacc caagatctac aagaagggcc
 420
 agttccgcag cgcctcggcc ttcttctggg gcctccacac cggccccac aagaccaagc
 480
 gcacgaggaa ggcccgacc gtgctcgggt acacgtcaga gcttatgacg cacatgcgca
 540
 tgggcaagaa gaagcgggag atgaagggca agaagccgtc cttcatgggt atccgcttcc
 600
 caggccgccc tggctacggc cgcctgcggc cgcgcgccc gtcactcagc aaagcgtcca
 660
 cggccatcaa ctggctcaca aaaaagtcc tcctcaagaa ggccgaggag tcgggcagcg
 720
 aacaggccac agtggacgcc tggtgcagc gctcgagctc ccgcatgggc tcccgaaaac
 780

tccccctccc gtcgggtgcc gagatcctgc ggcttggggg ccggctccgg aggttcccc
 840
 gcagccgcag catctacgcg tcaggcgagc ccctgggctt cctgcccttc gaggacgagg
 900
 cccattcca tcaactcgggc tcccgcaagt cgctgtacgg gcttgagggc ttccaggacc
 960
 tgggcgagta ttatgactat caccgcgacg gcgacgacta ctacgaccgg cagtcaactcc
 1020
 accgctacga ggagcaggaa ccctacctgg cgggcctcgg ccctacagc ccggcctggc
 1080
 caccctacgg cgaccactac tacgggtacc cgcccaggga tccctacgac tactaccacc
 1140
 ccgactatta cgggtggcccc gttgatccgg ggtacaccta cggctacggc tacgacgatt
 1200
 acgaaccccc atatgcgcc ccgtcggggg actcgtctcc ttacagctac cacgatgggt
 1260
 acgagggcga ggcgcaccct tatggctact acctggat
 1298

<210> 964

<211> 235

<212> PRT

<213> Homo sapiens

<400> 964

Ser	Ala	Ser	Gln	Ala	Ala	Val	Ala	Thr	Ala	Ala	Cys	Gly	Arg	Ala	Pro
1			5					10						15	
Gly	His	Ser	Ala	Lys	Arg	Pro	Arg	Pro	Ser	Thr	Gly	Ser	Gln	Lys	Ser
			20					25					30		
Ser	Ser	Ser	Arg	Arg	Pro	Arg	Ser	Arg	Ala	Ala	Asn	Arg	Pro	Gln	Trp
			35				40					45			
Thr	Pro	Gly	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Trp	Ala	Pro	Ala	Asn	Ser
			50				55				60				
Pro	Ser	Arg	Arg	Val	Pro	Arg	Ser	Cys	Gly	Leu	Gly	Ala	Gly	Ser	Gly
65					70				75					80	
Gly	Ser	Pro	Ala	Ala	Ala	Ser	Thr	Arg	Gln	Ala	Ser	Pro	Trp	Ala	
			85					90					95		
Ser	Cys	Pro	Ser	Arg	Thr	Arg	Pro	His	Ser	Ile	Thr	Arg	Ala	Pro	Ala
			100				105					110			
Ser	Arg	Cys	Thr	Gly	Leu	Arg	Ala	Ser	Arg	Thr	Trp	Ala	Ser	Ile	Met
			115				120				125				
Thr	Ile	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Thr	Thr	Gly	Ser	His	Ser	Thr
			130				135				140				
Ala	Thr	Arg	Ser	Arg	Asn	Pro	Thr	Trp	Arg	Ala	Ser	Ala	Pro	Thr	Ala
145					150				155					160	
Arg	Pro	Gly	His	Pro	Thr	Ala	Thr	Thr	Thr	Thr	Gly	Thr	Arg	Pro	Arg
			165					170						175	
Ile	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Thr	Ile	Thr	Val	Ala	Pro	Leu	Ile
			180				185					190			
Arg	Gly	Thr	Pro	Thr	Ala	Thr	Ala	Thr	Thr	Ile	Thr	Asn	Pro	His	Met
			195				200					205			
Arg	Pro	Arg	Arg	Gly	Thr	Arg	Leu	Leu	Thr	Ala	Thr	Thr	Met	Gly	Thr
			210				215				220				
Arg	Ala	Arg	Arg	Thr	Leu	Met	Ala	Thr	Thr	Trp					

225

230

235

<210> 965

<211> 336

<212> DNA

<213> Homo sapiens

<400> 965

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nnngtgacca ttatgggtgg tgcccgtagc cgtgaagtgg aaggcggtga ttttggtggc
60
cgggtcagcg atgccgaaaa ggctgaaatc ctcggccgcg ccgatgtgta tgtcgccccc
120
aataccggcg gtgagagctt tggcattgtc ttggtggaag ccatggcggc aggcgcagcc
180
gttggtgctt cagacttgga ggccttccgc gcagtgtgca acgccgattc cgatgatgtt
240
gccggcgcgc tatatcgcaa tgaggatagt aatgaccttg ctcgtgtact caacgaggtg
300
ctcgaggatc ctgagtatcg tgcccgctta gtgcac
336

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<210> 966

<211> 112

<212> PRT

<213> Homo sapiens

<400> 966

Xaa	Val	Thr	Ile	Met	Gly	Gly	Ala	Arg	Thr	Arg	Glu	Val	Glu	Gly	Val
1				5				10					15		
Asp	Phe	Val	Gly	Arg	Val	Ser	Asp	Ala	Glu	Lys	Ala	Glu	Ile	Leu	Gly
		20						25					30		
Arg	Ala	Asp	Val	Tyr	Val	Ala	Pro	Asn	Thr	Gly	Gly	Glu	Ser	Phe	Gly
		35					40					45			
Ile	Val	Leu	Val	Glu	Ala	Met	Ala	Ala	Gly	Ala	Ala	Val	Val	Ala	Ser
	50					55				60					
Asp	Leu	Glu	Ala	Phe	Arg	Ala	Val	Cys	Asn	Ala	Asp	Ser	Asp	Asp	Val
65					70					75					80
Ala	Gly	Ala	Leu	Tyr	Arg	Asn	Glu	Asp	Ser	Asn	Asp	Leu	Ala	Arg	Val
			85					90					95		
Leu	Asn	Glu	Val	Leu	Glu	Asp	Pro	Glu	Tyr	Arg	Ala	Arg	Leu	Val	His
			100					105					110		

<210> 967

<211> 393

<212> DNA

<213> Homo sapiens

<400> 967

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ncaaattggca attcatagcc cgccagatcg gacacggagc tgggtggtatc cacggattcg
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ggcgcggagg cgtcgggctc aagctccgct tcggcaccgg tcggcactga ggaatctccg
120
tcggcctccg cttcggccgc agcctgggct gcgccagact ctgcgggagg caccttctcc
180

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cgggttcgcc agccaaatgg cgttgcaggc tccagcatcc agtccggtgc cttcggcacc
 240
 cccgcactgc gcagagaggc cgccagaaac gatggcaccg gcggcgcggg aggtgataca
 300
 ggcgcttcgg ccggagcgct cacggactcc ggcactacag gtgcagcttg cgcttcctgc
 360
 ggcggagcaa cagggtcact tcgaggcggg gat
 393

<210> 968

<211> 125

<212> PRT

<213> Homo sapiens

<400> 968

Pro	Ala	Arg	Ser	Asp	Thr	Glu	Leu	Val	Val	Ser	Thr	Asp	Ser	Gly	Ala
1				5					10					15	
Glu	Ala	Ser	Gly	Ser	Ser	Ser	Ala	Ser	Ala	Pro	Val	Gly	Thr	Glu	Glu
			20					25					30		
Ser	Pro	Ser	Ala	Ser	Ala	Ser	Ala	Ala	Ala	Trp	Ala	Ala	Pro	Asp	Ser
		35					40					45			
Ala	Gly	Gly	Thr	Phe	Ser	Arg	Val	Arg	Gln	Pro	Asn	Gly	Val	Ala	Gly
	50					55					60				
Ser	Ser	Ile	Gln	Ser	Gly	Ala	Phe	Gly	Thr	Pro	Ala	Leu	Arg	Arg	Glu
65					70				75					80	
Ala	Ala	Arg	Asn	Asp	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Asp	Thr	Gly	Ala
			85					90					95		
Ser	Ala	Gly	Ala	Leu	Thr	Asp	Ser	Gly	Thr	Thr	Gly	Ala	Ala	Cys	Ala
			100					105					110		
Ser	Cys	Gly	Gly	Ala	Thr	Gly	Ser	Leu	Arg	Gly	Gly	Asp			
		115					120					125			

<210> 969

<211> 880

<212> DNA

<213> Homo sapiens

<400> 969

caattgtcat gcaggacacc aaagatgaac acaggcttca cagtggcaaa ctctgtctga
 60
 ttatccttac atgtattgca gaggatcaat atgaccatgc atttttgcat gatgatcaac
 120
 atgaattttc gagtaaactt acatagaatg cctatgagac acaggaagaa ggcagcagac
 180
 aagaatctta ccctgccgtc tttagtatgt gaagtactgg acctgatggg agagtttatt
 240
 gtaacacaca tgatgaagga gtttcctatg gatctctata tacgctgcat ccaggtagta
 300
 cacaaactgc tctgctacca gaagaagtgt cgggtacgcc tgcattacac ctggcggggag
 360
 ctctggtcag ccttgataaa tttgctgaag ttccttatgt caaatgagac tgtacttttg
 420
 gccaaacaca acattttttac attagccctt atgattgtga acctatttaa tatgtttatc
 480

acatatggcg acacatttct gccaaacccc agcagctatg atgaacttta ctatgagatt
 540
 atccgcatgc accagagctt tgacaacctc tactccatgg tcttgaggct ttctaccaat
 600
 gcaggccagt ggaaggaagc agctagcaag gtgacccatg cattgggttaa tatcagagcc
 660
 atcatcaacc actttaaccc caaaattgag tcctacgctg ctgtgaatca catatcccaa
 720
 ctgtcagagg agcaggtgct ggaggtggtg agagccaact atgacacgct cacgctgaag
 780
 ctgcaggatg gcctggacca gtatgagcgc tactcagagc agcacaagga agctgccttc
 840
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 880

<210> 970

<211> 263

<212> PRT

<213> Homo sapiens

<400> 970

Met	Thr	Met	His	Phe	Cys	Met	Met	Ile	Asn	Met	Asn	Phe	Arg	Val	Asn
1				5					10					15	
Leu	His	Arg	Met	Pro	Met	Arg	His	Arg	Lys	Lys	Ala	Ala	Asp	Lys	Asn
			20					25					30		
Leu	Thr	Leu	Pro	Ser	Leu	Val	Cys	Glu	Val	Leu	Asp	Leu	Met	Val	Glu
		35					40					45			
Phe	Ile	Val	Thr	His	Met	Met	Lys	Glu	Phe	Pro	Met	Asp	Leu	Tyr	Ile
	50					55					60				
Arg	Cys	Ile	Gln	Val	Val	His	Lys	Leu	Leu	Cys	Tyr	Gln	Lys	Lys	Cys
65					70					75					80
Arg	Val	Arg	Leu	His	Tyr	Thr	Trp	Arg	Glu	Leu	Trp	Ser	Ala	Leu	Ile
				85					90					95	
Asn	Leu	Leu	Lys	Phe	Leu	Met	Ser	Asn	Glu	Thr	Val	Leu	Leu	Ala	Lys
			100					105						110	
His	Asn	Ile	Phe	Thr	Leu	Ala	Leu	Met	Ile	Val	Asn	Leu	Phe	Asn	Met
		115					120					125			
Phe	Ile	Thr	Tyr	Gly	Asp	Thr	Phe	Leu	Pro	Thr	Pro	Ser	Ser	Tyr	Asp
	130					135					140				
Glu	Leu	Tyr	Tyr	Glu	Ile	Ile	Arg	Met	His	Gln	Ser	Phe	Asp	Asn	Leu
145					150					155					160
Tyr	Ser	Met	Val	Leu	Arg	Leu	Ser	Thr	Asn	Ala	Gly	Gln	Trp	Lys	Glu
				165					170					175	
Ala	Ala	Ser	Lys	Val	Thr	His	Ala	Leu	Val	Asn	Ile	Arg	Ala	Ile	Ile
			180					185					190		
Asn	His	Phe	Asn	Pro	Lys	Ile	Glu	Ser	Tyr	Ala	Ala	Val	Asn	His	Ile
		195					200					205			
Ser	Gln	Leu	Ser	Glu	Glu	Gln	Val	Leu	Glu	Val	Val	Arg	Ala	Asn	Tyr
	210					215						220			
Asp	Thr	Leu	Thr	Leu	Lys	Leu	Gln	Asp	Gly	Leu	Asp	Gln	Tyr	Glu	Arg
225					230					235					240
Tyr	Ser	Glu	Gln	His	Lys	Glu	Ala	Ala	Phe	Phe	Lys	Glu	Leu	Val	Arg
				245					250					255	
Ser	Ile	Ser	Thr	Asn	Val	Arg									

260

<210> 971
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 971
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 cgcggtcgtg gtggtgcagg cttccccact ggggtgaaat ggtcctttgt tccccaaaac
 120
 aatcccaacc ccaaatacct ggttggttaac ggagacgaat ccgaaccgga cacgtgcaag
 180
 gacatgccgc tcattatggc aagcccgac acgcttgctg aaggtgctct tatctccgc
 240
 tacgctttcg gatccgagca ggctttcatc tacctccgtg gagaagttgt tcaggtagcc
 300
 cggcgcttg aagaaaaaaa aaaaatgcga nnnnnnn
 337

<210> 972
 <211> 112
 <212> PRT
 <213> Homo sapiens

<400> 972
 Ser Arg Gly Leu Thr Met Glu Pro Ser Glu Val Leu Asn Leu Ile Lys
 1 5 10 15
 Asp Ser Gly Leu Arg Gly Arg Gly Gly Ala Gly Phe Pro Thr Gly Val
 20 25 30
 Lys Trp Ser Phe Val Pro Gln Asn Asn Pro Asn Pro Lys Tyr Leu Val
 35 40 45
 Val Asn Gly Asp Glu Ser Glu Pro Gly Thr Cys Lys Asp Met Pro Leu
 50 55 60
 Ile Met Ala Ser Pro His Thr Leu Val Glu Gly Ala Leu Ile Ser Arg
 65 70 75 80
 Tyr Ala Phe Gly Ser Glu Gln Ala Phe Ile Tyr Leu Arg Gly Glu Val
 85 90 95
 Val Gln Val Ala Arg Arg Leu Glu Glu Lys Lys Lys Met Arg Xaa Xaa
 100 105 110

<210> 973
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 973
 acgcgtgaag gggaaagggg gagtcgtctc cttggttcct aagtgcgccc tctccaggtt
 60
 ccagcagggc ggcacagcca aggaaatggc atggctcctgc tgcattgggtc tcagtggggt
 120
 ccgggacctt ctgtataggc atcacttagg aaccagtcag accatcagat tctcaggacc
 180

cactggatca actgagtcag gaactcaggg ttttcaacac atcctccggg gggattccag
 240
 tggctgtgta actttgagga ccactggcaa agtggctctg gggtcagaga tccgagttca
 300
 tattctgggt ctgcctctga ctgactgcaa cgggtgggcaa gtcacttgcc gtgcccagcc
 360

<210> 974
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 974
 Met Ala Trp Ser Cys Cys Met Val Leu Ser Gly Val Arg Asp Leu Leu
 1 5 10 15
 Tyr Arg His His Leu Gly Thr Ser Gln Thr Ile Arg Phe Ser Gly Pro
 20 25 30
 Thr Gly Ser Thr Glu Ser Gly Thr Gln Gly Phe Gln His Ile Leu Arg
 35 40 45
 Gly Asp Ser Ser Gly Cys Val Thr Leu Arg Thr Thr Gly Lys Val Ala
 50 55 60
 Leu Gly Ser Glu Ile Arg Val His Ile Leu Gly Leu Pro Leu Thr Asp
 65 70 75 80
 Cys Asn Gly Gly Gln Val Thr Cys Arg Ala Gln
 85 90

<210> 975
 <211> 2604
 <212> DNA
 <213> Homo sapiens

<400> 975
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 120
 ccttggataa gtggtttctg attttgagag gacagcagag ggctgtatca cacaagacat
 180
 ttggcattag cctggaagag gtccctgggtga acgagtttac ccgccgcaag catcttgaac
 240
 tgaccagcca cgatgcaggt tgaagaagcc accgggtcagg ctgcggggccg tcgtcgggga
 300
 aacgtgggtgc gaaggggtgtt tggccgcata cggcgctttt tcagtcgcag gcggaatgag
 360
 cccaccttgc cccgggagtt cactcgccgt gggcgctcag gtgcagtgtc tgtggatagt
 420
 ctggctgagc tggaagacgg agccctgctg ctgcagaccc tgcagctttc aaaaatttcc
 480
 tttccaattg gccaacgact tctgggatcc aaaaggaaga tgagtctcaa tccgattgag
 540
 aaacaaatcc cccaggttgt tgaggcttgc tgccaattca ttgaaaaaca tggcttaagc
 600
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<210> 976
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 976
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 Leu Leu Leu Gln Thr Leu Gln Leu Ser Lys Ile Ser Phe Pro Ile Gly
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 His Gly Leu Ser Ala Val Gly Ile Phe Thr Leu Glu Tyr Ser Val Gln
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 Thr Asn Leu Ala Leu Val Phe Gly Ser Ala Leu Leu Lys Lys Gly Lys
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 Phe Gly Lys Arg Glu Ser Arg Lys Thr Lys Leu Gly Ile Asp His Tyr
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<210> 977
 <211> 378
 <212> DNA
 <213> Homo sapiens

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<210> 978
 <211> 126
 <212> PRT
 <213> Homo sapiens

<400> 978
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 50 55 60
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 <212> DNA
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<210> 980
 <211> 73
 <212> PRT
 <213> Homo sapiens

<400> 980
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 Glu Arg Asn Ala Trp Leu Arg Ala Ala Glu His Ser Glu Ala Ser Arg
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 Glu Asp Ser Arg Pro Ala Arg Ala Pro
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<210> 981
 <211> 404
 <212> DNA
 <213> Homo sapiens

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<210> 982

<211> 134

<212> PRT

<213> Homo sapiens

<400> 982

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Asp	Asp	Glu	Asp	Val	Asp	Asp	Glu	Asn	Thr	Asp	Ile	Thr	Ala	Leu	Ala
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Arg	Pro	Gly	Ser	Asp	Arg	Val	Leu	Gly	Arg	Gln	Arg	Leu	Gln	Gln	Pro
				85					90					95	
Arg	His	Leu	Gln	Pro	Ser	Gly	Ala	Pro	Asp	Gln	Ala	Cys	Gly	Gly	Thr
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Ala	Ser	Gly	Ala	Gln	Gly	Gly	Ala	Pro	Leu	Pro	Pro	Ala	His	Cys	Pro
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<210> 983

<211> 579

<212> DNA

<213> Homo sapiens

<400> 983

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<210> 984
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 984
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 Leu Phe Pro Lys Arg Ala Arg Tyr Pro Ser Phe Ser Gly Pro Leu Tyr
 50 55 60
 Leu Phe Phe Ser Leu Pro Glu Thr Pro Phe Leu Leu Asn Asn Leu Met
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<210> 985
 <211> 313
 <212> DNA
 <213> Homo sapiens

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<210> 986
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 986
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Leu Asp Asn Gln Ile Phe Ile Asp Tyr Ala Lys Leu Ile Lys Glu Ser			
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Asp Ala Leu Pro Val Asp Gln Gln Val Ala Phe Phe Leu Asn Asn Met			
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<210> 987

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<212> DNA

<213> Homo sapiens

<400> 987

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2640

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<210> 988
 <211> 873
 <212> PRT
 <213> Homo sapiens

<400> 988

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Met	Leu	Leu	Arg	Gly	Leu	Thr	Gln	Ile	Gln	Ser	Arg	Ile	Leu	Gly	Pro
		35					40					45			
Gly	Arg	Lys	Cys	Cys	Ala	Leu	Ala	Asn	Leu	Ala	Asp	Met	Leu	Thr	Val
	50					55					60				
Phe	Ala	Leu	Thr	Glu	Asp	Pro	Gln	Glu	Val	Ser	Ala	Thr	Val	Tyr	
65					70				75					80	
Leu	Asp	Lys	Leu	Ala	Thr	Val	Ile	Ser	Val	Trp	Asn	Ser	Asp	Thr	Gln
				85					90					95	
Asn	Pro	Tyr	His	Gln	Gln	Ala	Leu	Ala	Glu	Lys	Val	Lys	Glu	Ala	Glu
			100						105				110		
Arg	Asp	Val	Ser	Leu	Thr	Ser	Leu	Ala	Lys	Leu	Pro	Ser	Glu	Thr	Ile
		115						120					125		
Phe	Val	Gly	Cys	Glu	Phe	Leu	His	His	Leu	Leu	Arg	Glu	Trp	Gly	Glu
	130					135					140				
Glu	Leu	Gln	Ala	Val	Leu	Arg	Ser	Ser	Gln	Gly	Thr	Ser	Tyr	Asp	Ser
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Tyr	Arg	Leu	Cys	Asp	Ser	Leu	Thr	Ser	Phe	Ser	Gln	Asn	Ala	Thr	Leu
				165					170					175	
Tyr	Leu	Asn	Arg	Thr	Ser	Leu	Ser	Lys	Glu	Asp	Arg	Gln	Val	Val	Ser
			180						185				190		
Glu	Leu	Ala	Glu	Cys	Val	Arg	Asp	Phe	Leu	Arg	Lys	Thr	Ser	Thr	Val
		195					200					205			
Leu	Lys	Asn	Arg	Ala	Leu	Glu	Asp	Ile	Thr	Ala	Ser	Ile	Ala	Met	Ala
	210					215					220				
Val	Ile	Gln	Gln	Lys	Met	Asp	Arg	His	Met	Glu	Val	Cys	Tyr	Ile	Phe
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Ala	Ser	Glu	Lys	Lys	Trp	Ala	Phe	Ser	Asp	Glu	Trp	Val	Ala	Cys	Leu
				245					250					255	
Gly	Ser	Asn	Arg	Ala	Leu	Phe	Arg	Glu	Pro	Asp	Leu	Val	Leu	Arg	Leu
			260					265					270		
Leu	Glu	Thr	Val	Ile	Asp	Val	Ser	Thr	Ala	Asp	Arg	Ala	Ile	Pro	Glu
		275						280				285			
Ser	Gln	Ile	Arg	Gln	Val	Ile	His	Leu	Ile	Leu	Glu	Cys	Tyr	Ala	Asp
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Leu	Ser	Leu	Pro	Gly	Lys	Asn	Lys	Val	Leu	Ala	Gly	Ile	Leu	Arg	Ser
305					310					315					320
Trp	Gly	Arg	Lys	Gly	Leu	Ser	Glu	Lys	Leu	Leu	Ala	Tyr	Val	Glu	Gly
				325					330					335	
Phe	Gln	Glu	Asp	Leu	Asn	Thr	Thr	Phe	Asn	Gln	Leu	Thr	Gln	Ser	Ala
			340					345					350		
Ser	Glu	Gln	Gly	Leu	Ala	Lys	Ala	Val	Ala	Ser	Val	Ala	Arg	Leu	Val
		355					360					365			
Ile	Val	His	Pro	Glu	Val	Thr	Val	Lys	Lys	Met	Cys	Ser	Leu	Ala	Val

370	375	380																	
Val	Asn	Leu	Gly	Thr	His	Lys	Phe	Leu	Ala	Gln	Ile	Leu	Thr	Ala	Phe				
385					390					395					400				
Pro	Ala	Leu	Arg	Phe	Val	Glu	Val	Gln	Gly	Pro	Asn	Ser	Ser	Ala	Thr				
				405					410						415				
Phe	Met	Val	Ser	Cys	Leu	Lys	Glu	Thr	Val	Trp	Met	Lys	Phe	Ser	Thr				
			420					425					430						
Pro	Lys	Glu	Glu	Lys	Gln	Phe	Leu	Glu	Leu	Leu	Asn	Cys	Leu	Met	Ser				
	435					440					445								
Pro	Val	Lys	Pro	Gln	Gly	Ile	Pro	Val	Ala	Ala	Leu	Leu	Glu	Pro	Asp				
	450				455						460								
Glu	Val	Leu	Lys	Glu	Phe	Val	Leu	Pro	Phe	Leu	Arg	Leu	Asp	Val	Glu				
465					470					475					480				
Glu	Val	Asp	Leu	Ser	Leu	Arg	Ile	Phe	Ile	Gln	Thr	Leu	Glu	Ala	Asn				
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Ala	Cys	Arg	Glu	Glu	Tyr	Trp	Leu	Gln	Thr	Cys	Ser	Pro	Phe	Pro	Leu				
			500					505					510						
Leu	Phe	Ser	Leu	Cys	Gln	Leu	Leu	Asp	Arg	Phe	Ser	Lys	Tyr	Trp	Gln				
	515					520					525								
Leu	Pro	Lys	Glu	Lys	Arg	Cys	Leu	Ser	Leu	Asp	Arg	Lys	Asp	Leu	Ala				
	530				535					540									
Ile	His	Ile	Leu	Glu	Leu	Leu	Cys	Glu	Ile	Val	Ser	Ala	Asn	Ala	Glu				
545				550					555						560				
Thr	Phe	Ser	Pro	Asp	Val	Trp	Ile	Lys	Ser	Leu	Ser	Trp	Leu	His	Arg				
			565					570					575						
Lys	Leu	Glu	Gln	Leu	Asp	Trp	Thr	Val	Gly	Leu	Arg	Leu	Lys	Ser	Phe				
			580					585					590						
Phe	Glu	Gly	His	Phe	Lys	Cys	Glu	Val	Pro	Ala	Thr	Leu	Phe	Glu	Ile				
	595					600					605								
Cys	Lys	Leu	Ser	Glu	Asp	Glu	Trp	Thr	Ser	Gln	Ala	His	Pro	Gly	Tyr				
	610				615					620									
Gly	Ala	Gly	Thr	Gly	Leu	Leu	Ala	Trp	Met	Glu	Cys	Cys	Cys	Val	Ser				
625				630					635						640				
Ser	Gly	Ile	Ser	Glu	Arg	Met	Leu	Ser	Leu	Leu	Val	Val	Asp	Val	Gly				
			645					650					655						
Asn	Pro	Glu	Glu	Val	Arg	Leu	Phe	Ser	Lys	Gly	Phe	Leu	Val	Ala	Leu				
		660				665					670								
Val	Gln	Val	Met	Pro	Trp	Cys	Ser	Pro	Gln	Glu	Trp	Gln	Arg	Leu	His				
	675				680					685									
Gln	Leu	Thr	Arg	Arg	Leu	Leu	Glu	Lys	Gln	Leu	Leu	His	Val	Pro	Tyr				
	690				695				700										
Ser	Leu	Glu	Tyr	Ile	Gln	Phe	Val	Pro	Leu	Leu	Asn	Leu	Lys	Pro	Phe				
705				710					715						720				
Ala	Gln	Glu	Leu	Gln	Leu	Ser	Val	Leu	Phe	Leu	Arg	Thr	Phe	Gln	Phe				
			725					730					735						
Leu	Cys	Ser	His	Ser	Cys	Arg	Asn	Trp	Leu	Pro	Leu	Glu	Gly	Trp	Asn				
		740				745				750									
His	Val	Val	Lys	Leu	Leu	Cys	Gly	Ser	Leu	Thr	Arg	Leu	Leu	Asp	Ser				
	755					760				765									
Val	Arg	Ala	Ile	Gln	Ala	Ala	Gly	Pro	Trp	Val	Gln	Gly	Pro	Glu	Gln				
	770				775				780										
Asp	Leu	Thr	Gln	Glu	Ala	Leu	Phe	Val	Tyr	Thr	Gln	Val	Phe	Cys	His				
785				790					795					800					
Ala	Leu	His	Ile	Met	Ala	Met	Leu	His	Pro	Glu	Val	Cys	Glu	Pro	Leu				

				805					810					815			
Tyr	Val	Leu	Ala	Leu	Glu	Thr	Leu	Thr	Cys	Tyr	Glu	Thr	Leu	Ser	Lys		
			820						825					830			
Thr	Asn	Pro	Ser	Val	Ser	Ser	Leu	Leu	Gln	Arg	Ala	His	Glu	Gln	Cys		
		835					840					845					
Phe	Leu	Lys	Ser	Ile	Ala	Glu	Gly	Ile	Gly	Pro	Glu	Glu	Arg	Arg	Gln		
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Thr	Leu	Leu	Gln	Lys	Met	Ser	Ser	Phe									
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<210> 989

<211> 402

<212> DNA

<213> Homo sapiens

<400> 989

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240
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300
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<210> 990

<211> 134

<212> PRT

<213> Homo sapiens

<400> 990

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Cys	Pro	Pro	Gly	Asp	Thr	Pro	Val	Asp	Val	Leu	Ser	Gly	Gly	Glu	Arg		
			20					25					30				
Arg	Arg	Val	Ala	Leu	Cys	Lys	Leu	Leu	Ile	Glu	Gln	Pro	Asp	Leu	Leu		
		35					40					45					
Leu	Leu	Asp	Glu	Pro	Thr	Asn	His	Leu	Asp	Ala	Glu	Ser	Val	Asn	Trp		
	50					55					60						
Leu	Glu	Gly	His	Leu	Lys	Ser	Tyr	Pro	Gly	Ala	Val	Leu	Ala	Val	Thr		
65					70					75					80		
His	Asp	Arg	Tyr	Phe	Leu	Asp	His	Val	Ala	Glu	Trp	Ile	Cys	Glu	Val		
				85					90					95			
Asp	Arg	Gly	Gln	Leu	His	Pro	Tyr	Glu	Gly	Asn	Tyr	Ser	Thr	Tyr	Leu		
		100						105					110				
Asp	Thr	Lys	Arg	Lys	Arg	Leu	Gln	Ile	Glu	Gly	Lys	Lys	Asp	Ala	Lys		
		115					120						125				
Arg	Ala	Lys	Ile	Leu	Glu												

130

<210> 991
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 991
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 180
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 240
 tggattgaag ttgtagaagc taacttttct tgcgggacag gtgaatctat tgaatttcac
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<210> 992
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 992
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 20 25 30
 Lys Ser Ala Phe Leu Pro Leu Ile Ala Gln Phe Leu Gly Val Asp Gly
 35 40 45
 Tyr Trp Leu Thr Thr Gly Asn Thr Glu Asp Ser Phe Arg Glu Ser Asp
 50 55 60
 Val Phe Ser Pro Thr Val Val Ser Ala Glu Ser Thr Asp Gln Tyr Val
 65 70 75 80
 Trp Ile Glu Val Val Glu Ala Asn Phe Ser Cys Gly Thr Gly Glu Ser
 85 90 95
 Ile Glu Phe His Phe Asp Ala Ile Asn Gly Lys Ile Pro Phe Pro Ala
 100 105 110
 Ser Phe Phe Lys Glu Lys Arg
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<210> 993
 <211> 450
 <212> DNA
 <213> Homo sapiens

<400> 993
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 120

atgcgctcgct ttggcgccacg aggtttacgc cgtggggagt tcataaggga aataccagca
 180
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 240
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 300
 ccgaacgaac tgtttgccac gtggtttaaa gaagccgttg agaacgaagt cggcgaccct
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 420
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 450

<210> 994
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 994
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 20 25 30
 Tyr Leu Ser Gln Asp Tyr Ile Gly Glu Leu Pro Lys Gln His Ile Ser
 35 40 45
 Leu Gly Lys Phe Asp Pro Asp Asn Ile Pro Ala Asp Pro Asn Glu Leu
 50 55 60
 Phe Ala Thr Trp Phe Lys Glu Ala Val Glu Asn Glu Val Gly Asp Pro
 65 70 75 80
 Thr Ala Val Thr Val Ala Thr Val Asp Asp Asn Gly Gln Pro Asp Ala
 85 90 95
 Arg Val Val Asp Leu Leu Tyr Leu Asn Ser Asp Gly Phe His
 100 105 110

<210> 995
 <211> 924
 <212> DNA
 <213> Homo sapiens

<400> 995
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 aactacgaca tgctcatcgg cgtcaaccag ggagagggcc tcaagttcgt ggaggactct
 180
 gcagagagcg aggacggtgt gtctgccagc gcctttgact tcaactgtctc caactttgtg
 240
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 420

cagtctcccg tctactttta caccttctac caccactgcc aggcggaggg ccggcctgag
 480
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 660
 accaagttca tccacaccaa gcccaatcgc ttcgaggagg tgggtgtggag caaattcaac
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<210> 996

<211> 308

<212> PRT

<213> Homo sapiens

<400> 996

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Phe	Gly	Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile
		20						25					30		
Leu	Met	Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val
		35					40					45			
Asn	Gln	Gly	Glu	Gly	Leu	Lys	Phe	Val	Glu	Asp	Ser	Ala	Glu	Ser	Glu
		50				55					60				
Asp	Gly	Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val
65				70					75					80	
Asp	Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Val	Leu	Arg	Glu	Thr
			85					90						95	
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met
		100					105					110			
Arg	Arg	Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala
		115				120						125			
Pro	Ala	Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val
		130				135					140				
Tyr	Phe	Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu
145				150					155					160	
Trp	Ala	Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val
			165					170						175	
Pro	Met	Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn
		180					185					190			
Asp	Val	Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala
		195				200						205			
Lys	Thr	Gly	Asp	Pro	Asn	Gln	Pro	Val	Pro	Gln	Asp	Thr	Lys	Phe	Ile
	210				215						220				
His	Thr	Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn


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225          230          235          240
Ser Lys Glu Lys Gln Tyr Leu His Ile Gly Leu Lys Pro Arg Val Arg
          245          250          255
Asp Asn Tyr Arg Ala Asn Lys Val Ala Phe Trp Leu Glu Leu Val Pro
          260          265          270
His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg Leu
          275          280          285
Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala Pro
          290          295          300
Gly Thr Arg Arg
305

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<210> 997
 <211> 320
 <212> DNA
 <213> Homo sapiens

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<400> 997
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120
gccttggtctt tggtcggtgc ctttgccgct attatgtacg gtctcattct acttgattct
180
acctgggttag ccttactcgg tatcgatgta cgagggtggtg ccatcgaata ttgggcgaag
240
atgttcaaaa taggtattgg tactgaagag cttcggttacc ctatctttat gcaagatatg
300
tttgatttgc gccacgcgt
320

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<210> 998
 <211> 106
 <212> PRT
 <213> Homo sapiens

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<400> 998
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20          25          30
Ala Val Pro Lys Arg Val Ser Arg Ala Leu Ser Leu Phe Gly Ala Phe
35          40          45
Ala Ala Ile Met Tyr Gly Leu Ile Leu Leu Asp Ser Thr Trp Leu Ala
50          55          60
Leu Leu Gly Ile Asp Val Arg Gly Gly Ala Ile Glu Tyr Trp Ala Lys
65          70          75          80
Met Phe Lys Ile Gly Ile Gly Thr Glu Glu Leu Arg Tyr Pro Ile Phe
85          90          95
Met Gln Asp Met Phe Asp Leu Arg Pro Arg
100          105

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<210> 999
 <211> 401

<212> DNA

<213> Homo sapiens

<400> 999

acgcgttcag gcggttaaca atcgcgctaa gaagctgacc aaggaaaatg tcggcatggg
60
acatctgagc aagagcttca tcggtgttta tctctactca gaaggcaagt ttgtgaccag
120
caactatctc aatcgtggct acaaggacat tctgagctat gcagacgatg ctagtctttt
180
gcaaaagcct ccagcagtgg cttcagatga tctggataca ggtctcttga agagggcctt
240
ggatgagtgg gtggctgatg ctaagaacca cattctcaat actgaaaact tcttttagcgg
300
gtcaaccggg ctcaacattg acagtttcta cgtctttggg gaccaagaca tctgctggca
360
gttggcagct attctgaagc agagcatgaa tcgggaattg t
401

<210> 1000

<211> 115

<212> PRT

<213> Homo sapiens

<400> 1000

Met	Val	His	Leu	Ser	Lys	Ser	Phe	Ile	Gly	Val	Tyr	Leu	Tyr	Ser	Glu
1				5					10					15	
Gly	Lys	Phe	Val	Thr	Ser	Asn	Tyr	Leu	Asn	Arg	Gly	Tyr	Lys	Asp	Ile
			20					25					30		
Leu	Ser	Tyr	Ala	Asp	Asp	Ala	Ser	Leu	Leu	Gln	Lys	Pro	Pro	Ala	Val
		35					40					45			
Ala	Ser	Asp	Asp	Leu	Asp	Thr	Gly	Leu	Leu	Lys	Arg	Ala	Leu	Asp	Glu
	50					55					60				
Trp	Val	Ala	Asp	Ala	Lys	Asn	His	Ile	Leu	Asn	Thr	Glu	Asn	Phe	Phe
65					70					75				80	
Ser	Gly	Ser	Thr	Gly	Leu	Asn	Ile	Asp	Ser	Phe	Tyr	Val	Phe	Gly	Asp
			85					90						95	
Gln	Asp	Ile	Cys	Trp	Gln	Leu	Ala	Ala	Ile	Leu	Lys	Gln	Ser	Met	Asn
			100					105						110	
Arg	Glu	Leu													
			115												

<210> 1001

<211> 351

<212> DNA

<213> Homo sapiens

<400> 1001

cgcgggtattg caatgcgcct ggtgccgaat gctaaacctg ctcttgattg cccgggtactg
60
ttcccttatg ccctaatgc ggtgattggt ggcttcttgg ccactaccgt tggttcaatt
120
atcgggtatga ttgtcttccc gctgtttggg ctggcgatga tccttcggg tctgctaact
180

aacttcttcg ctggtggtgc cgctggagtc tttggcaacg cgatgggagg acgtaaaggg
 240
 gcaattattg gcggcgtagt gcacgggctg tttatcaccc tggaccagc gatgctaac
 300
 cccttactgg aaaccttcgg cttcaaaggg gtcaccttca gtgattccga t
 351

<210> 1002
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1002
 Arg Gly Ile Ala Met Arg Leu Val Pro Asn Ala Lys Pro Ala Leu Asp
 1 5 10 15
 Cys Pro Val Leu Phe Pro Tyr Ala Pro Asn Ala Val Ile Val Gly Phe
 20 25 30
 Leu Ala Thr Thr Val Gly Ser Ile Ile Gly Met Ile Val Phe Pro Leu
 35 40 45
 Phe Gly Leu Ala Met Ile Leu Pro Gly Leu Leu Thr Asn Phe Phe Ala
 50 55 60
 Gly Gly Ala Ala Gly Val Phe Gly Asn Ala Met Gly Gly Arg Lys Gly
 65 70 75 80
 Ala Ile Ile Gly Gly Val Val His Gly Leu Phe Ile Thr Leu Leu Pro
 85 90 95
 Ala Met Leu Ile Pro Leu Leu Glu Thr Phe Gly Phe Lys Gly Val Thr
 100 105 110
 Phe Ser Asp Ser Asp
 115

<210> 1003
 <211> 444
 <212> DNA
 <213> Homo sapiens

<400> 1003
 acgcgtcctc ctttagtcga tcgcgaatat gataggcgaa gcgacgtgat ggtgtgacgc
 60
 acgagcactg ccccatctcc taggcttagg gttatgcaga ctcccatcga cgctacctcc
 120
 acccccgcacat ggggcacact ctccggccta aagtcgccgct tcgctgacgg gccacataaa
 180
 ctgcgccggtt tgttcgacgc cgaccctcac cgcgctgagc gctacacctt tgacgtcgcg
 240
 gatttgcacg tcgatttatc gaagaacctc cttaccgacg agattcgtga cgctctcctc
 300
 gaactggctg cgcagatgcg cgtcaccgag cgtcgtgacg cgatgtatgc cggtgagcac
 360
 atcaacgtca ccgaggaccg cgccgtcctc cataccgcgc tgtgtcgtcc ccgcactgac
 420
 gagctgcatg ttgacgggtca ggat
 444

<210> 1004

<211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1004

```

Met Gln Thr Pro Ile Asp Ala Thr Ser Thr Pro Ala Trp Gly Thr Leu
 1           5           10           15
Ser Gly Leu Lys Ser Arg Phe Ala Asp Gly Pro His Lys Leu Arg Arg
      20           25           30
Leu Phe Asp Ala Asp Pro His Arg Ala Glu Arg Tyr Thr Phe Asp Val
      35           40           45
Ala Asp Leu His Val Asp Leu Ser Lys Asn Leu Leu Thr Asp Glu Ile
      50           55           60
Arg Asp Ala Leu Leu Glu Leu Ala Ala Gln Met Arg Val Thr Glu Arg
      65           70           75           80
Arg Asp Ala Met Tyr Ala Gly Glu His Ile Asn Val Thr Glu Asp Arg
      85           90           95
Ala Val Leu His Thr Ala Leu Cys Arg Pro Arg Thr Asp Glu Leu His
      100           105           110
Val Asp Gly Gln Asp
      115

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<210> 1005
 <211> 299
 <212> DNA
 <213> Homo sapiens

<400> 1005

```

ccatggccat tcctctggtg actgcatcca gtccgatgga tttaaaccac cccaatgtgc
60
tggtgactcc caagtttaca cctccagcca gggcttctct cctggggttg cataccacc
120
tatctatctg ccttagccac tcgtgtctga cgagcacctc acacctccag aggctcctca
180
tttcttccca tgctgcttc tcccacactc ctccctctca catgagggca acttcacct
240
cccagttgct caggcccca acctccatca gttttgactc ttctctcgca cactactcg
299

```

<210> 1006
 <211> 99
 <212> PRT
 <213> Homo sapiens

<400> 1006

```

Met Ala Ile Pro Leu Val Thr Ala Ser Ser Pro Met Asp Leu Asn Thr
 1           5           10           15
Pro Asn Val Leu Val Thr Pro Lys Phe Thr Pro Pro Ala Arg Ala Ser
      20           25           30
Leu Leu Gly Leu His Thr His Leu Ser Ile Cys Leu Ser His Ser Cys
      35           40           45
Leu Thr Ser Thr Ser His Leu Gln Arg Leu Leu Ile Ser Ser His Ala
      50           55           60
Cys Phe Ser His Thr Pro Pro Ser His Met Arg Ala Thr Ser Ser Ser

```

Gln Leu Leu Arg Pro Gln Thr Ser Ile Ser Phe Asp Ser Ser Leu Ala
85 90 95

His Tyr Ser

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<210> 1007
<211> 389
<212> DNA
<213> Homo sapiens
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<400> 1007
gccggcgcgca agatctaaag agctggaaag gcaaccgcaa gagagcgggg ttcttgcttg
60
atgagcgcgcg tttcatggac tccatcttctg gcccgggggcc tgggtgtgacg gtctctgaaa
120
tcaacgacgcg caccgaggca cccagaggtg tgacgttgag tgatggccga cgacagggca
180
acgccgggagc aatcggtgac ttcttcgcat cgaaggacta caagccgtcc gcggcgagcc
240
tccgaggtcc ggcgagggat ccgaaatgga tcgacgttca acgctcattc cacgagaacg
300
aagaaggccc gtacagctgg tacacctggc gcgggcaggc ttttgacacg ggcgctggat
360
ggcgtaaata cgtccatgcc gcgacaacg
389

```

```
<210> 1008
<211> 105
<212> PRT
<213> Homo sapiens
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<400> 1008															
Met	Asp	Ser	Ile	Phe	Gly	Pro	Gly	Pro	Gly	Val	Thr	Val	Ser	Glu	Ile.
1				5					10					15	
Asn	Asp	Ala	Thr	Glu	Ala	Pro	Arg	Gly	Val	Thr	Leu	Ser	Asp	Gly	Arg
			20					25					30		
Arg	Gln	Gly	Asn	Ala	Gly	Ala	Ile	Gly	Asp	Phe	Phe	Ala	Ser	Lys	Asp
		35					40					45			
Tyr	Lys	Pro	Ser	Ala	Ala	Ser	Leu	Arg	Gly	Pro	Ala	Arg	Asp	Pro	Lys
	50					55					60				
Trp	Ile	Asp	Val	Gln	Arg	Ser	Phe	His	Glu	Asn	Glu	Glu	Gly	Pro	Tyr
65				70					75					80	
Ser	Trp	Tyr	Thr	Trp	Arg	Gly	Gln	Ala	Phe	Asp	Thr	Gly	Ala	Gly	Trp
			85						90					95	
Arg	Lys	Tyr	Val	His	Ala	Ala	Thr	Thr							
			100					105							

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<210> 1009
<211> 324
<212> DNA
<213> Homo sapiens
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<400> 1009

ngccttcacg gctgntatgc ctggcctcat ccccatccct ggcacccgtg acgatagcca
 60
 cattccactg gtgtttcccc aggaaagcca accctacctg catctcagca gagcttccac
 120
 ggagttggaa ccccgctccg agaggggtgtg ggctcagggg ccaggggtca cacaaactcc
 180
 agaaggagga cgtagttggt ttgcaaggct gtcctttgcc ctggttgaat aaccttcggt
 240
 ctgccccgag aggaacgtgg gcattagget gcacccgcag gaagccatgt attttctgag
 300
 aaacttgccc catggtgcag atct
 324

<210> 1010
 <211> 104
 <212> PRT
 <213> Homo sapiens

<400> 1010
 Met Gly Gln Val Ser Gln Lys Ile His Gly Phe Leu Arg Val Gln Pro
 1 5 10 15
 Asn Ala His Val Pro Leu Gly Ala Asp Arg Arg Leu Phe Asn Gln Gly
 20 25 30
 Lys Gly Gln Pro Cys Lys Pro Thr Thr Ser Ser Phe Trp Ser Leu Cys
 35 40 45
 Asp Pro Trp Pro Leu Ser Pro His Pro Leu Gly Ala Gly Phe Gln Leu
 50 55 60
 Arg Gly Ser Ser Ala Glu Met Gln Val Gly Leu Ala Phe Leu Gly Lys
 65 70 75 80
 His Gln Trp Asn Val Ala Ile Val Thr Gly Ala Arg Asp Gly Asp Glu
 85 90 95
 Ala Arg His Xaa Ser His Glu Gly
 100

<210> 1011
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1011
 ctgcagaaaa ggaggggggtt cccatgccaa ggcagaactg tctgggacag acgctgcccc
 60
 gatccctgcg gctgcctgca ctctggacca cgagctctga gagcagcagg ttgagggccg
 120
 gtgggcagca gctcggaggc tccgcgaggt gcaggagacg caggcatggc cggtagagctg
 180
 actcctgagg aggaggccca gtacaaaaag gctttctccg cggttgacac ggatggaaac
 240
 ggcaccatca atgcccagga gctgggcgcg gcgctgaagg ccacgggcaa gaacctctcg
 300
 gaggcccagc taaagaaact catctccgag
 330

<210> 1012

<211> 55
 <212> PRT
 <213> Homo sapiens

<400> 1012
 Met Ala Gly Glu Leu Thr Pro Glu Glu Glu Ala Gln Tyr Lys Lys Ala
 1 5 10 15
 Phe Ser Ala Val Asp Thr Asp Gly Asn Gly Thr Ile Asn Ala Gln Glu
 20 25 30
 Leu Gly Ala Ala Leu Lys Ala Thr Gly Lys Asn Leu Ser Glu Ala Gln
 35 40 45
 Leu Lys Lys Leu Ile Ser Glu
 50 55

<210> 1013
 <211> 432
 <212> DNA
 <213> Homo sapiens

<400> 1013
 nacttgacaca tcgtggtggc gtcgctgcgt gcggcactga caatgtgact ggcgcatctcg
 60
 tggcggcgctc tcctcgtcgc cgggagcggc gaggaaggat taacgatgac cagcgacgctc
 120
 cccgggattg gctcgaacgc cgccactttg gcgcgttccc aggetcgcag tgacaaggctc
 180
 gaggctgatt tggcgggtcca tcccgacaag tggcgcattc tggggggggga ccgtcctact
 240
 ggcagcctgc acatcgggtca ctacttcggg tcgctggcga atcgggtacg cgtgcagaac
 300
 aagggcattg agtctttcct tgtcgtcgt gactaccagg ttatctatga ccgcgggggg
 360
 ggtggtgacc tgcaggccaa tgttatgtcg aatgtcgccg attacctggc aatcggcatt
 420
 gacccaacgc gt
 432

<210> 1014
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1014
 Met Thr Ser Asp Val Pro Gly Ile Gly Ser Asn Ala Ala Thr Leu Ala
 1 5 10 15
 Arg Ser Gln Ala Arg Ser Asp Lys Val Glu Ala Asp Leu Ala Val His
 20 25 30
 Pro Asp Lys Trp Arg Ile Leu Gly Gly Asp Arg Pro Thr Gly Ser Leu
 35 40 45
 His Ile Gly His Tyr Phe Gly Ser Leu Ala Asn Arg Val Arg Val Gln
 50 55 60
 Asn Lys Gly Ile Glu Ser Phe Leu Val Val Ala Asp Tyr Gln Val Ile
 65 70 75 80
 Tyr Asp Arg Gly Gly Gly Gly Asp Leu Gln Ala Asn Val Met Ser Asn

85 90 95
 Val Ala Asp Tyr Leu Ala Ile Gly Ile Asp Pro Thr Arg
 100 105

<210> 1015

<211> 467

<212> DNA

<213> Homo sapiens

<400> 1015

nngaattcga tggctgtgaa aggtcgagct cttaagtgtt ttcatatccc ctgtgtgggt
 60
 gaaaacttcc cgatgaaagc gcgcacgggt gaagagctga aagaattgga aagagtttta
 120
 cagcaaaaga agattgaagc agagtgtcctt aaactacgga aggaaattgt agaggctcag
 180
 tctggagtta agttgattaa acagcgtcat gaagaggatg atgaagaaga ggaagaggaa
 240
 gacaagacag taaaatatag caatttgccc aattacctgc ttggtagtct gagtactgat
 300
 tttggggtag atacctcttt attgtcaagc caattggagc ttcattccag agaagagaaa
 360
 atcaacccaaa ttatattatt gaaagatata atttacaagg taaaaactgt tttcaataat
 420
 gagtttgacg ctgcatataa acaaaaagag tttgaaattg cacgcgt
 467

<210> 1016

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1016

Xaa Asn Ser Met Ala Val Lys Gly Arg Ala Leu Lys Cys Phe His Ile
 1 5 10 15
 Pro Cys Val Val Glu Asn Phe Pro Met Lys Ala Arg Thr Val Glu Glu
 20 25 30
 Leu Lys Glu Leu Glu Arg Val Leu Gln Gln Lys Lys Ile Glu Ala Glu
 35 40 45
 Cys Leu Lys Leu Arg Lys Glu Ile Val Glu Ala Gln Ser Gly Val Lys
 50 55 60
 Leu Ile Lys Gln Arg His Glu Glu Asp Asp Glu Glu Glu Glu Glu Glu
 65 70 75 80
 Asp Lys Thr Val Lys Tyr Ser Asn Leu Pro Asn Tyr Leu Leu Gly Ser
 85 90 95
 Leu Ser Thr Asp Phe Gly Val Asp Thr Ser Leu Leu Ser Ser Gln Leu
 100 105 110
 Glu Leu His Ser Arg Glu Glu Lys Ile Asn Gln Ile Ile Leu Leu Lys
 115 120 125
 Asp Ile Ile Tyr Lys Val Lys Thr Val Phe Asn Asn Glu Phe Asp Ala
 130 135 140
 Ala Tyr Lys Gln Lys Glu Phe Glu Ile Ala Arg
 145 150 155

<210> 1017
 <211> 335
 <212> DNA
 <213> Homo sapiens

<400> 1017
 acgcgtggct gggtgggtat gtggaacat gtgcgcgcta atgagaagga tgcgaagggg
 60
 aacattaaag tgggtcgccc cggctacttt gcggagggtca tggatttcta tgcgcattat
 120
 ctgaaggggtg cggttaccgc tttccgtccg aattttattg tgcaggataa tacggggccgt
 180
 tggcgtgttc agtcgtcgtg gccgcagccg aatcgcactg ttacttttgc gggaccccg
 240
 ggcattgtcc gctacggtac gacgttggcg gcccgcacgc atgggaatgg tcaggctatt
 300
 ccgcaggcgg atgcacagtc tcttaaccgc gagaa
 335

<210> 1018
 <211> 105
 <212> PRT
 <213> Homo sapiens

<400> 1018
 Met Trp Asn His Val Arg Ala Asn Glu Lys Asp Ala Lys Gly Asn Ile
 1 5 10 15
 Lys Val Gly Arg Pro Gly Tyr Phe Ala Glu Val Met Asp Phe Tyr Ala
 20 25 30
 His Tyr Leu Lys Gly Ala Val Thr Arg Phe Arg Pro Asn Phe Ile Val
 35 40 45
 Gln Asp Asn Thr Gly Arg Trp Arg Val Gln Ser Ser Trp Pro Gln Pro
 50 55 60
 Asn Arg Thr Val Thr Phe Ala Gly Pro Arg Gly Ile Val Arg Tyr Gly
 65 70 75 80
 Thr Thr Leu Ala Ala Arg Thr His Gly Asn Gly Gln Ala Ile Pro Gln
 85 90 95
 Ala Asp Ala Gln Ser Leu Asn Arg Glu
 100 105

<210> 1019
 <211> 454
 <212> DNA
 <213> Homo sapiens

<400> 1019
 acgcgtgaag gggtagtcgt agtagaagtc gtccacaaac acggggccccg gcagggtccag
 60
 ctctggagcc tcctcctcaa tggcgttgcc catggtgcct ggcttgggtg atgaggcggg
 120
 tgaagggcgt ggggccaggt ggtgcgggat gaagtcagcc tcgttgaaga gctcgtggct
 180
 ggaggagccg ctgcctgagc cttcagggcc cagtgtgccc agggggccacc gacagagtgg
 240

cagagagcag gtgacttcct ggcactgcgg agcgaggacc cggagaagta cttcctcaat
 300
 ggtggctgga ccatccagtg gaacggggac taccaggtgg cagggaccac cttcacatac
 360
 gcacgcaggg gcaactggga gaacctcacg tccccgggtc ccaccaagga gcctgtctgg
 420
 atccagctgc tgttccagga gagcaaccct gggg
 454

<210> 1020

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1020

Met	Ala	Leu	Pro	Met	Val	Pro	Gly	Leu	Gly	Asp	Glu	Ala	Gly	Glu	Gly
1				5				10						15	
Arg	Gly	Ala	Arg	Trp	Cys	Gly	Met	Lys	Ser	Ala	Ser	Leu	Lys	Ser	Ser
			20					25					30		
Trp	Leu	Glu	Glu	Pro	Leu	Pro	Glu	Pro	Ser	Gly	Pro	Ser	Val	Pro	Arg
		35					40					45			
Gly	His	Arg	Gln	Ser	Gly	Arg	Glu	Gln	Val	Thr	Ser	Trp	His	Cys	Gly
	50					55					60				
Ala	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Ser	Met	Val	Ala	Gly	Pro	Ser	Ser
65					70					75				80	
Gly	Thr	Gly	Thr	Thr	Arg	Trp	Gln	Gly	Pro	Pro	Ser	His	Thr	His	Ala
			85					90						95	
Gly	Ala	Thr	Gly	Arg	Thr	Ser	Arg	Pro	Arg	Val	Pro	Pro	Arg	Ser	Leu
			100					105					110		
Ser	Gly	Ser	Ser	Cys	Cys	Ser	Arg	Arg	Ala	Thr	Leu	Gly			
		115					120					125			

<210> 1021

<211> 366

<212> DNA

<213> Homo sapiens

<400> 1021

cagctgtgtc gtgacctcct gtagaccaga gagaggtaga gcatgaaaaa tgctcattga
 60
 gccgagatta tctgacagga ccaaagcata taaagttgac tgaagcagga gcaaacacgc
 120
 tgggtgaggg tcaagtgtcg gggcagcagc aacaacaaac caaaaaaag ccctttgaac
 180
 tcccttaatg ttgoccaaag gttctggtag agaacaagtc acatgcctaa gaaggtcttt
 240
 taaagggcac tcttgagtt tcagcatttg gtccggggaa ttgcacaagg ctctgcttaa
 300
 atgcagagct ctttctagca tcttcatatt caaggcggaa aaactgagct tggcgaggaa
 360
 ccctgt
 366

<210> 1022

<211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1022
 Met Lys Met Leu Glu Arg Ala Leu His Leu Ser Arg Ala Leu Cys Asn
 1 5 10 15
 Ser Pro Asp Gln Met Leu Lys Leu Gln Glu Cys Pro Leu Lys Asp Leu
 20 25 30
 Leu Arg His Val Thr Cys Ser Leu Pro Glu Pro Leu Gly Asn Ile Lys
 35 40 45
 Gly Val Gln Arg Ala Phe Phe Trp Phe Val Val Ala Ala Ala Pro Ala
 50 55 60
 Leu Asp Pro Gln Pro Ala Cys Leu Leu Leu Leu Gln Ser Thr Leu Tyr
 65 70 75 80
 Ala Leu Val Leu Ser Asp Asn Leu Gly Ser Met Ser Ile Phe His Ala
 85 90 95
 Leu Pro Leu Ser Gly Leu Gln Glu Val Thr Thr Gln Leu
 100 105

<210> 1023
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1023
 gccgggcttc gggctctctga agcgatcaac ctggccgact cggatgcaga tctggacggc
 60
 ggcacacctga ccatacagca gaccaagttt ggcaagtccc gcatggtgcc gctacacccc
 120
 agcgtgatcg gtccgatggc agcctaccgg gccttgcgcc gccagtacgt gcctgcgaag
 180
 ccgcagatga cattcttcgt gggctcgcgt ggcgtgcacc ggggtgaacc gctgggagat
 240
 aggcaggtgc atcgagtgtt ctgtcagctg cgcgagcaat tgggttgat cgatcgcggc
 300
 ggccatggcc gaccgcgggt gcatgacctg cgccatagct tcgccgtgag acggatgatc
 360
 ctgtggcacc agcagggagc gaaccttgac caacgaatgc tggccctgtc cacgtacatg
 420
 ggccac
 426

<210> 1024
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 1024
 Ala Gly Leu Arg Val Ser Glu Ala Ile Asn Leu Ala Asp Ser Asp Ala
 1 5 10 15
 Asp Leu Asp Gly Gly Ile Leu Thr Ile Gln Gln Thr Lys Phe Gly Lys
 20 25 30
 Ser Arg Met Val Pro Leu His Pro Ser Val Ile Gly Pro Met Ala Ala

```

      35          40          45
Tyr Arg Ala Leu Arg Arg Gln Tyr Val Pro Ala Lys Pro Gln Met Thr
      50          55          60
Phe Phe Val Gly Ser Arg Gly Val His Arg Gly Glu Pro Leu Gly Asp
65          70          75          80
Arg Gln Val His Arg Val Phe Cys Gln Leu Arg Glu Gln Leu Gly Trp
      85          90          95
Ile Asp Arg Gly Gly His Gly Arg Pro Arg Val His Asp Leu Arg His
      100          105          110
Ser Phe Ala Val Arg Arg Met Ile Leu Trp His Gln Gln Gly Ala Asn
      115          120          125
Leu Asp Gln Arg Met Leu Ala Leu Ser Thr Tyr Met Gly His
      130          135          140

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<210> 1025
 <211> 518
 <212> DNA
 <213> Homo sapiens

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<400> 1025
nacgcgtggt gcgcgcaggt ggcgccgcgg tccctttgct ccctgcgcaa gccggagggg
60
tgcccagaag gctaccacta gcctcagcga aggggtgcgcc ctgagagccg ggtagcctcg
120
gatagcggcg ctgcgtacgc gatgatggat gagccgtggt ggggaagggcg cgtcgccctcg
180
gacgtccact gcaccctgcg cgagaaggaa ctgaagctgc ccaccttccg agcccactcc
240
ccactcctga agagccgccc gttcttcgtg gacatcctga ccctgctgag cagccactgc
300
cagctctgcc ctgcagcccg gcacctggcc gtctacctgc tggaccactt catggatcgc
360
tacaacgtca ccacctccaa gcagctctac accgtggccg tctcctgcct cctgcttgca
420
agtaagtctg aggatcggga agaccacgtc cccaagttgg agcaaataaa cagcacgagg
480
atcctgagca gccagaactt caccctcacc aagaagga
518

```

<210> 1026
 <211> 125
 <212> PRT
 <213> Homo sapiens

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<400> 1026
Met Met Asp Glu Pro Trp Trp Glu Gly Arg Val Ala Ser Asp Val His
1          5          10          15
Cys Thr Leu Arg Glu Lys Glu Leu Lys Leu Pro Thr Phe Arg Ala His
20          25          30
Ser Pro Leu Leu Lys Ser Arg Arg Phe Phe Val Asp Ile Leu Thr Leu
35          40          45
Leu Ser Ser His Cys Gln Leu Cys Pro Ala Ala Arg His Leu Ala Val
50          55          60
Tyr Leu Leu Asp His Phe Met Asp Arg Tyr Asn Val Thr Thr Ser Lys

```

```

65          70          75          80
Gln Leu Tyr Thr Val Ala Val Ser Cys Leu Leu Leu Ala Ser Lys Phe
          85          90          95
Glu Asp Arg Glu Asp His Val Pro Lys Leu Glu Gln Ile Asn Ser Thr
          100          105          110
Arg Ile Leu Ser Ser Gln Asn Phe Thr Leu Thr Lys Lys
          115          120          125

```

<210> 1027

<211> 465

<212> DNA

<213> Homo sapiens

<400> 1027

```

ggcccaaaag tcatcaaaga aaagctgaca caggagctga aggaccacaa cgccaccagc
60
atcctgcagc agctgccgct gctcaaggcc atgcgggaaa agccagccgg aggcattcct
120
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<210> 1028

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1028

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Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser Leu Val Asn Thr
          35          40          45
Xaa Pro Glu Ala His His Xaa Trp Leu Lys Val Ile Thr Ala Asn Ile
          50          55          60
Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp Gln Glu Leu Leu Val
65          70          75          80
Lys Ile Pro Leu Asp Met Val Ala Gly Phe Asn Thr Pro Leu Val Lys
          85          90          95
Thr Ile Val Glu Phe His Met Thr Thr Glu Ala Gln Ala Thr Ile Arg
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Met Asp Thr Ser Ala Ser Gly Pro Thr Arg Leu Val Leu Ser Asp Cys
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Ala Thr Ser His Gly Ser Leu Arg Ile Gln Leu Leu His Lys Leu Ser

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 Ala Asn Arg Trp Gly Lys Ser Phe Thr Gly Gly Asn Pro Leu Gly Ser
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 Pro Cys Asp Ser Cys Thr Arg Ser Ser Gly Pro Ala Arg Asp Asn Phe
 50 55 60
 Pro His Leu Val Ser Asn Asn Asn Asn Asn Tyr Thr Leu Met Ser Ser
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 <212> DNA
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 35 40 45
 Asp Pro Ala Ser Arg Ala Gln Ala Asn Asp Val His Gly Trp Ser Val
 50 55 60
 Val Val Asp Pro Leu Ala Tyr Gln Trp Arg His Pro Asn Trp Gln Gly
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 420

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 480
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 Val Ile Asp Val Gly Val Gln Ala Gly Asp Asp Thr Leu Tyr Pro Arg
 35 40 45
 Ile Gly Ile Lys Gly Ala His Val Ile Lys Asp Gly Lys Ala Asp Arg
 50 55 60
 Gly Ile Phe Phe Cys Gly Thr Gly Met Gly Met Ala Ile Thr Ala Asn
 65 70 75 80
 Lys Val Pro Gly Ile Arg Ala Cys Thr Ala His Asp Ser Phe Ser Val
 85 90 95
 Glu Arg Leu Ile Met Ser Asn Asp Ala His Val Leu Cys Leu Gly Gln
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<210> 1035
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<213> Homo sapiens

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Val Cys Val Xaa Glu Ala Val Cys Ile Cys Xaa Cys Leu Cys Ala Cys
          35          40          45
Thr Xaa Met Cys Ala Cys Met Glu Cys Ile Cys Val Cys Val Trp Thr
          50          55          60
Val Cys Val Ile Met Gln Tyr Val Arg Val Cys Val Trp Ser Val Ser
65          70          75          80
Val Trp His Val Cys Val Tyr Leu Leu Cys Val Ser Val Cys Val Xaa
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Thr Cys Ile Cys Ile Glu Ser Val Cys Ala Val Cys Met Cys Val Ser
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<210> 1037

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<212> DNA

<213> Homo sapiens

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 Ser Tyr Ser Gly Pro Gly Pro Gly Met Gly Ile Ser Ala Asn Asn Gln
 50 55 60
 Met His Gly Gln Gly Pro Ser Gln Pro Cys Gly Ala Val Pro Leu Gly
 65 70 75 80
 Arg Met Pro Ser Ala Gly Met Gln Asn Arg Pro Phe Pro Gly Asn Met
 85 90 95
 Ser Ser Met Thr Pro Ser Ser Pro Gly Met Ser Gln Gln Gly Gly Pro
 100 105 110
 Gly Met Gly Pro Pro Met Pro Thr Val Asn Arg Lys Ala Gln Glu Ala
 115 120 125
 Ala Ala Ala Val Met Gln Ala Ala Ala Asn Ser Ala Gln Ser Arg Gln
 130 135 140
 Gly Ser Phe Pro Gly Met Asn Gln Ser Gly Leu Met Ala Ser Ser Ser
 145 150 155 160
 Pro Tyr Ser Gln Pro Met Asn Asn Ser Ser Ser Leu Met Asn Thr Gln
 165 170 175
 Ala Pro Pro Tyr Ser Met Ala Pro Ala Met Val Asn Ser Ser Ala Ala
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 Ser Val Gly Leu Ala Asp Met Met Ser Pro Gly Glu Ser Lys Leu Pro
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 210 215 220
 Ser Lys Ser Lys Asp Ser Tyr Ser Ser Gln Gly Ile Ser Gln Pro Pro
 225 230 235 240
 Thr Pro Gly Asn Leu Pro Val Pro Ser Pro Met Ser Pro Ser Ser Ala
 245 250 255
 Ser Ile Ser Ser Phe His Gly Asp Glu Ser Asp Ser Ile Ser Ser Pro
 260 265 270
 Gly Trp Pro Lys Thr Pro Ser Ser Pro Lys Ser Ser Ser Ser Thr Thr
 275 280 285
 Thr Gly Glu Lys Ile Thr Lys Val Tyr Glu Leu Gly Asn Glu Pro Glu
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 Arg Lys Leu Trp Val Asp Arg Tyr Leu Thr Phe Met Glu Glu Arg Gly
 305 310 315 320
 Ser Pro Val Ser Ser Leu Pro Ala Val Gly Lys Lys Pro Leu Asp Leu

325 330 335
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 370 375 380
 Leu Phe Ala Phe Glu Cys Lys Ile Glu Arg Gly Glu Glu Pro Pro Pro
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 Ser Thr Gly Ser Asn Ser Met Ala Glu Val Pro Gly Asp Leu Lys Pro
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 Pro Thr Pro Ala Ser Thr Pro His Gly Gln Met Thr Pro Met Gln Gly
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 Asp Ser Ser Phe Pro Lys Arg Asn Ser Met Thr Pro Asn Ala Pro Tyr
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 Gln Gln Gly Met Ser Met Pro Asp Val Met Gly Arg Met Pro Tyr Glu
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 Pro Asn Lys Asp Pro Phe Gly Gly Met Arg Lys Val Pro Gly Ser Ser
 515 520 525
 Glu Pro Phe Met Thr Gln Gly Gln Met Pro Asn Ser Ser Met Gln Asp
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 Met Tyr Asn Gln Ser Pro Ser Gly Ala Met Ser Asn Leu Gly Met Gly
 545 550 555 560
 Gln Arg Gln Gln Phe Pro Tyr Gly Ala Ser Tyr Asp Arg Arg His Glu
 565 570 575
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 Pro Tyr Gly Gly His Gln Pro Gly Leu Tyr Pro Gln Gln Pro Asn Tyr
 595 600 605
 Lys Arg His Met Asp Gly Met Tyr Gly Pro Pro Ala Lys Arg His Glu
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 645 650 655
 Gly Gln Tyr Pro Tyr Pro Tyr Ser Arg Glu Arg Met Gln Gly Pro Gly
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 690 695 700
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Lys	Asp	Ile	Val	Thr	Pro	Glu	Ala	Trp	Arg	Val	Met	Met	Ser	Leu	Lys
865					870					875					880
Ser	Gly	Leu	Leu	Ala	Glu	Ser	Thr	Trp	Ala	Leu	Asp	Thr	Ile	Asn	Ile
				885					890					895	
Leu	Leu	Tyr	Asp	Asp	Ser	Thr	Val	Ala	Thr	Phe	Asn	Leu	Ser	Gln	Leu
			900					905					910		
Ser	Gly	Phe	Leu	Glu	Leu	Leu	Val	Glu	Tyr	Phe	Arg	Lys	Cys	Leu	Ile
	915						920					925			
Asp	Ile	Phe	Gly	Ile	Leu	Met	Glu	Tyr	Glu	Val	Gly	Asp	Pro	Ser	Gln
	930					935					940				
Lys	Ala	Leu	Asp	His	Asn	Ala	Ala	Arg	Lys	Asp	Asp	Ser	Gln	Ser	Leu
945					950					955					960
Ala	Asp	Asp	Ser	Gly	Lys	Glu	Glu	Glu	Asp	Ala	Glu	Cys	Ile	Asp	Asp
				965					970					975	
Asp	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Ser	Glu	Lys	Thr	Glu
			980				985					990			
Ser	Asp	Glu	Lys	Ser	Ser	Ile	Ala	Leu	Thr	Ala	Pro	Asp	Ala	Ala	Ala
	995						1000					1005			
Asp	Pro	Lys	Glu	Lys	Pro	Lys	Gln	Ala	Ser	Lys	Phe	Asp	Lys	Leu	Pro
	1010					1015					1020				
Ile	Lys	Ile	Val	Lys	Lys	Asn	Asn	Leu	Phe	Val	Val	Asp	Arg	Ser	Asp
1025					1030					1035					1040
Lys	Leu	Gly	Arg	Val	Gln	Glu	Phe	Asn	Ser	Gly	Leu	Leu	His	Trp	Gln
				1045					1050					1055	
Leu	Gly	Gly	Gly	Asp	Thr	Thr	Glu	His	Ile	Gln	Thr	His	Phe	Glu	Ser
			1060				1065						1070		
Lys	Met	Glu	Ile	Pro	Pro	Arg	Arg	Arg	Pro	Pro	Pro	Pro	Leu	Ser	Ser
	1075						1080					1085			
Ala	Gly	Lys	Lys	Lys	Glu	Leu	Ala	Gly	Lys	Gly	Asp	Ser	Glu	Glu	Gln
	1090					1095					1100				
Gln	Glu	Lys	Ser	Ile	Ile	Ala	Thr	Ile	Asp	Asp	Val	Leu	Ser	Ala	Arg
1105					1110					1115					1120
Pro	Gly	Ala	Leu	Pro	Glu	Asp	Ala	Asn	Pro	Gly	Pro	Gln	Thr	Glu	Ser
				1125					1130					1135	
Ser	Lys	Phe	Pro	Phe	Gly	Ile	Gln	Gln	Ala	Lys	Ser	His	Arg	Asn	Ile
			1140				1145					1150			
Lys	Leu	Leu	Glu	Asp	Glu	Pro	Arg	Ser	Arg	Asp	Glu	Thr	Pro	Leu	Cys
	1155						1160					1165			
Thr	Ile	Ala	His	Trp	Gln	Asp	Ser	Leu	Ala	Lys	Arg	Cys	Ile	Cys	Val
	1170					1175					1180				
Ser	Asn	Ile	Val	Arg	Ser	Leu	Ser	Phe	Val	Pro	Gly	Asn	Asp	Ala	Glu

1185 1190 1195 1200
 Met Ser Lys His Pro Gly Leu Val Leu Ile Leu Gly Lys Leu Ile Leu
 1205 1210 1215
 Leu His His Glu His Pro Glu Arg Lys Arg Ala Pro Gln Thr Tyr Glu
 1220 1225 1230
 Lys Glu Glu Asp Glu Asp Lys Gly Val Ala Cys Ser Lys Asp Glu Trp
 1235 1240 1245
 Trp Trp Asp Cys Leu Glu Val Leu Arg Asp Asn Thr Leu Val Thr Leu
 1250 1255 1260
 Ala Asn Ile Ser Gly Gln Leu Asp Leu Ser Ala Tyr Thr Glu Ser Ile
 1265 1270 1275 1280
 Cys Leu Pro Ile Leu Asp Gly Leu Leu His Trp Met Val Cys Pro Ser
 1285 1290 1295
 Ala Glu Ala Gln Asp Pro Phe Pro Thr Val Gly Pro Asn Ser Val Pro
 1300 1305 1310
 Ser Pro Gln Arg Leu Val Leu Glu Thr Leu Cys Lys Leu Ser Ile Gln
 1315 1320 1325
 Asp Asn Asn Val Asp Leu Ile Leu Ala Thr Pro Pro Phe Ser Arg Gln
 1330 1335 1340
 Glu Lys Phe Tyr Ala Thr Leu Val Arg Tyr Val Gly Asp Arg Lys Asn
 1345 1350 1355 1360
 Pro Val Cys Arg Glu Met Ser Met Ala Leu Leu Ser Asn Leu Ala Gln
 1365 1370 1375
 Gly Asp Ala Leu Ala Ala Arg Ala Ile Ala Val Gln Lys Gly Ser Ile
 1380 1385 1390
 Gly Asn Leu Ile Ser Phe Leu Glu Asp Gly Val Thr Met Ala Gln Tyr
 1395 1400 1405
 Gln Gln Ser Gln His Asn Leu Met His Met Gln Pro Pro Pro Leu Glu
 1410 1415 1420
 Pro Pro Ser Val Asp Met Met Cys Arg Ala Ala Lys Ala Leu Leu Ala
 1425 1430 1435 1440
 Met Ala Arg Val Asp Glu Asn Arg Ser Glu Phe Leu Leu His Glu Gly
 1445 1450 1455
 Arg Leu Leu Asp Ile Ser Ile Ser Ala Val Leu Asn Ser Leu Val Ala
 1460 1465 1470
 Ser Val Ile Cys Asp Val Leu Phe Gln Ile Gly Gln Leu
 1475 1480 1485

<210> 1039
 <211> 379
 <212> DNA
 <213> Homo sapiens

<400> 1039
 gcaggagcca gggatgctgc tgaacatccc gcagtgcacg agacaggcct ccaccacacg
 60
 gaattacctt ggcctgaggt gttacgagag cacagagaga aaccaggtac agacgcgggg
 120
 cagaggggag agagggagag agtgtgagag ctaaggtttc gggagaagac tttgtggaaa
 180
 aagtcttttg ctgggtcctg caacatagcc aggattcagt gacaggtgag gaccactcca
 240
 gattttgtat gtattgaagg ccctgaatac ttttttgaaa gagaatgaca tgagtacacc
 300

tggtcagcca cacgtgagag ggggtggagg aggggaagtac cagaggcagg gagaccaggt
 360
 agaaagacct cgccatagt
 379

<210> 1040
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 1040
 Met Ala Arg Ser Phe Tyr Leu Val Ser Leu Pro Leu Val Leu Pro Ser
 1 5 10 15
 Ser Asn Pro Ser His Val Trp Leu Thr Arg Cys Thr His Val Ile Leu
 20 25 30
 Phe Gln Lys Ser Ile Gln Gly Leu Gln Tyr Ile Gln Asn Leu Glu Trp
 35 40 45
 Ser Ser Pro Val Thr Glu Ser Trp Leu Cys Cys Arg Thr Gln Pro Lys
 50 55 60
 Thr Phe Ser Thr Lys Ser Ser Pro Glu Thr Leu Ala Leu Thr Leu Ser
 65 70 75 80
 Pro Ser Leu Pro Ser Ala Pro Arg Leu Tyr Leu Val Ser Leu Cys Ala
 85 90 95
 Leu Val Thr Pro Gln Ala Lys Val Ile Pro Cys Gly Gly Gly Leu Ser
 100 105 110
 Arg Ala Leu Arg Asp Val Gln Gln His Pro Trp Leu Leu
 115 120 125

<210> 1041
 <211> 388
 <212> DNA
 <213> Homo sapiens

<400> 1041
 ttagtgcccg tggaggccat cggctacatc gcgagtattg acaaggccga tatgtcaatc
 60
 gaaacggcgt acctgccgcg gctgttggtt tccctggccc tgaccatccc ggtgctcgcc
 120
 ttgtcgatga tcccggccct gcacttcccg cattggccgt tgtgggcgtt ggcgcttacc
 180
 accccgggtgg tggtctgggg tgcttgcccg ctgcaccacg ccgctgggac caacctgcgg
 240
 caggcgcgcg ccatcatgga caccctggtg tcgctcgggc tctcacttc gtacctctgg
 300
 tcggtatgga tgctgaccac aggcggcgag cacctctacc tggaggtagc cgtccaccgt
 360
 cagcagctg atcctggccg gcaaattt
 388

<210> 1042
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 1042

```

Leu Val Ala Val Glu Ala Ile Gly Tyr Ile Ala Ser Ile Asp Lys Ala
 1           5           10           15
Asp Met Ser Ile Glu Thr Ala Tyr Leu Pro Arg Leu Leu Val Ser Leu
 20           25           30
Ala Leu Thr Ile Pro Val Leu Ala Leu Ser Met Ile Pro Ala Leu His
 35           40           45
Phe Pro His Trp Pro Leu Trp Ala Leu Ala Leu Thr Thr Pro Val Val
 50           55           60
Phe Trp Gly Ala Trp Pro Leu His His Ala Ala Trp Thr Asn Leu Arg
 65           70           75           80
His Gly Ala Ala Ile Met Asp Thr Leu Val Ser Leu Gly Val Leu Thr
 85           90           95
Ser Tyr Leu Trp Ser Val Trp Met Leu Thr Thr Gly Gly Glu His Leu
 100          105          110
Tyr Leu Glu Val Ala Val His Arg His Asp Ala Asp Pro Gly Arg Gln
 115          120          125
Ile

```

<210> 1043

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1043

```

accggtgaaa ccctgatcgg ccaatcgttt tccaccgttc ccggcggcaa gggcgcaaac
 60
caggcgggtcg ctctggcgcg tcttgggggcc gaagtcgcga tggtcggttg cgtgggtacc
 120
gatgcctacg gcgcgcaatt acgcgacgca ttgttggtgg aaggcatcga ttgccaggcc
 180
gtcagcaccg tcgacggttc cagcgggtgtg gcgctgatcg tgggtggatga cagcagccag
 240
aatgcgatcg ttatcgtcgc cggtagcaat ggcgagctga ctccggccaa gttacagacc
 300
tttgacagcg tgctgcaggc tgccgacgtg attgtctgcc agcttgagac gccgatggac
 360
actgtcggcc atgcgcctaa gcgcggtcgc gaactgggca agacggtgat cctcaatccg
 420
gcgccggcca ggggcccgct gcctgaggat tggtagcccg ccatcgatta cctgattccc
 480
aacgaaagcg aagcctcggc cttgagtggc gtggtggtgg attcactgga cagcgccaag
 540
gtcgtgcta cgcgt
 555

```

<210> 1044

<211> 185

<212> PRT

<213> Homo sapiens

<400> 1044

```

Thr Gly Glu Thr Leu Ile Gly Gln Ser Phe Ser Thr Val Pro Gly Gly

```

```

      1           5           10           15
Lys Gly Ala Asn Gln Ala Val Ala Ser Ala Arg Leu Gly Ala Glu Val
      20           25           30
Ala Met Val Gly Cys Val Gly Thr Asp Ala Tyr Gly Ala Gln Leu Arg
      35           40           45
Asp Ala Leu Leu Val Glu Gly Ile Asp Cys Gln Ala Val Ser Thr Val
      50           55           60
Asp Gly Ser Ser Gly Val Ala Leu Ile Val Val Asp Asp Ser Ser Gln
      65           70           75           80
Asn Ala Ile Val Ile Val Ala Gly Ser Asn Gly Glu Leu Thr Pro Ala
      85           90           95
Lys Leu Gln Thr Phe Asp Ser Val Leu Gln Ala Ala Asp Val Ile Val
      100           105           110
Cys Gln Leu Glu Thr Pro Met Asp Thr Val Gly His Ala Pro Lys Arg
      115           120           125
Gly Arg Glu Leu Gly Lys Thr Val Ile Leu Asn Pro Ala Pro Ala Ser
      130           135           140
Gly Pro Leu Pro Glu Asp Trp Tyr Ala Ala Ile Asp Tyr Leu Ile Pro
      145           150           155           160
Asn Glu Ser Glu Ala Ser Ala Leu Ser Gly Val Val Val Asp Ser Leu
      165           170           175
Asp Ser Ala Lys Val Ala Ala Thr Arg
      180           185

```

<210> 1045

<211> 371

<212> DNA

<213> Homo sapiens

<400> 1045

```

ctattgccat actaccgccg cggcaaccta caggacatga tcaacgccaa cctcttcaat
60
cactccaaat tccccgagac gcaccttatg aatctatttc tcggcgctctg caaggccctg
120
cgcgccatgc acgattacca cgcaccgccg gcagagcgca tgccaattgg gcaccgaagg
180
cagaccacca cccaggtgca aagcaacagt ggtagagcgg tcgctcatcg acgaaacgta
240
cggaagaaga cgaagagacg gagcaggaaa gacctgttat ggaatcacag aaccacatcg
300
ggcagggcgg cgagcacaaa accatatgcg catcgcgaca ttaaaccagg tacgtgctgc
360
aagctcctcg g
371

```

<210> 1046

<211> 123

<212> PRT

<213> Homo sapiens

<400> 1046

```

Leu Leu Pro Tyr Tyr Arg Arg Gly Asn Leu Gln Asp Met Ile Asn Ala
1           5           10           15
Asn Leu Phe Asn His Ser Lys Phe Pro Glu Thr His Leu Met Asn Leu

```

	20		25		30										
Phe	Leu	Gly	Val	Cys	Lys	Ala	Leu	Arg	Ala	Met	His	Asp	Tyr	His	Ala
	35		40		45										
Pro	Pro	Ala	Glu	Arg	Met	Pro	Ile	Gly	His	Arg	Arg	Gln	Thr	Thr	Thr
	50		55		60										
Gln	Val	Gln	Ser	Asn	Ser	Gly	Arg	Ala	Val	Ala	His	Arg	Arg	Asn	Val
65			70		75									80	
Arg	Lys	Lys	Thr	Lys	Arg	Arg	Ser	Arg	Lys	Asp	Leu	Leu	Trp	Asn	His
			85		90									95	
Arg	Thr	Thr	Ser	Gly	Arg	Ala	Ala	Ser	Thr	Lys	Pro	Tyr	Ala	His	Arg
			100		105									110	
Asp	Ile	Lys	Pro	Gly	Thr	Cys	Cys	Lys	Leu	Leu					
	115				120										

<210> 1047
 <211> 754
 <212> DNA
 <213> Homo sapiens

<400> 1047
 natgcccaga aggacctgga cgaggcggtg ccagccctgg atgcggctct ggccagccta
 60
 cgcaacctca acaagaacga agtgaccag gtacgtgcca tgcagcggcc acccccgggt
 120
 gtgaaactgg tcatagaagc tgtgtgcatt atgaaaggca tcaagcccaa gaaggtgcct
 180
 ggagaaaagc caggcaccaa ggtggatgac tactgggagc ctggcaaggg gctgctgcag
 240
 gacccgggccc acttccttga gagcctcttc aagtttgaca aggacaacat tggagatgtg
 300
 gtgatcaaag ccatccagcc gtacatcgat aatgaagagt tccagccagc caccattgcc
 360
 aaggtgtcca agggttgccc cttcatttgg ccgtgggggg gggcaatgcc caagtacccc
 420
 tttgtggcca aggccgtgga gcccaagcgg caagccctgc tggaggccca ggatgacctg
 480
 ggggtgacac agaggatcct ggatgaggca aaacagcgcc ttcgtgaggt ggaggacggc
 540
 atcgccacaa tgcaggctaa gtaccgggaa tgcattacca agaaggagga gctggagctg
 600
 aagtgtgagc agtgtgagca gcggctgggc cacgctggca aggtgcgcac cctcctctg
 660
 caaggcctgc aagcggggccc ggcccagaca ggggccagaa aggaccaggg cgccggtggg
 720
 tcctgggggtg gctgtccaac cccctccctg gcaa
 754

<210> 1048
 <211> 251
 <212> PRT
 <213> Homo sapiens

<400> 1048
 Xaa Ala Gln Lys Asp Leu Asp Glu Ala Leu Pro Ala Leu Asp Ala Ala

```

1           5           10           15
Leu Ala Ser  Leu Arg Asn Leu Asn Lys Asn Glu Val Thr Gln Val Arg
20           25           30
Ala Met Gln Arg Pro Pro Pro Gly Val Lys Leu Val Ile Glu Ala Val
35           40           45
Cys Ile Met Lys Gly Ile Lys Pro Lys Lys Val Pro Gly Glu Lys Pro
50           55           60
Gly Thr Lys Val Asp Asp Tyr Trp Glu Pro Gly Lys Gly Leu Leu Gln
65           70           75           80
Asp Pro Gly His Phe Leu Glu Ser Leu Phe Lys Phe Asp Lys Asp Asn
85           90           95
Ile Gly Asp Val Val Ile Lys Ala Ile Gln Pro Tyr Ile Asp Asn Glu
100          105          110
Glu Phe Gln Pro Ala Thr Ile Ala Lys Val Ser Lys Gly Cys Pro Phe
115          120          125
Ile Trp Pro Trp Gly Gly Ala Met Pro Lys Tyr Pro Phe Val Ala Lys
130          135          140
Ala Val Glu Pro Lys Arg Gln Ala Leu Leu Glu Ala Gln Asp Asp Leu
145          150          155          160
Gly Val Thr Gln Arg Ile Leu Asp Glu Ala Lys Gln Arg Leu Arg Glu
165          170          175
Val Glu Asp Gly Ile Ala Thr Met Gln Ala Lys Tyr Arg Glu Cys Ile
180          185          190
Thr Lys Lys Glu Glu Leu Glu Leu Lys Cys Glu Gln Cys Glu Gln Arg
195          200          205
Leu Gly His Ala Gly Lys Val Arg Thr Leu Leu Leu Gln Gly Leu Gln
210          215          220
Ala Gly Pro Ala Gln Thr Gly Ala Arg Lys Asp Gln Gly Ala Gly Gly
225          230          235          240
Ser Trp Gly Gly Cys Pro Thr Pro Ser Leu Ala
245          250

```

<210> 1049

<211> 558

<212> DNA

<213> Homo sapiens

<400> 1049

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cgcagcaata gctgcacttg accagactgg gctttgcaat aagcgcatte cccgggctga
60
atgctgcaga tccttacagg ctgactgcag ggtgtttcag attctcctgg agtcacacgt
120
gccagcttga tttcaagaaa caactagaat aacagttttc tgataagaag tctatagcac
180
tttatggctt acataatcca gagatagatg ggctgggcat gattcccatt ttctgttggg
240
gaaaccgact cacagagaag ttaagggaca agtataaagt gatgaaactg tgtactgaac
300
ctcatgtctc ccagactccc ggggtccccg gctttttctc ggggcgggccc cattcacatt
360
gcaattcatg gccggggcaa atgctcacc acagagatat taagcactcc aacactccat
420
ccaccagggt gcagccaaag gattcagaag acaatgatca ttccatcagc atgcactatg
480

```

cagctaaaga aaggttttgg catgctctgc tttattgttt cacagaagat aagaaaataa

540

actgcaaagt aacttaag

558

<210> 1050

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1050

Met	Ile	Pro	Ile	Phe	Cys	Trp	Gly	Asn	Arg	Leu	Thr	Glu	Lys	Leu	Arg
1				5				10						15	
Asp	Lys	Tyr	Lys	Val	Met	Lys	Leu	Cys	Thr	Glu	Pro	His	Val	Ser	Gln
			20					25					30		
Thr	Pro	Gly	Ser	Pro	Gly	Phe	Phe	Ser	Gly	Arg	Pro	His	Ser	His	Cys
		35				40					45				
Asn	Ser	Trp	Pro	Gly	Gln	Met	Leu	Thr	His	Arg	Asp	Ile	Lys	His	Ser
	50				55					60					
Asn	Thr	Pro	Ser	Thr	Arg	Leu	Gln	Pro	Lys	Asp	Ser	Glu	Asp	Asn	Asp
65				70					75					80	
His	Ser	Ile	Ser	Met	His	Tyr	Ala	Ala	Lys	Glu	Arg	Phe	Trp	His	Ala
			85					90					95		
Leu	Leu	Tyr	Cys	Phe	Thr	Glu	Asp	Lys	Lys	Ile	Asn	Cys	Lys	Val	Thr
			100					105					110		

<210> 1051

<211> 317

<212> DNA

<213> Homo sapiens

<400> 1051

gcggttgagtc gggatgtcgc attcatgccc ggcgaacctt tttttgccga accggagcgt
60
aatccgggta atcttcgtct caatttcagt cacatcgcac cggagcgtct ggacgaaggt
120
ctcaagcgcc tggtctgtgt catccgtcac gcacaggctg cacaagcggc ttaaggggag
180
ggccatgtac aaggtttatg gcgattacca gtcgggcaat tgctacaaga tcaagctgat
240
gctgcacctg ctggggcagg aatatcgctg gcacccgggg gacatcctca aggtgacacc
300
gagaccccg aattttt
317

<210> 1052

<211> 57

<212> PRT

<213> Homo sapiens

<400> 1052

Ala	Leu	Ser	Arg	Asp	Val	Ala	Phe	Met	Pro	Gly	Glu	Pro	Phe	Phe	Ala
1				5				10					15		
Glu	Pro	Glu	Arg	Asn	Pro	Gly	Asn	Leu	Arg	Leu	Asn	Phe	Ser	His	Ile

```

                20                25                30
Ala Pro Glu Arg Leu Asp Glu Gly Leu Lys Arg Leu Ala Ala Val Ile
           35                40                45
Arg His Ala Gln Ala Ala Gln Ala Ala
      50                55

```

<210> 1053
 <211> 318
 <212> DNA
 <213> Homo sapiens

```

<400> 1053
caattggcta cgcgatccga acgggcgcat gggctctctat gactggcaag ccgtcgctcg
60
cggggagtg ggcctcgact atgcctacgc gatgtcgggtg aacctgacca ccgagaaccg
120
gcgtgcctgg gaacgcgacc tgctcgagcg ttatctgtgg cgcctcgccg aagaggggtgt
180
cgccaaccg cctcggttcg agcaagcgtg gctacgctac cggcaacagc cgttcacgt
240
cgggatcttc tcaactcttga ccatcggcgc cggacgcttt caaccggcca tgcaaccggc
300
ggactcnnnn ccccnenc
318

```

<210> 1054
 <211> 96
 <212> PRT
 <213> Homo sapiens

```

<400> 1054
Met Gly Leu Tyr Asp Trp Gln Ala Val Ala Arg Gly Glu Trp Ala Leu
1      5      10      15
Asp Tyr Ala Tyr Ala Met Ser Val Asn Leu Thr Thr Glu Asn Arg Arg
      20      25      30
Ala Trp Glu Arg Asp Leu Leu Glu Arg Tyr Leu Trp Arg Leu Ala Glu
      35      40      45
Glu Gly Val Ala Asn Pro Pro Ser Phe Glu Gln Ala Trp Leu Arg Tyr
      50      55      60
Arg Gln Gln Pro Phe His Val Gly Ile Phe Ser Leu Leu Thr Ile Gly
65      70      75      80
Ala Gly Arg Phe Gln Pro Ala Met Gln Pro Ala Asp Ser Xaa Pro Xaa
      85      90      95

```

<210> 1055
 <211> 391
 <212> DNA
 <213> Homo sapiens

```

<400> 1055
tacaatgtat catcaaccag aaatacaatg agaaccacct gccagtctcc caaatactat
60
ctgcagccac tcatttaact ctctgggcta gctccacgtg ggccgtctga actctcttag
120

```

aagaatcatc tctctgctca ggcaccggga gcaaggggca tctgtcgctc tgcagaacgg
 180
 aggggaccag gcctgatgaa caccatcctg ggcccagaaa cctgggaggg taaagagaac
 240
 tgccaggggt gaagtccaag gatgggaaaa aggcctccgg ggcagagtcc tgaaatgtca
 300
 gaagtacacc aaagaggaaa cagcatcacg ttattgctga ggcagggcct cattctgttg
 360
 ccaaggctgc agtgcagtgg tgacaccatg g
 391

<210> 1056

<211> 83

<212> PRT

<213> Homo sapiens

<400> 1056

Met	Val	Ser	Pro	Leu	His	Cys	Ser	Leu	Gly	Asn	Arg	Met	Arg	Pro	Cys
1				5				10					15		
Leu	Ser	Asn	Asn	Val	Met	Leu	Phe	Pro	Leu	Trp	Cys	Thr	Ser	Asp	Ile
		20						25				30			
Ser	Gly	Leu	Cys	Pro	Gly	Gly	Leu	Phe	Pro	Ile	Leu	Gly	Leu	His	Pro
		35				40					45				
Trp	Gln	Phe	Ser	Leu	Pro	Ser	Gln	Val	Ser	Gly	Pro	Arg	Met	Val	Phe
	50					55				60					
Ile	Arg	Pro	Gly	Pro	Leu	Arg	Ser	Ala	Glu	Arg	Gln	Met	Pro	Leu	Ala
65					70					75					80
Pro	Gly	Ala													

<210> 1057

<211> 341

<212> DNA

<213> Homo sapiens

<400> 1057

gaattccctg cgcgtgtgac gccggtcgcc gagcaactcg gcgtgtcgct gacgctgcat
 60
 cccgatgatc cgccgcgtcc gctgttcggg ttgccgcgca ttgcgtccag cgccgaggac
 120
 tatcaggcgc tggtcgatgc ggtaccgtcc aaggcgaacg gcatctgcct gtgcacgggt
 180
 tcgctcggcg tgcgcgcgga gaacgatctg cctgaaatgg ccgaacgttt cggcccgcgt
 240
 atcgcccttg cgcattctgcg cgcgaccaag cgcgacgccg atggcctgtc gtttcatgaa
 300
 tccgaccatc tcgacggcga tgtcgacatg gtcgcgtgct c
 341

<210> 1058

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1058

Glu Phe Pro Ala Arg Val Thr Pro Val Ala Glu Gln Leu Gly Val Ser
 1 5 10 15
 Leu Thr Leu His Pro Asp Asp Pro Pro Arg Pro Leu Phe Gly Leu Pro
 20 25 30
 Arg Ile Ala Ser Ser Ala Glu Asp Tyr Gln Ala Leu Phe Asp Ala Val
 35 40 45
 Pro Ser Lys Ala Asn Gly Ile Cys Leu Cys Thr Gly Ser Leu Gly Val
 50 55 60
 Arg Ala Glu Asn Asp Leu Pro Glu Met Ala Glu Arg Phe Gly Pro Arg
 65 70 75 80
 Ile Ala Phe Ala His Leu Arg Ala Thr Lys Arg Asp Ala Asp Gly Leu
 85 90 95
 Ser Phe His Glu Ser Asp His Leu Asp Gly Asp Val Asp Met Val Ala
 100 105 110
 Cys

<210> 1059

<211> 372

<212> DNA

<213> Homo sapiens

<400> 1059

nagctgaccg gctggcagat caacatcatg acgccggaag aaagcgtgaa ccgccgggaa
 60
 gtcgagcggtt cgggcctgcg caccacgttc atgaacaagc tggacgtcga tgaggaagtc
 120
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 180
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 240
 gcccgcaatg cgctgctgac cgaggccatc gcccaggaag agcgccttga gaccgcgcag
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<210> 1060

<211> 124

<212> PRT

<213> Homo sapiens

<400> 1060

Xaa Leu Thr Gly Trp Gln Ile Asn Ile Met Thr Pro Glu Glu Ser Val
 1 5 10 15
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 20 25 30
 Lys Leu Asp Val Asp Glu Glu Val Ala Asp Ile Leu Ile Asp Glu Gly
 35 40 45
 Phe Thr Gly Ile Glu Glu Ile Ala Tyr Val Pro Met Gln Glu Leu Leu
 50 55 60
 Glu Ile Glu Ala Phe Asp Glu Asp Thr Ile Asn Glu Leu Arg Ala Arg

```

65              70              75              80
Ala Arg Asn Ala Leu Leu Thr Glu Ala Ile Ala Gln Glu Glu Arg Leu
              85              90              95
Glu Thr Ala Gln Asp Leu Leu Glu Leu Glu Gly Val Thr Pro Glu Leu
              100              105              110
Ala Ala Lys Leu Ala Glu Arg Gln Val Arg Thr Arg
              115              120

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<210> 1061
 <211> 456
 <212> DNA
 <213> Homo sapiens

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<400> 1061
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120
gagaaggagg attctggagc attgtatttg gcagccggag cgggcagtgg gcgggggggtt
180
gggacacgaa gggctcttcg gacccctgtg cctcttctgc cccaagggcg agaagacggg
240
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300
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360
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420
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456

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<210> 1062
 <211> 125
 <212> PRT
 <213> Homo sapiens

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<400> 1062
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1              5              10              15
Phe Leu Leu Pro Ile Gln Val Gln Thr Trp Glu Glu Arg Gly Gly Glu
20              25              30
Gly Arg Arg Leu His Gly Pro Pro Arg Val Ala Ala Lys Pro Val Phe
35              40              45
Ser Pro Leu Gly Gln Lys Arg His Arg Gly Pro Lys Ser Pro Ser Cys
50              55              60
Pro Asn Pro Pro Pro Thr Ala Arg Ser Gly Cys Gln Ile Gln Cys Ser
65              70              75              80
Arg Ile Leu Leu Leu Leu Ser Ala Pro Lys His Leu Gln Pro Leu Leu
85              90              95
Gly Leu Gln Lys Gly Phe Leu Glu Gly Ala Lys Gly Thr Phe Tyr Leu
100              105              110
Ser Tyr Leu Pro Ala Gln Pro Gly Ala Met Glu Ser Arg
115              120              125

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<210> 1063
<211> 3760
<212> DNA
<213> Homo sapiens

<400> 1063
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120
taaggcttta taactagtaa atatctgcat taaagaacga gttgaatgaa aattctgata
180
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240
attcagaaga atgagctttg taattcttaa aaattagtct cagaatagaa aggattttaa
300
aagtaattga gtaaagtcac aggaaatgtg accatataaa ggaatggctc taaatgtatt
360
aatccagaag gaagcaacag gttaaacagt aagaggtaag aaacaaaaaa taaggaacga
420
gagagagaga gtgacagga gagagagaca gagcggggaa ggagagaatg agaaggaaaa
480
tcaggaaaac gaggagaaac agaattaagg aggtgatact ggaatagtat cagaccattc
540
tgaatcaatt taagaattgc catgtctaata tcttatatgg aagatttgaa atacaaggat
600
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660
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720
ttacaaaatt attatgctct ataattcttc catatgcaaa tatttcatat tccctctttt
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1020
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1140
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1320
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1380
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1440

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2160
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2340
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2460
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2700
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2760
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 3660
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 3760

<210> 1064

<211> 483

<212> PRT

<213> Homo sapiens

<400> 1064

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His	Gly	Ser	Pro	Ser	Cys	Thr	Leu	Arg	Arg	Ser	Ala	Val	Lys	Ser	Arg
			20					25					30		
Leu	Gly	Cys	Ala	Val	Ala	Gly	Ser	Phe	Thr	Ser	Thr	Trp	Asn	Phe	
		35				40					45				
Leu	Lys	Ser	Ser	Leu	Leu	Pro	Gly	Met	Gln	His	Ala	Val	Phe	Ser	Ser
	50					55					60				
Met	Gly	Met	Phe	Ser	Ala	Ser	Ser	Leu	Val	Thr	Ala	Leu	Leu	Leu	Leu
65					70					75					80
Arg	Thr	Pro	Leu	Thr	Pro	Ser	Ser	Arg	Pro	Arg	Ala	Gly	Arg	Trp	His
				85					90					95	
Leu	Ser	Cys	Ser	Ser	Ser	Ala	Ser	Ser	Phe	Arg	Ala	Leu	Leu	Cys	Trp
			100					105					110		
Thr	Ser	Arg	Leu	Leu	Leu	Ser	Arg	Ser	Leu	Cys	Ser	Val	Ala	Arg	Ser
		115					120					125			
Ser	Ala	Ser	Ser	Arg	Leu	Ser	Tyr	Gln	Val	Lys	Leu	Gln	Met	Ala	Leu
	130					135					140				
Glu	Leu	Met	Arg	Lys	Glu	Leu	Glu	Asp	Ala	Leu	Thr	Gln	Glu	Ala	Asn
145				150						155					160
Val	Gly	Lys	Lys	Thr	Val	Ile	Trp	Lys	Glu	Lys	Val	Glu	Met	Gln	Arg
				165				170						175	
Gln	Arg	Phe	Arg	Leu	Glu	Phe	Glu	Lys	His	Arg	Gly	Phe	Leu	Ala	Gln

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<210> 1065
<211> 892
<212> DNA
<213> Homo sapiens
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1006

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 360
 caccagagc agcatcaaga tgcagtggc ggggtactgg aactggcttg gcaagggctg
 420
 cgcaggcaac aggtcccagc aagagtcagc tagcctagct cagccctgca cacctggaga
 480
 cctgggggtg ctccagacac ctcgccctt taggtccctt taattgaatg tgtgtggatc
 540
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 600
 ttagtacctg ccagcttttc ctctcttaca taaatttcat gccagagcct ggaaatgtgt
 660
 gccctttgta ggaggggcat cacaggctgg ctcacctcag cagtgccagg cagagcccgt
 720
 ccctctcatt gcaggaggcg catgaagcgt gtctgggacc gagctgtgga gttcctggcc
 780
 tccaacgaat cccggatcca gacggagtcc caccgcgttg caggagagga catgctgggtg
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 892

<210> 1066

<211> 76

<212> PRT

<213> Homo sapiens

<400> 1066

Met	Cys	Ala	Leu	Cys	Arg	Arg	Gly	Ile	Thr	Gly	Trp	Leu	Thr	Ser	Ala
1				5					10					15	
Val	Pro	Gly	Arg	Ala	Arg	Pro	Ser	His	Cys	Arg	Arg	Arg	Met	Lys	Arg
			20					25					30		
Val	Trp	Asp	Arg	Ala	Val	Glu	Phe	Leu	Ala	Ser	Asn	Glu	Ser	Arg	Ile
		35					40					45			
Gln	Thr	Glu	Ser	His	Arg	Val	Ala	Gly	Glu	Asp	Met	Leu	Val	Leu	Arg
		50				55					60				
Trp	Thr	Lys	Pro	Ser	Ser	Phe	Ser	Asp	Ser	Glu	Arg				
65					70					75					

<210> 1067

<211> 418

<212> DNA

<213> Homo sapiens

<400> 1067

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 120
 ggactagaca tctggaaagc ccgagtctcc gctgacatcg aaggcgactg gactatgcac
 180
 gttgaaggct ggtcagacac ctggggcacg tggcatcaca atgccaatgc caagctcgcc
 240

gctgccatcg acgtcgaact ggtgtgcgcc gaaggccatg ccctcataaa cgaggcggtc
 300
 cggcacgccg agcaatccgg ggatactgac gcgatcacgg ctctgcgcga gaccgatgcc
 360
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 418

<210> 1068
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1068
 Glu Phe Glu Val Thr Ala Asn Val Phe Arg Glu Gly His Asp Ala Val
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 Gly Ala Ser Val Val Leu Thr Asp Pro Glu Gly Asn Arg His Leu Thr
 20 25 30
 Asp Met His Gln Val Glu Pro Trp Gly Leu Asp Ile Trp Lys Ala Arg
 35 40 45
 Val Ser Ala Asp Ile Glu Gly Asp Trp Thr Met His Val Glu Gly Trp
 50 55 60
 Ser Asp Thr Trp Gly Thr Trp His His Asn Ala Asn Ala Lys Leu Ala
 65 70 75 80
 Ala Ala Ile Asp Val Glu Leu Val Cys Ala Glu Gly His Ala Leu Ile
 85 90 95
 Asn Glu Ala Val Arg His Ala Glu Gln Ser Gly Asp Thr Asp Ala Ile
 100 105 110
 Thr Ala Leu Arg Glu Thr Asp Ala Asn Leu Thr Leu Asp Arg Ala Pro
 115 120 125
 Asp Ser Leu Gln Gln Val Ile Asn Thr Tyr Ala
 130 135

<210> 1069
 <211> 371
 <212> DNA
 <213> Homo sapiens

<400> 1069
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 120
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 180
 ctgcggttatc acctgcaaca gaacgtccac ttcaaggaag aaacagtgaa gctcttcac
 240
 tgtgagctgg tcatggcctt ggactacctg cagaaccagc gcatcattca cagggatatg
 300
 aagcctgaca atattttact tgacgaacat gggcacgtgc acatcacaga tttcaacatt
 360
 gctgcgatgc t
 371

<210> 1070

<211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1070

Xaa	Tyr	Asn	Phe	Leu	Ala	Gly	Ser	Thr	Gly	Ala	Asn	Met	Ile	Arg	Ser
1				5					10					15	
Pro	Ala	Ser	Gln	Gln	Phe	Ile	Cys	Arg	His	Ser	Gln	Gly	Pro	Pro	Val
		20						25					30		
Asn	Ser	Lys	Gly	Ile	Ala	Cys	Ser	Phe	Ser	Gly	Ala	Glu	His	Leu	Arg
	35						40					45			
Cys	His	Val	Arg	Leu	Gly	Ala	Ser	His	Gly	Gly	Asp	Leu	Arg	Tyr	His
	50					55					60				
Leu	Gln	Gln	Asn	Val	His	Phe	Lys	Glu	Glu	Thr	Val	Lys	Leu	Phe	Ile
65					70					75					80
Cys	Glu	Leu	Val	Met	Ala	Leu	Asp	Tyr	Leu	Gln	Asn	Gln	Arg	Ile	Ile
			85					90						95	
His	Arg	Asp	Met	Lys	Pro	Asp	Asn	Ile	Leu	Leu	Asp	Glu	His	Gly	His
		100					105						110		
Val	His	Ile	Thr	Asp	Phe	Asn	Ile	Ala	Ala	Met					
		115					120								

<210> 1071
 <211> 998
 <212> DNA
 <213> Homo sapiens

<400> 1071

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120
cccacccgaa gtacgtggcc ttggagtgc attcgcactc cacttgGCCA ccgtttgcat
180
tcgacctaac cagcaattgc atctcgtttg acctgctcgc gttgtcaaca tcatagcaac
240
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300
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360
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420
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480
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540
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600
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660
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720
cgagattagc cacatacatg accatgtggt ccttgggtca gcacgcgaag aaaatgccaa
780

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gcgtaccctt tgggttggtg cgcttacggt ggtgatgatg gttggcgaaa tcgtcgccgg
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<210> 1072

<211> 72

<212> PRT

<213> Homo sapiens

<400> 1072

Met	Gly	His	Thr	Ala	Ser	Asn	Lys	Asp	Asp	Leu	Leu	Lys	Arg	Val	Lys
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Arg	Ile	Ala	Gly	Gln	Ile	Gln	Ala	Val	Glu	Arg	Ala	Leu	Glu	Ser	Asp
		20					25					30			
Ala	Asp	Cys	Ala	Lys	Thr	Leu	His	Leu	Val	Ala	Ala	Thr	Arg	Gly	Ala
		35				40						45			
Ile	Asn	Gly	Leu	Met	Asp	Glu	Ile	Ile	Glu	Asp	His	Ala	Arg	Lys	His
	50				55						60				
Val	Ala	Ser	Pro	Thr	Leu	Ser	Asp								
65					70										

<210> 1073

<211> 468

<212> DNA

<213> Homo sapiens

<400> 1073

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120
ttcccccaact gataaaatct tgcttctctt caaactccta ggcaaatttc tcctacttca
180
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300
catcctctgt ataatatattg gttttcacct ctttatgaac tcttttgtat tctcattact
360
ggctctggaa cccagaacat accacggggt caaggatatgt tttaatgaat tgaatggaat
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468

<210> 1074

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1074

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Gly Cys Phe Ser Pro Thr Asp Lys Ile Leu Leu Leu Phe Lys Leu Leu
          20           25           30
Gly Lys Phe Leu Leu Leu Gln Lys Val Leu Phe Leu His Ile Leu Arg
          35           40           45
Asn His His Leu Val His Met Leu Lys Ala Glu Phe Ile Val Ser Ser
          50           55           60
Pro Ser Leu Ser Asn Ser Phe Ala Gln Thr Leu Arg Tyr Ser Phe Ile
65           70           75           80
Leu Cys Ile Ile Phe Gly Phe His Leu Phe Met Asn Ser Phe Val Phe
          85           90           95
Ser Leu Leu Ala Leu Glu Pro Arg Thr Tyr His Gly Phe Lys Val Cys
          100          105          110
Phe Asn Glu Leu Asn Gly Ile Asn Phe Val Val Leu Met Gln Ile Gln
          115          120          125
Met Pro Leu Asn Thr Asp
          130

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<210> 1075

<211> 1633

<212> DNA

<213> Homo sapiens

<400> 1075

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180
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240
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300
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420
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720
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780
gactgtggac aacgtgcacc tggaacacgg cgtggtgtat gagtatgtga gcacggcagg
840

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cgtcaggtgc catgtgctgg agaagatcgt ggagccccgc ggctgcttcg gcctcaccgc
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 1200
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 1620
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<210> 1076
 <211> 87
 <212> PRT
 <213> Homo sapiens

<400> 1076
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 20 25 30
 Pro Gly Ala Pro Pro Ala Val Trp Pro Thr Ser Ala Pro Pro Ile Ala
 35 40 45
 Thr Ser Thr Ser Trp Lys Cys Pro Thr Pro Arg Pro Pro Pro Gln Trp
 50 55 60
 Ala Gly Pro Ser Ala Ser Ala Leu Asp Ala Asn Pro Pro Ser Ser Ala
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 Leu Thr Arg Ser Lys Ala Thr
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<210> 1077
 <211> 419
 <212> DNA
 <213> Homo sapiens

<400> 1077

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 180
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 240
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<210> 1078

<211> 139

<212> PRT

<213> Homo sapiens

<400> 1078

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Trp	Thr	Cys	Asn	Ala	Asn	Glu	Ala	Thr	Cys	Leu	Arg	Leu	Ala	Gly	Ala
			20					25					30		
Pro	Ser	Pro	Ser	Asp	Ala	Leu	Phe	His	Pro	Glu	Phe	Thr	Tyr	Pro	Ile
			35				40					45			
Phe	Gly	Glu	Ala	Glu	Ala	Ile	Tyr	Gly	Tyr	Asn	Gly	Leu	His	Met	Asn
	50					55				60					
Leu	Ala	Phe	Ala	Ser	Gly	Ser	Leu	Val	Pro	Ser	Leu	Glu	Ile	Thr	Tyr
65					70				75					80	
Arg	Ala	Lys	Asn	Thr	Thr	Thr	Ser	Ala	Lys	Val	Asp	Asp	Val	Glu	Gln
			85					90					95		
Ala	Leu	Arg	Gly	Val	Leu	Pro	Pro	Asp	Val	Val	Thr	Pro	Ala	Glu	Leu
			100					105				110			
Asp	Ala	Ile	Val	Ala	Arg	Asp	Ala	Arg	Ala	Val	Arg	Ala	His	Leu	Arg
		115				120					125				
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	130					135									

<210> 1079

<211> 584

<212> DNA

<213> Homo sapiens

<400> 1079

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 120
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 180
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 240

tttaccccaa gttccccccag gccctccctt tcgtctgcaa agacacacat ctgtttcact
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 420
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 480
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<210> 1080
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1080
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 20 25 30
 Phe Pro Ser Gln Gln Gly Gly Glu Pro Cys Cys Leu Leu Thr Trp Val
 35 40 45
 Val Leu Phe Arg Ser Cys Asp Thr Thr Val Gly Lys Val Met Pro Ser
 50 55 60
 Val Thr Lys Ser Ile Tyr Pro Lys Phe Pro Gln Ala Leu Pro Phe Val
 65 70 75 80
 Cys Lys Asp Thr His Leu Phe His Cys Val Phe Cys Lys Asp Thr His
 85 90 95
 Leu Phe His Trp Gly Phe Leu Gln Arg His Pro Phe Val Ser Pro Phe
 100 105 110
 Lys Gly Phe Pro Leu His Leu Val Tyr Phe
 115 120

<210> 1081
 <211> 3077
 <212> DNA
 <213> Homo sapiens

<400> 1081
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 120
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 180
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 240
 tatactctgta atcaatgtgg tgctaagtac acatccctag acagctttca gactcaccta
 300
 aaaactcatc tcgacactgt gcttccaaaa ttgacctgtc ctcagtgcaa caaggaattc
 360

cccaaccaag aatccttgct gaagcatggt accattcact ttatgatcac ttcaacgtat
420
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480
ctggacatgc acacctttgt cttcttttcgc tgcacctctt gccaggaagt ttttgactca
540
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720
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1020
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1920
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1980
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2040

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 2160
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 2280
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 2400
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 2580
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 2760
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 2820
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 3077

<210> 1082

<211> 757

<212> PRT

<213> Homo sapiens

<400> 1082

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		20						25					30		
Lys	Asn	Ile	Pro	Leu	Ala	Leu	Asn	Tyr	Ile	His	Asn	Gly	Lys	Lys	Ser
	35					40					45				
Arg	Ala	Leu	Ser	Pro	Leu	Ser	Pro	Val	Ala	Ile	Glu	Gln	Thr	Ser	Leu
	50					55					60				
Lys	Met	Met	Gln	Ala	Val	Gly	Gly	Ala	Pro	Ala	Arg	Pro	Thr	Gly	Glu
65				70					75					80	
Tyr	Ile	Cys	Asn	Gln	Cys	Gly	Ala	Lys	Tyr	Thr	Ser	Leu	Asp	Ser	Phe

				85					90					95					
Gln	Thr	His	Leu	Lys	Thr	His	Leu	Asp	Thr	Val	Leu	Pro	Lys	Leu	Thr				
			100					105					110						
Cys	Pro	Gln	Cys	Asn	Lys	Glu	Phe	Pro	Asn	Gln	Glu	Ser	Leu	Leu	Lys				
		115					120					125							
His	Val	Thr	Ile	His	Phe	Met	Ile	Thr	Ser	Thr	Tyr	Tyr	Ile	Cys	Glu				
	130					135					140								
Ser	Cys	Asp	Lys	Gln	Phe	Thr	Ser	Val	Asp	Asp	Leu	Gln	Lys	His	Leu				
145					150				155						160				
Leu	Asp	Met	His	Thr	Phe	Val	Phe	Phe	Arg	Cys	Thr	Leu	Cys	Gln	Glu				
				165				170						175					
Val	Phe	Asp	Ser	Lys	Val	Ser	Ile	Gln	Leu	His	Leu	Ala	Val	Lys	His				
			180					185					190						
Ser	Asn	Glu	Lys	Lys	Val	Tyr	Arg	Cys	Thr	Ser	Cys	Asn	Trp	Asp	Phe				
	195						200					205							
Arg	Asn	Glu	Thr	Asp	Leu	Gln	Leu	His	Val	Lys	His	Asn	His	Leu	Glu				
	210					215					220								
Asn	Gln	Gly	Lys	Val	His	Lys	Cys	Ile	Phe	Cys	Gly	Glu	Ser	Phe	Gly				
225					230				235						240				
Thr	Glu	Val	Glu	Leu	Gln	Cys	His	Ile	Thr	Thr	His	Ser	Lys	Lys	Tyr				
				245					250					255					
Asn	Cys	Lys	Phe	Cys	Ser	Lys	Ala	Phe	His	Ala	Ile	Ile	Leu	Leu	Glu				
			260					265					270						
Lys	His	Leu	Arg	Glu	Lys	His	Cys	Val	Phe	Glu	Thr	Lys	Thr	Pro	Asn				
	275						280					285							
Cys	Gly	Thr	Asn	Gly	Ala	Ser	Glu	Gln	Val	Gln	Lys	Glu	Glu	Val	Glu				
	290					295					300								
Leu	Gln	Thr	Leu	Leu	Thr	Asn	Ser	Gln	Glu	Ser	His	Asn	Ser	His	Asp				
305					310					315					320				
Gly	Ser	Glu	Glu	Asp	Val	Asp	Thr	Ser	Glu	Pro	Met	Tyr	Gly	Cys	Asp				
				325					330					335					
Ile	Cys	Gly	Ala	Ala	Tyr	Thr	Met	Glu	Thr	Leu	Leu	Gln	Asn	His	Gln				
			340					345					350						
Leu	Arg	Asp	His	Asn	Ile	Arg	Pro	Gly	Glu	Ser	Ala	Ile	Val	Lys	Lys				
	355						360					365							
Lys	Ala	Glu	Leu	Ile	Lys	Gly	Asn	Tyr	Lys	Cys	Ser	Val	Cys	Ser	Arg				
	370				375						380								
Thr	Phe	Phe	Ser	Glu	Asn	Gly	Leu	Arg	Glu	His	Met	Gln	Thr	His	Leu				
385					390					395					400				
Gly	Pro	Val	Lys	His	Tyr	Met	Cys	Pro	Ile	Cys	Gly	Glu	Arg	Phe	Pro				
				405					410					415					
Ser	Leu	Leu	Thr	Leu	Thr	Glu	His	Lys	Val	Thr	His	Ser	Lys	Ser	Leu				
			420					425					430						
Asp	Thr	Gly	Asn	Cys	Arg	Ile	Cys	Lys	Met	Pro	Leu	Gln	Ser	Glu	Glu				
	435						440					445							
Glu	Phe	Leu	Glu	His	Cys	Gln	Met	His	Pro	Asp	Leu	Arg	Asn	Ser	Leu				
	450					455					460								
Thr	Gly	Phe	Arg	Cys	Val	Val	Cys	Met	Gln	Thr	Val	Thr	Ser	Thr	Leu				
465					470					475					480				
Glu	Leu	Lys	Ile	His	Gly	Thr	Phe	His	Met	Gln	Lys	Thr	Gly	Asn	Gly				
				485					490					495					
Ser	Ala	Val	Gln	Thr	Thr	Gly	Arg	Gly	Gln	His	Val	Gln	Lys	Leu	Tyr				
			500					505					510						
Lys	Cys	Ala	Ser	Cys	Leu	Lys	Glu	Phe	Arg	Ser	Lys	Gln	Asp	Leu	Val				

515 520 525
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 530 535 540
 Asn Leu Ser Lys Ser Ala Ser Pro Gly Ile Asn Val Pro Pro Gly Thr
 545 550 555 560
 Asn Arg Pro Gly Leu Gly Gln Asn Glu Asn Leu Ser Ala Ile Gly Glu
 565 570 575
 Arg Gln Gly Gly Thr Glu Thr Arg Cys Ser Ser Cys Asn Val Lys
 580 585 590
 Phe Glu Ser Glu Ser Glu Leu Gln Asn His Ile Gln Thr Ile His Arg
 595 600 605
 Glu Leu Val Pro Asp Ser Asn Ser Thr Gln Leu Lys Thr Pro Gln Val
 610 615 620
 Ser Pro Met Pro Arg Ile Ser Pro Ser Gln Ser Asp Glu Lys Lys Thr
 625 630 635 640
 Tyr Gln Cys Ile Lys Cys Gln Met Val Phe Tyr Asn Glu Trp Asp Ile
 645 650 655
 Gln Val His Val Ala Asn His Met Ile Asp Glu Gly Leu Asn His Glu
 660 665 670
 Cys Lys Leu Cys Ser Gln Thr Phe Asp Ser Pro Ala Lys Leu Gln Cys
 675 680 685
 His Leu Ile Glu His Ser Phe Glu Gly Met Gly Gly Thr Phe Lys Cys
 690 695 700
 Pro Val Cys Phe Thr Val Phe Val Gln Ala Asn Lys Leu Gln Gln His
 705 710 715 720
 Ile Phe Ser Ala His Gly Gln Glu Asp Lys Ile Tyr Asp Cys Thr Gln
 725 730 735
 Cys Pro Gln Lys Phe Phe Phe Gln Thr Glu Leu Gln Asn His Thr Met
 740 745 750
 Thr Gln His Ser Ser
 755

<210> 1083

<211> 516

<212> DNA

<213> Homo sapiens

<400> 1083

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 ccactgaccc cggttctgtc ggccaattgg gatgaagagc gcagttggaa gctgcttaac
 180
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 360
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 420
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516

<210> 1084

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1084

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Ser	Ala	Asn	Trp	Asp	Glu	Glu	Arg	Ser	Trp	Lys	Leu	Leu	Asn	Tyr	Glu
		20						25					30		
Arg	Gln	Gly	Gly	Tyr	Thr	Gly	Leu	Arg	Lys	Ala	Leu	Thr	Met	Pro	Pro
		35					40					45			
Asp	Asp	Val	Val	Ser	Leu	Val	Lys	Asp	Ala	Asn	Leu	Arg	Gly	Arg	Gly
	50					55					60				
Gly	Ala	Gly	Phe	Pro	Thr	Gly	Met	Lys	Trp	Ser	Phe	Val	Pro	Lys	Asp
65					70				75					80	
Asn	Pro	Asn	Pro	Thr	Tyr	Leu	Val	Val	Asn	Gly	Asp	Glu	Ser	Glu	Pro
				85					90					95	
Gly	Thr	Cys	Lys	Asp	Met	Pro	Leu	Met	Met	Ala	Ser	Pro	His	Thr	Leu
		100						105					110		
Val	Glu	Gly	Val	Ile	Ile	Ala	Ser	Tyr	Ala	Ile	Lys	Ala	Lys	Met	Ala
		115						120				125			
Phe	Ile	Tyr	Ile	Arg	Gly	Glu	Val	Leu	His	Val	Val	Arg	Arg		
	130					135						140			

<210> 1085

<211> 374

<212> DNA

<213> Homo sapiens

<400> 1085

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374

<210> 1086

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1086

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Phe Phe Tyr Arg Asp Ile Tyr Lys Ser Asp Tyr Ser Phe Asp Leu His
          35           40           45
Gln Asp Tyr Glu Arg Ser Lys Glu Asn Phe Leu Lys Met Ile Gly Asp
          50           55           60
Ser Leu Leu Ala Glu Leu Asn Leu Val Asp Ile Asp Thr Val Arg Lys
65           70           75           80
Ile Ala Asn Ser Pro Leu Gly Ser Ser Glu Thr Leu Tyr Asp Phe Glu
          85           90           95
Arg Met Thr His Met Glu Val Trp Leu Arg Glu Asn Tyr Val
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<210> 1087

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1087

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120
nggcaccact gtgcctggcc catccaccgg agtctagggg tgcaatccac cgcccgtgca
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240
gccccgggaat ttttcggagt gcattaggat tgggtctgaac gtgaaccttg aatccatgta
300
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420
ctt
423

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<210> 1088

<211> 88

<212> PRT

<213> Homo sapiens

<400> 1088

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Met Thr Ile Val Ala Pro Pro Pro Pro Thr Ala Gly Ala Ala Ile Ser
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Phe Leu Val Asp Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp
          20           25           30
Asp His Gly Val Ser Ile Arg Val Xaa His His Cys Ala Trp Pro Ile
          35           40           45
His Arg Ser Leu Gly Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Phe
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<210> 1089

<211> 750

<212> DNA

<213> Homo sapiens

<400> 1089

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750					

<210> 1090

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1090

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			20					25					30		
Arg	Val	Val	Arg	Met	Gly	Leu	Gly	Glu	Glu	Ala	Leu	Pro	Leu	Phe	Phe
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Phe	Asn	Leu	Ala	Lys	Gly	Leu	Leu	Gly	Gln	Gly	His	Pro	Ser	Leu	Leu
	50					55					60				
Leu	Gly	Ala	Ser	Ile	Phe	Leu	His	Ser	Val	Lys	Asn	Gly	Gly	Val	Ile
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Gln	Lys	Tyr	Pro	Pro	Tyr	Cys	Gln	Gly	Phe	Gly	Glu	Gly	Ser	Lys	Lys

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<210> 1092
<211> 146
<212> PRT
<213> Homo sapiens

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35 40 45
His Phe Phe Gly Arg Pro Leu Lys Glu Leu Asn Ile Asp Glu Phe Ala
50 55 60
Leu Leu Val Gly Met Val Lys Gly Pro Ser Ile Tyr Asn Pro Glu Arg
65 70 75 80
His Pro Lys Arg Ala Leu Ser Arg Arg Asn Thr Val Leu Ala Ile Leu
85 90 95
Lys Ser Gln Asp Arg Leu Thr Glu Ser Asp Tyr Asn Ile Leu Arg Lys
100 105 110
Gln Pro Ile Arg Leu Ala Asp Lys His Gln Glu Arg Ser Val Tyr Gly
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Cys Met
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<210> 1093
 <211> 351
 <212> DNA
 <213> Homo sapiens

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 35 40 45
 Val Arg Glu Leu Leu His Ala Ile Asp Leu Glu His Glu Ile Gly Arg
 50 55 60
 Leu Arg Glu Gln Ile Pro Gln Thr Asn Ser Glu Thr Lys Ile Lys Lys
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 Leu Ser Lys Arg Leu Lys Leu Met Glu Ala Phe Gln Gly Ser Gly Asn
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 100 105 110
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<210> 1095
 <211> 619
 <212> DNA
 <213> Homo sapiens

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<210> 1096

<211> 195

<212> PRT

<213> Homo sapiens

<400> 1096

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Ser	Ser	Arg	Leu	Glu	His	Leu	Glu	Lys	Glu	Leu	Ser	Glu	Lys	Ser	Gly
			20					25					30		
Gln	Leu	Arg	Gln	Gly	Ser	Ala	Gln	Ser	Gln	Arg	Gln	Ile	Arg	Gly	Glu
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Ala	Ile	Glu	Tyr	Lys	Asn	Glu	Ala	Ile	Thr	Cys	Arg	Gln	Arg	Val	Leu
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His	Gly	Thr	Cys	Gly	Glu	Val	Ser	His	Gly	Ser	Cys	Ser	Ser	Gly	Tyr
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Pro	Val	Ser	Ser	Gln	Thr	Gly	Gly	Gln	Asn	Gln	Asp	Gln	Leu	Ile	Cys
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<210> 1097

<211> 5108

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Ser	Glu	Asn	Pro	Pro	Ala	Gly	Ile	Ala	His	Lys	Gly	Lys	Pro	His	Tyr
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			165					170					175		
Glu	Glu	Leu	Asp	Leu	Ile	Gln	Ala	Val	Gly	Cys	Leu	Glu	Glu	Phe	Gly
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Val	Lys	Ile	Leu	Pro	Leu	Gln	Val	Arg	Leu	Cys	Pro	Asp	Arg	Ile	Ser
	195					200					205				
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Thr	Lys	Leu	Leu	Gly	Leu	Ala	Glu	Leu	Leu	Arg	Val	Ala	Gly	Glu	Asn
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Pro	Glu	Glu	Arg	Arg	Gly	Gln	Val	Leu	Ile	Leu	Leu	Val	Glu	Gln	Ala
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Leu	Arg	Phe	His	Asp	Tyr	Lys	Ala	Ala	Ser	Met	His	Cys	Gln	Glu	Leu
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Phe	Ala	Leu	Thr	His	Cys	Pro	Pro	Ser	Ser	Ile	Glu	Leu	Leu	Leu	Ala
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					325					330					335
Gln	Ile	His	His	Glu	Gly	Gly	Glu	Asn	Ile	Ser	Ala	Ser	Pro	Leu	Thr
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Glu	Lys	Gln	Gly	Cys	His	Pro	Phe	Tyr	Glu	Ser	Val	Ile	Ser	Asn	Pro
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Ala	Lys	Asn	Lys	Gly	Glu	Val	Phe	Pro	Thr	Thr	Glu	Val	Leu	Leu	Gln
					485					490					495
Leu	Ala	Ser	Glu	Ala	Leu	Pro	Asn	Asp	Met	Thr	Leu	Ala	Leu	Ala	Tyr
					500					505					510
Leu	Leu	Ala	Leu	Pro	Gln	Val	Leu	Asp	Ala	Asn	Arg	Cys	Phe	Glu	Lys
					515					520					525
Gln	Ser	Pro	Ser	Ala	Leu	Ser	Leu	Gln	Leu	Ala	Ala	Tyr	Tyr	Tyr	Ser
530					535					540					
Leu	Gln	Ile	Tyr	Ala	Arg	Leu	Ala	Pro	Cys	Phe	Arg	Asp	Lys	Cys	His
545					550					555					560
Pro	Leu	Tyr	Arg	Ala	Asp	Pro	Lys	Glu	Leu	Ile	Lys	Met	Val	Thr	Arg
					565					570					575
His	Val	Thr	Arg	His	Glu	His	Glu	Ala	Trp	Pro	Glu	Asp	Leu	Ile	Ser
					580					585					590
Leu	Thr	Lys	Gln	Leu	His	Cys	Tyr	Asn	Glu	Arg	Leu	Leu	Asp	Phe	Thr
					595					600					605
Gln	Ala	Gln	Ile	Leu	Gln	Gly	Leu	Arg	Lys	Gly	Val	Asp	Val	Gln	Arg
610					615					620					
Phe	Thr	Ala	Asp	Asp	Gln	Tyr	Lys	Arg	Glu	Thr	Ile	Leu	Gly	Leu	Ala
625					630					635					640
Glu	Thr	Leu	Glu	Glu	Ser	Val	Tyr	Ser	Ile	Ala	Ile	Ser	Leu	Ala	Gln
					645					650					655
Arg	Tyr	Ser	Val	Ser	Arg	Trp	Glu	Val	Phe	Met	Thr	His	Leu	Glu	Phe
					660					665					670
Pro	Phe	Thr	Asp	Ser	Gly	Leu	Ser	Thr	Leu	Glu	Ile	Glu	Asn	Arg	Ala
					675					680					685
Gln	Asp	Leu	His	Leu	Phe	Glu	Thr	Leu	Lys	Thr	Asp	Pro	Glu	Ala	Phe
690					695					700					
His	Gln	His	Met	Val	Lys	Tyr	Ile	Tyr	Pro	Thr	Ile	Gly	Gly	Phe	Asp

1030

	1140		1145		1150										
Ser	Glu	Tyr	Val	Ile	Thr	Asn	Asn	Pro	Trp	Val	Arg	Leu	Ala	Thr	Val
	1155						1160					1165			
Met	Leu	Thr	Arg	Cys	Thr	Met	Glu	Asn	Lys	Glu	Gly	Leu	Gly	Asn	Glu
	1170						1175					1180			
Val	Leu	Lys	Met	Cys	Arg	Ser	Leu	Tyr	Asn	Thr	Lys	Gln	Met	Leu	Pro
1185					1190					1195					1200
Ala	Glu	Gly	Val	Lys	Glu	Leu	Cys	Leu	Leu	Leu	Leu	Asn	Gln	Ser	Leu
			1205						1210					1215	
Leu	Leu	Pro	Ser	Leu	Lys	Leu	Leu	Leu	Glu	Ser	Arg	Asp	Glu	His	Leu
		1220						1225					1230		
His	Glu	Met	Ala	Leu	Glu	Gln	Ile	Thr	Ala	Val	Thr	Thr	Val	Asn	Asp
	1235						1240					1245			
Ser	Asn	Cys	Asp	Gln	Glu	Leu	Leu	Ser	Leu	Leu	Leu	Asp	Ala	Lys	Leu
	1250						1255				1260				
Leu	Val	Lys	Cys	Val	Ser	Thr	Pro	Phe	Tyr	Pro	Arg	Ile	Val	Asp	His
1265					1270					1275					1280
Leu	Leu	Ala	Ser	Leu	Gln	Gln	Gly	Arg	Trp	Asp	Ala	Glu	Glu	Leu	Gly
			1285					1290					1295		
Arg	His	Leu	Arg	Glu	Ala	Gly	His	Glu	Ala	Glu	Ala	Gly	Ser	Leu	Leu
		1300					1305					1310			
Leu	Ala	Val	Arg	Gly	Thr	His	Gln	Ala	Phe	Arg	Thr	Phe	Ser	Thr	Ala
	1315						1320					1325			
Leu	Arg	Ala	Ala	Gln	His	Trp	Val								
	1330					1335									

<210> 1099

<211> 309

<212> DNA

<213> Homo sapiens

<400> 1099

acgcgtgctc tctcccgctt ggcaatcagc atggcctttt cgagctcggc ggtgcgcaat
60

tgaaccattt cttccagttg cgatttttca gaaagcagcg tcgattgacc ttcggtcagc
120

ttgcgcacat agcgcttggt gcggctggca aggatatagg cgagtatcaa tgcacctgcy
180

agggcgagga tcgaggcaat ggtcagccag aagcgcaact tgtccatggc tatgttgcyg
240

gcgattagcc gacgatcttc ttcaccagc aaactgttga tggttttcct gacgtcatcc
300

atctggcca

309

<210> 1100

<211> 100

<212> PRT

<213> Homo sapiens

<400> 1100

Met Asp Asp Val Arg Lys Thr Ile Asn Ser Phe Leu Gly Glu Glu Asp
1 5 10 15

Arg Arg Leu Ile Ala Arg Asn Ile Ala Met Asp Lys Leu Arg Phe Trp

```

      20      25      30
Leu Thr Ile Ala Ser Ile Leu Ala Leu Ala Gly Ala Leu Ile Leu Ala
      35      40      45
Tyr Ile Leu Ala Ser Arg Thr Lys Arg Tyr Val Arg Lys Leu Thr Glu
      50      55      60
Gly Gln Ser Thr Leu Leu Ser Glu Lys Ser Gln Leu Glu Glu Met Val
65      70      75      80
Gln Leu Arg Thr Ala Glu Leu Glu Lys Ala Met Leu Ile Ala Lys Arg
      85      90      95
Glu Arg Ala Arg
      100

```

<210> 1101
 <211> 540
 <212> DNA
 <213> Homo sapiens

```

<400> 1101
gtcgacgtta ccaactacgt catgttggag tctggtcagc cgcttcatgc ctatgatgcc
60
gacaacgtca gcgggacgat tgtggtccgt aaggcccacg agggtgagca tctattgacc
120
ctcgacgaca ccgatcgcac cctcgatcct gacgatctag tcatcgccga cgactcggga
180
gccattggcc tggctggcgt catgggtggt gcggccaccg aagtgactgc tgagacgacg
240
tcaatcatcc tcgagggcgc tcacttcgac ccgatgacgg gcgctcgtgc ttaccgacgc
300
cacaagctcg gttcggaggc ctcccgcgc tttgagcggg gcgttgatcc gatttgcgcc
360
cataccgcag ccgttcgcgc agcgggaattg ctcgcccagt acggcggtgc caccgtcggt
420
gagcccaccg tcgttgggtga ggtccccgag atgccacgtc aaacgatcaa cgctgattta
480
cctaaccgga ttctcggcac gaaggtgcca actgaagagg tcatcgagat cttgacgcgt
540

```

<210> 1102
 <211> 180
 <212> PRT
 <213> Homo sapiens

```

<400> 1102
Val Asp Val Thr Asn Tyr Val Met Leu Glu Ser Gly Gln Pro Leu His
1      5      10      15
Ala Tyr Asp Ala Asp Asn Val Ser Gly Thr Ile Val Val Arg Lys Ala
      20      25      30
His Glu Gly Glu His Leu Leu Thr Leu Asp Asp Thr Asp Arg Thr Leu
      35      40      45
Asp Pro Asp Asp Leu Val Ile Ala Asp Asp Ser Gly Ala Ile Gly Leu
      50      55      60
Ala Gly Val Met Gly Gly Ala Ala Thr Glu Val Thr Ala Glu Thr Thr
65      70      75      80
Ser Ile Ile Leu Glu Gly Ala His Phe Asp Pro Met Thr Gly Ala Arg

```


				85					90					95			
Ala	Tyr	Arg	Arg	His	Lys	Leu	Gly	Ser	Glu	Ala	Ser	Arg	Arg	Phe	Glu		
			100					105					110				
Arg	Gly	Val	Asp	Pro	Ile	Cys	Ala	His	Thr	Ala	Ala	Val	Arg	Ala	Ala		
		115					120					125					
Glu	Leu	Leu	Ala	Gln	Tyr	Gly	Gly	Ala	Thr	Val	Gly	Glu	Pro	Thr	Val		
	130					135					140						
Val	Gly	Glu	Val	Pro	Glu	Met	Pro	Arg	Gln	Thr	Ile	Asn	Ala	Asp	Leu		
145					150				155					160			
Pro	Asn	Arg	Ile	Leu	Gly	Thr	Lys	Val	Pro	Thr	Glu	Glu	Val	Ile	Glu		
			165					170					175				
Ile	Leu	Thr	Arg														
			180														

<210> 1103

<211> 537

<212> DNA

<213> Homo sapiens

<400> 1103

```

cctttcctcc aaccaggcgc tgcggcgccg gcacttgccc gacgttataa aacaattcaa
60
cgtcaggttt accatcgctg tactcaacca aatggtagcc gtatccacct tccccaccga
120
tcgcgacca ggtgatcttt ccctcggcat agattgacgt ggcattctcg tcggagtga
180
tcaagcagcg cttaggcagc tgctgggccc gcggcttcgc ctagctcgcc ggagcacacg
240
aacccttccc gaagataacc gccaaaggcct ggcacacctt ctgctgcacc cattccggct
300
tgacgccgac cgccaccgca ctggtgaaca tagccgcaat aaggagaatt gcgatgtatt
360
cggcgcgggc ggcaccccca tcgtcccttg tccgcatggg tctccctccc actacctacc
420
caatacaggg gagagcataa aaagaaaccc atagccgcac ctgagcccat ggccccaaac
480
cggggcccga gccgggcccc aaccatggga tcaaccggat gtccgtacat caccgcgt
537

```

<210> 1104

<211> 112

<212> PRT

<213> Homo sapiens

<400> 1104

Met	Tyr	Gly	His	Pro	Val	Asp	Pro	Met	Val	Trp	Ala	Arg	Leu	Gly	Pro		
1				5				10					15				
Arg	Phe	Gly	Ala	Met	Gly	Ser	Gly	Ala	Ala	Met	Gly	Phe	Phe	Leu	Cys		
		20					25				30						
Ser	Pro	Leu	Tyr	Trp	Val	Gly	Ser	Gly	Gly	Glu	Thr	His	Ala	Asp	Lys		
	35					40				45							
Gly	Arg	Ser	Gly	Cys	Arg	Arg	Ala	Gly	Ile	His	Arg	Asn	Ser	Pro	Tyr		
	50				55			60									
Cys	Gly	Tyr	Val	His	Gln	Cys	Gly	Gly	Gly	Arg	Arg	Gln	Ala	Gly	Met		

```

65          70          75          80
Gly Ala Ala Glu Gly Val Pro Gly Leu Gly Gly Tyr Leu Arg Glu Gly
          85          90          95
Phe Val Cys Ser Gly Glu Leu Gly Glu Ala Ala Gly Pro Ala Ala Ala
          100          105          110

```

<210> 1105
 <211> 448
 <212> DNA
 <213> Homo sapiens

```

<400> 1105
agggacctgg ggcagcacgt gcacgtgggt gggaggctcc ttgctaccga cagccagcca
60
tgggggtgggc ccttccgagg ctgcctccag gacctgogac tcgatggctg ccacctcccc
120
ttctttcttc tgccactgga taactcaagc cagcccagcg agctcggcgg caggcagtcc
180
tggaacctca ctgcgggctg cgtctccgag gacatgtgca gtcttgaccc ctgtttcaat
240
ggtgggactt gcctcgtcac ctggaatgac ttccactgta cctgccctgc caatttcacg
300
gggcctacat gtgccagca gctgtggtgt cccggccagc cctgtctccc acctgccacg
360
tgtgaggagg tccctgatgg ctttgtgtgt gtggcggagg ccacgttccg cgagggtccc
420
cccgccgcgt tcagcgggca caacgcgt
448

```

<210> 1106
 <211> 149
 <212> PRT
 <213> Homo sapiens

```

<400> 1106
Arg Asp Leu Gly Gln His Val His Val Gly Gly Arg Leu Leu Ala Thr
1          5          10          15
Asp Ser Gln Pro Trp Gly Gly Pro Phe Arg Gly Cys Leu Gln Asp Leu
20          25          30
Arg Leu Asp Gly Cys His Leu Pro Phe Phe Pro Leu Pro Leu Asp Asn
35          40          45
Ser Ser Gln Pro Ser Glu Leu Gly Gly Arg Gln Ser Trp Asn Leu Thr
50          55          60
Ala Gly Cys Val Ser Glu Asp Met Cys Ser Pro Asp Pro Cys Phe Asn
65          70          75          80
Gly Gly Thr Cys Leu Val Thr Trp Asn Asp Phe His Cys Thr Cys Pro
85          90          95
Ala Asn Phe Thr Gly Pro Thr Cys Ala Gln Gln Leu Trp Cys Pro Gly
100          105          110
Gln Pro Cys Leu Pro Pro Ala Thr Cys Glu Glu Val Pro Asp Gly Phe
115          120          125
Val Cys Val Ala Glu Ala Thr Phe Arg Glu Gly Pro Pro Ala Ala Phe
130          135          140
Ser Gly His Asn Ala

```

145

<210> 1107

<211> 618

<212> DNA

<213> Homo sapiens

<400> 1107

```

acgcgttgat gaagtacctg ccacgcttca gcaatgacgg ctcggtgaac ggcttctata
60
tctttgttat cgatgagacc gaacgcaaac tcaccgaaga ggccctgcgc cacctcaacg
120
agaacctcga agagcgcgct gcccagcgca cacaggcgct ggctgaagcc aaccaacgcc
180
tggcaaaaaca aaatgttcaa acgcaagcgc gccgaagacg cgctgcgtca cgcgcagaaa
240
atggaagccg ggggccagct caccggcggc atcgcccatg atttcaacaa catgctgacc
300
gggattatcg gcagcctgga cttgatgcag cgctacatcn aggccgggcg cagcgacgaa
360
atcggccgnc ttactgacgc cgccgtatcg tccgcccacg gcgcggccgc cctcacccat
420
cggctgctgg cgttctcgcg ccgccagtcg ctggcccccc gcccgctgga cccaaccag
480
ctggtagcgt ccctggagga tctgttccag cgaaccaaag gcgcgcatat cacgctcaaa
540
gtgcaactgg gccgcgatat ctggcccgtg aataccgatg ccagccagtt ggaaaacgcc
600
ctgctcaacc tggcgatc
618

```

<210> 1108

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1108

```

Met Arg Pro Asn Ala Asn Ser Pro Lys Arg Pro Cys Ala Thr Ser Thr
1           5           10           15
Arg Thr Ser Lys Ser Ala Ser Pro Ser Ala His Arg Arg Trp Leu Lys
20           25           30
Pro Thr Asn Ala Trp Gln Asn Lys Met Phe Lys Arg Lys Arg Ala Glu
35           40           45
Asp Ala Leu Arg His Ala Gln Lys Met Glu Ala Gly Gly Gln Leu Thr
50           55           60
Gly Gly Ile Ala His Asp Phe Asn Asn Met Leu Thr Gly Ile Ile Gly
65           70           75           80
Ser Leu Asp Leu Met Gln Arg Tyr Ile Xaa Ala Gly Arg Ser Asp Glu
85           90           95
Ile Gly Arg Leu Thr Asp Ala Ala Val Ser Ser Ala His Arg Ala Ala
100          105          110
Ala Leu Thr His Arg Leu Leu Ala Phe Ser Arg Arg Gln Ser Leu Ala
115          120          125
Pro Arg Pro Leu Asp Pro Asn Gln Leu Val Ala Ser Leu Glu Asp Leu

```

130		135		140											
Phe	Gln	Arg	Thr	Lys	Gly	Ala	His	Ile	Thr	Leu	Lys	Val	Gln	Leu	Gly
145				150					155						160
Arg	Asp	Ile	Trp	Pro	Val	Asn	Thr	Asp	Ala	Ser	Gln	Leu	Glu	Asn	Ala
			165						170					175	
Leu	Leu	Asn	Leu	Ala	Ile										
		180													

<210> 1109
 <211> 325
 <212> DNA
 <213> Homo sapiens

<400> 1109
 accggtgagc atcagggagg caccatgcag acgactctcc catccagtct caagccgtcc
 60
 agcctcaaga tcgtcgcacc gctgggggggc atcctcgtgc ccctggatca ggtgcccgat
 120
 cccgtttttcg ccagaagat ggtgggagac gggatctccc tggaccccat ctcaaacgaa
 180
 ttgctggcgc cggtcgccgg caccgtgacc cagctccaca acgcccacca cgcgctcacg
 240
 atcacgaccc cggaaggcat cgaggttctg gtccatatcg gactggatac cgtgatgctg
 300
 cgcggcgaca gctatccccc ccccn
 325

<210> 1110
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 1110	
Thr Gly Glu His Gln Gly Gly Thr Met Gln Thr Thr Leu Pro Ser Ser	
1 5 10 15	
Leu Lys Pro Ser Leu Lys Ile Val Ala Pro Leu Gly Gly Ile Leu	
20 25 30	
Val Pro Leu Asp Gln Val Pro Asp Pro Val Phe Ala Gln Lys Met Val	
35 40 45	
Gly Asp Gly Ile Ser Leu Asp Pro Ile Ser Asn Glu Leu Leu Ala Pro	
50 55 60	
Val Ala Gly Thr Val Thr Gln Leu His Asn Ala His His Ala Leu Thr	
65 70 75 80	
Ile Thr Thr Pro Glu Gly Ile Glu Val Leu Val His Ile Gly Leu Asp	
85 90 95	
Thr Val Met Leu Arg Gly Asp Ser Tyr Pro Pro Pro	
100 105	

<210> 1111
 <211> 385
 <212> DNA
 <213> Homo sapiens

<400> 1111

nnacgcgtcg ccccggtgcg cctggcagtg ggagaagagc atgaccttac cgagctcgcg
 60
 actgaactcg tcaacgccgc ctatagccgg gttgacatgg tggaacgccg tggcgaattc
 120
 gcagtacgtg gcggcatcgt cgacgtcttc ccaccggtgc tagaacaccc ggtccgtatc
 180
 gatttttttg gtgacgagat cgaggaaatg acctccttcg cggtagccga ccagcgatcc
 240
 accgacgaga ctcaccaaga actgatctgc gctccttgcc gtgagctcat cctcaccgac
 300
 gaggtacgtt cccgagccaa ggctttgctg accgaccatc ccgaattagc tgacatgttg
 360
 gagcggatcg gcaacggtca agctt
 385

<210> 1112

<211> 128

<212> PRT

<213> Homo sapiens

<400> 1112

Xaa	Arg	Val	Ala	Pro	Val	Arg	Leu	Ala	Val	Gly	Glu	Glu	His	Asp	Leu
1				5					10					15	
Thr	Glu	Leu	Ala	Thr	Glu	Leu	Val	Asn	Ala	Ala	Tyr	Ser	Arg	Val	Asp
			20					25					30		
Met	Val	Glu	Arg	Arg	Gly	Glu	Phe	Ala	Val	Arg	Gly	Gly	Ile	Val	Asp
		35					40					45			
Val	Phe	Pro	Pro	Val	Leu	Glu	His	Pro	Val	Arg	Ile	Asp	Phe	Phe	Gly
	50					55					60				
Asp	Glu	Ile	Glu	Glu	Met	Thr	Ser	Phe	Ala	Val	Ala	Asp	Gln	Arg	Ser
65					70				75					80	
Thr	Asp	Glu	Thr	His	Gln	Glu	Leu	Ile	Cys	Ala	Pro	Cys	Arg	Glu	Leu
				85					90					95	
Ile	Leu	Thr	Asp	Glu	Val	Arg	Ser	Arg	Ala	Lys	Ala	Leu	Leu	Thr	Asp
			100					105					110		
His	Pro	Glu	Leu	Ala	Asp	Met	Leu	Glu	Arg	Ile	Gly	Asn	Gly	Gln	Ala
		115					120					125			

<210> 1113

<211> 400

<212> DNA

<213> Homo sapiens

<400> 1113

nnncgaccga tgagcgatcg cgaacccgtc aacctgggat acccctacgt cgagtctttc
 60
 cactcggact tctcggggac cggcgggagtc gatcagaccg accgttctac caatatcgac
 120
 gagcacacca tcgaggagat gcatcagatc gcctcgcggt accccgactc ccgttcggcg
 180
 ttgctgccga tcttgacact ggttcagtcg gtggacggac gcatctcgcc ggctcggtatt
 240
 gagactgcgg ctgaagtgct cggcattacc accgcccagg tatccgggggt ggcgaccttc
 300

tacaccatgt ataagaagca ccctgcgggc cagcatcaca tcggtgtctg caccacggcg
 360
 ctgtgcgccg tcatgggtgg cgaggaggtg cttgcccgtn
 400

<210> 1114
 <211> 133
 <212> PRT
 <213> Homo sapiens

<400> 1114
 Xaa Arg Pro Met Ser Asp Arg Glu Pro Val Asn Leu Gly Tyr Pro Tyr
 1 5 10 15
 Val Glu Ser Phe His Ser Asp Phe Ser Gly Thr Gly Gly Val Asp Gln
 20 25 30
 Thr Asp Arg Ser Thr Asn Ile Asp Glu His Thr Ile Glu Glu Met His
 35 40 45
 Gln Ile Ala Ser Arg Tyr Pro Asp Ser Arg Ser Ala Leu Leu Pro Ile
 50 55 60
 Leu His Leu Val Gln Ser Val Asp Gly Arg Ile Ser Pro Val Gly Ile
 65 70 75 80
 Glu Thr Ala Ala Glu Val Leu Gly Ile Thr Thr Ala Gln Val Ser Gly
 85 90 95
 Val Ala Thr Phe Tyr Thr Met Tyr Lys Lys His Pro Ala Gly Gln His
 100 105 110
 His Ile Gly Val Cys Thr Thr Ala Leu Cys Ala Val Met Gly Gly Glu
 115 120 125
 Glu Val Leu Ala Arg
 130

<210> 1115
 <211> 402
 <212> DNA
 <213> Homo sapiens

<400> 1115
 tctccgactg cacagattag agaaaggact gcgatgacca ttcgcaccac tcatgttggt
 60
 tccctgcccc gcacccccga gctgatcgag gcgaatcgtg cgcgccgtga gggttcgctc
 120
 ggcgaggctg acttcacgtc gctgctgcag gatcagggtg acggcggttg gaagcgtcag
 180
 gctgagattg gcctggatat cgtcaatgac ggcgagtag gtcacgcgat gcttgacacg
 240
 gttgattacg gcgcgtggtg gacgtattcc atctctcggt tcggcgggct gtcctttgag
 300
 gacgtgcagc gttttgatgt gcgtcccccg gctggccgtg acggtcgcct gtctttctcg
 360
 tcgttcgctg agcgccgcga ctggcagcgt ttccggacgc gt
 402

<210> 1116
 <211> 134
 <212> PRT

<213> Homo sapiens

<400> 1116

```

Ser Pro Thr Ala Gln Ile Arg Glu Arg Thr Ala Met Thr Ile Arg Thr
 1           5           10           15
Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Ile Glu Ala Asn
          20           25           30
Arg Ala Arg Arg Glu Gly Ser Leu Gly Glu Ala Asp Phe Thr Ser Leu
          35           40           45
Leu Gln Asp Gln Val Asp Gly Val Val Lys Arg Gln Ala Glu Ile Gly
 50           55           60
Leu Asp Ile Val Asn Asp Gly Glu Tyr Gly His Ala Met Leu Asp Thr
65           70           75           80
Val Asp Tyr Gly Ala Trp Trp Thr Tyr Ser Ile Ser Arg Phe Gly Gly
          85           90           95
Leu Ser Phe Glu Asp Val Gln Arg Phe Asp Val Arg Pro Pro Ala Gly
          100          105          110
Arg Asp Gly Arg Leu Ser Phe Ser Ser Phe Ala Glu Arg Arg Asp Trp
          115          120          125
Gln Arg Phe Arg Thr Arg
          130

```

<210> 1117

<211> 307

<212> DNA

<213> Homo sapiens

<400> 1117

```

ggcgccgggc ttgccctggc tggaagtggc atgcagacct tgggtgcggaa cccgctggct
60
gaccctacc tgctaggtgt atcggctggc gcaagtgtgg gagcaaccgc agtcctcgt
120
ttggggatgt tcacttcgtg gggaactcac cgactcactc ttggtgccct ttagggggcc
180
ttggcggcag ctgcattggt ctatctcatt tccatggcgc aaggaggcat gacgccgctt
240
cggttggtgc tgtcgggcgt ggtgttgctc tcggcgttct cgcgttggcg agtttctctg
300
tctttcg
307

```

<210> 1118

<211> 102

<212> PRT

<213> Homo sapiens

<400> 1118

```

Gly Ala Gly Leu Ala Leu Ala Gly Ser Gly Met Gln Thr Leu Val Arg
 1           5           10           15
Asn Pro Leu Ala Asp Pro Tyr Leu Leu Gly Val Ser Ala Gly Ala Ser
          20           25           30
Val Gly Ala Thr Ala Val Ile Ala Leu Gly Met Phe Thr Ser Trp Gly
          35           40           45
Thr His Arg Leu Thr Leu Gly Ala Leu Val Gly Ala Leu Ala Ala Ala

```

```

      50              55              60
Ala Leu Val Tyr Leu Ile Ser Met Ala Gln Gly Gly Met Thr Pro Leu
65              70              75              80
Arg Leu Val Leu Ser Gly Val Val Leu Ser Ser Ala Phe Ser Arg Trp
      85              90              95
Arg Val Ser Ser Ser Phe
      100

```

<210> 1119
 <211> 353
 <212> DNA
 <213> Homo sapiens

```

<400> 1119
cgcgctccttg agatgcttga gcaggctcggt attgaggatc cagccagggt gatggattcc
60
tatccgcatc aactgtccgg tggccagcgt caacgggttc tgcttgccat ggcgttggtg
120
aactcgccgg atctgctcat ttgtgacgag ccgacgaccg ccttggaactg cacggtgcag
180
tctcaggtac tggcgactat cgatgaggtg cttgactcgg ttggtgccgc atgcctattt
240
attaccacag atttggcggt tgtctcgac atctgccggg agcttatcgt gatgacgtcg
300
ggcaaggtcg ttgaagccgg atcagcgcgt gatgtgttat ctcaccctga tca
353

```

<210> 1120
 <211> 117
 <212> PRT
 <213> Homo sapiens

```

<400> 1120
Arg Val Leu Glu Met Leu Glu Gln Val Gly Ile Glu Asp Pro Ala Arg
1      5      10      15
Val Met Asp Ser Tyr Pro His Gln Leu Ser Gly Gly Gln Arg Gln Arg
20     25     30
Val Leu Leu Ala Met Ala Leu Val Asn Ser Pro Asp Leu Leu Ile Cys
35     40     45
Asp Glu Pro Thr Thr Ala Leu Asp Val Thr Val Gln Ser Gln Val Leu
50     55     60
Ala Thr Ile Asp Glu Val Leu Asp Ser Val Gly Ala Ala Cys Leu Phe
65     70     75     80
Ile Thr His Asp Leu Ala Val Val Ser His Ile Cys Arg Glu Leu Ile
85     90     95
Val Met Thr Ser Gly Lys Val Val Glu Ala Gly Ser Ala Arg Asp Val
100    105    110
Leu Ser His Pro Asp
115

```

<210> 1121
 <211> 406
 <212> DNA
 <213> Homo sapiens

<400> 1121

tgatcaccca tgctccactc gaccgcgcgc tcgacgatgc gacggctgag acgatgctcg
60
cccagggcac ggtgttcata ccgaccttga cgatgatgaa aggcgtcgcc gcgaatctca
120
ccgcagcggg cgttcccggg gtgagctatg cacacgcca cgagagcacg cgcgcgatgc
180
atgccgcggg cgttccgggc ctggccggca ccgacgccta catcgggtcc ttcacacggg
240
catcgcgcgc atacggcgag agcatgcacg acgaagacgc ctacatcggg ctccctcgaac
300
gggcaatgcc gccatacggc gagagcatgc acgacgaact cgctctgctc gtggacgccg
360
gcctgtcaac agccgaagcg ctgcgcgctg ccacctcgac gggcgc
406

<210> 1122

<211> 117

<212> PRT

<213> Homo sapiens

<400> 1122

Met	Leu	Ala	Gln	Gly	Thr	Val	Phe	Ile	Pro	Thr	Leu	Thr	Met	Met	Lys
1				5					10				15		
Gly	Val	Ala	Ala	Asn	Leu	Thr	Ala	Ala	Gly	Val	Pro	Gly	Val	Ser	Tyr
			20					25				30			
Ala	His	Ala	His	Glu	Ser	Thr	Arg	Ala	Met	His	Ala	Ala	Gly	Val	Pro
		35					40				45				
Val	Leu	Ala	Gly	Thr	Asp	Ala	Tyr	Ile	Gly	Ser	Phe	Thr	Arg	Ala	Ser
	50					55					60				
Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Asp	Ala	Tyr	Ile	Gly	Leu
65					70				75					80	
Leu	Glu	Arg	Ala	Met	Pro	Pro	Tyr	Gly	Glu	Ser	Met	His	Asp	Glu	Leu
			85					90					95		
Ala	Leu	Leu	Val	Asp	Ala	Gly	Leu	Ser	Thr	Ala	Glu	Ala	Leu	Arg	Ala
			100				105						110		
Ala	Thr	Ser	Thr	Gly											
			115												

<210> 1123

<211> 337

<212> DNA

<213> Homo sapiens

<400> 1123

gccggcgatg cgttcattaa ggcctaagat gcgccgacgc ctccccgctt tccctgcacct
60
cgcctccacc gcccttgccg cagcggggat ggtgggggtgc tcgtccgagg gggcatcgcc
120
aagcgaatgc tcccctgttg atattgccgc agtgcgcgag gccctgccgc attcgctcgc
180
taaggcgaag ctgcacccgc actccaccaa cgaggatgaa cactcctttt ccatgctcta
240

ccgcgcgcaa gataaggagc aggtcagctt gctggggacg aagtatgagg ccgacggtgc
 300
 acccgtctgc cccgatgacc ccaatgaggc agcgcgc
 337

<210> 1124

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1124

Met	Arg	Ser	Leu	Arg	Pro	Lys	Met	Arg	Arg	Arg	Leu	Pro	Ala	Phe	Leu
1				5				10					15		
Ala	Leu	Ala	Ser	Thr	Ala	Leu	Ala	Ala	Ala	Gly	Met	Val	Gly	Cys	Ser
			20				25						30		
Ser	Glu	Gly	Ala	Ser	Pro	Ser	Glu	Cys	Ser	Pro	Val	Asp	Ile	Ala	Ala
		35					40					45			
Val	Arg	Glu	Ala	Leu	Pro	His	Ser	Leu	Ala	Lys	Ala	Lys	Leu	Asp	Pro
	50					55					60				
His	Ser	Thr	Asn	Glu	Asp	Glu	His	Ser	Phe	Ser	Met	Leu	Tyr	Arg	Ala
65				70					75					80	
Gln	Asp	Lys	Glu	Gln	Val	Ser	Leu	Leu	Gly	Thr	Lys	Tyr	Glu	Ala	Asp
			85						90					95	
Gly	Ala	Pro	Val	Cys	Pro	Asp	Asp	Pro	Asn	Glu	Ala	Ala	Arg		
		100						105					110		

<210> 1125

<211> 555

<212> DNA

<213> Homo sapiens

<400> 1125

nncttgaatc gaatcggcat tgcgtctaaa catgacgttg agacactctc tgctaagctc
 60
 gaagagctga cggcattgct agaacgtgtc gcgcgtaaac actaaggaga catcgggatg
 120
 gctgttaaaa agactactca gaaagaaggc agctcgtgga tcggggaagt tgaaaaatat
 180
 tcccgtaaaa tctggcttgc tggtttaggc gtgtactcga aggttagcag tgacggcggc
 240
 aaatacttcg agacgttggc caaggacggc gagaaggccg agaagttgac caagagccca
 300
 gtcggtaaaa aagtagaggc ggcaaaagcg agcgcgggtt ctgcgaaatc gagcatttcg
 360
 gatacctggg gcaagttgga agagactttc gacaagcgtc tcaacagtgc tatttcgcga
 420
 ttgggcgtgc ccagcaaagc ggaactgaag acgctgcaca gcaaggctga taccctgacc
 480
 aagcaaactc aaaaactcac cgggtgcaaa gtggccccgg ctaaaacggc agccgctaaa
 540
 cctgctgcca agctt
 555

<210> 1126

<211> 146
 <212> PRT
 <213> Homo sapiens

<400> 1126
 Met Ala Val Lys Lys Thr Thr Gln Lys Glu Gly Ser Ser Trp Ile Gly
 1 5 10 15
 Glu Val Glu Lys Tyr Ser Arg Lys Ile Trp Leu Ala Gly Leu Gly Val
 20 25 30
 Tyr Ser Lys Val Ser Ser Asp Gly Gly Lys Tyr Phe Glu Thr Leu Val
 35 40 45
 Lys Asp Gly Glu Lys Ala Glu Lys Leu Thr Lys Ser Pro Val Gly Lys
 50 55 60
 Lys Val Glu Ala Ala Lys Ala Ser Ala Gly Ser Ala Lys Ser Ser Ile
 65 70 75 80
 Ser Asp Thr Trp Gly Lys Leu Glu Glu Thr Phe Asp Lys Arg Leu Asn
 85 90 95
 Ser Ala Ile Ser Arg Leu Gly Val Pro Ser Lys Ala Glu Leu Lys Thr
 100 105 110
 Leu His Ser Lys Val Asp Thr Leu Thr Lys Gln Ile Glu Lys Leu Thr
 115 120 125
 Gly Ala Lys Val Ala Pro Ala Lys Thr Ala Ala Ala Lys Pro Ala Ala
 130 135 140
 Lys Leu
 145

<210> 1127
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 1127
 cccgaccgcg tactcgtggt cgggtgccgga gtgatgggtg cagcacacgc acacgcgctc
 60
 cgcggggtccc tccaggcagt cgtgtgcggc gtggtcgacc tgcaggagcg agcagcgcaa
 120
 tcactcgctt cggaagtggg cgtaccggg ttcaccgacc tgggtgaaggc gatcgagtcg
 180
 accgctccgg acgccgcggt catcgccacg ccggactcgg ctcaccgcca accggctgag
 240
 accgccatcg acgccggcct tgccgtcctg gtcgagaaac cgctcgccac gaccgtcgat
 300
 gacgccgaag cgatcgtgct ccgcgctgaa cgggcccggc tccgtctcat ga
 352

<210> 1128
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 1128
 Pro Asp Arg Val Leu Val Val Gly Ala Gly Val Met Gly Ala Ala His
 1 5 10 15
 Ala His Ala Leu Arg Gly Ser Leu Gln Ala Val Val Cys Gly Val Val

```

      20      25      30
Asp Leu Gln Glu Arg Ala Ala Gln Ser Leu Ala Ser Glu Val Gly Val
      35      40      45
Pro Gly Phe Thr Asp Leu Val Lys Ala Ile Glu Ser Thr Ala Pro Asp
      50      55      60
Ala Ala Val Ile Ala Thr Pro Asp Ser Ala His Arg Gln Pro Ala Glu
65      70      75      80
Thr Ala Ile Asp Ala Gly Leu Ala Val Leu Val Glu Lys Pro Leu Ala
      85      90      95
Thr Thr Val Asp Asp Ala Glu Ala Ile Val Leu Arg Ala Glu Arg Ala
      100      105      110
Gly Val Arg Leu Met
      115

```

<210> 1129
 <211> 336
 <212> DNA
 <213> Homo sapiens

```

<400> 1129
ntggcagccc tggaggagcc gatggtggac ctggacggcg agctgccttt cgtgcgggccc
60
ctgccccaca ttgccgtgct ccaggacgag ctgccgcaac tcttcagga tgacgacgtc
120
ggggccgatg aggaagaggc agagttgcgg ggcgaacaca cgctcacaga gaagtttgctc
180
tgcttgatg actcctttgg ccatgactgc agcttgacct gtgatgactg caggaacgga
240
gggacctgcc tcttgggcct ggatggctgg gattgccccg agggctggac tgggctcatc
300
tgcaatgaga cttggtcctc gggctgcatg gatatt
336

```

<210> 1130
 <211> 112
 <212> PRT
 <213> Homo sapiens

```

<400> 1130
Xaa Ala Ala Leu Glu Glu Pro Met Val Asp Leu Asp Gly Glu Leu Pro
1      5      10      15
Phe Val Arg Pro Leu Pro His Ile Ala Val Leu Gln Asp Glu Leu Pro
      20      25      30
Gln Leu Phe Gln Asp Asp Asp Val Gly Ala Asp Glu Glu Glu Ala Glu
      35      40      45
Leu Arg Gly Glu His Thr Leu Thr Glu Lys Phe Val Cys Leu Asp Asp
      50      55      60
Ser Phe Gly His Asp Cys Ser Leu Thr Cys Asp Asp Cys Arg Asn Gly
65      70      75      80
Gly Thr Cys Leu Leu Gly Leu Asp Gly Trp Asp Cys Pro Glu Gly Trp
      85      90      95
Thr Gly Leu Ile Cys Asn Glu Thr Trp Ser Ser Gly Cys Met Asp Ile
      100      105      110

```

<210> 1131

<211> 672

<212> DNA

<213> Homo sapiens

<400> 1131

```

gcgttggtgg tgctcatggc ccgggaaaat ccgctggatc aatacctctt tgagcacccc
60
gaattattgt tctcgtcctc ggtggaatcg actgtgttgc acccgataa cccgtatgtg
120
ctcggccccg acgtggccgc ggccgccag gaggcatacc tctcccctgc ggacgaagag
180
ttttacgggt cggcctttgc cgggatatgc aaaacgctga caggccagaa cgtactgcga
240
cgtcgcgga atcggctgtt ctggactcgt ccggaacggg ctgtcgacgc catcgacctg
300
cgatcggcgg caggcaaagg gattgacatt atcgacgtgt ccaccgggag ggtcatcggg
360
gtagtgcacg aagccgccgc agaccgtacc gtgcatccag gcgcggtgta cctgcatcag
420
ggggatcagt ggctggtcga cgaatacaac ccggtcgagc accacgccct ggtgcaccag
480
gacctgccgg gatattggac tcaaccgcag tcagcgtcga cggtgagaat ccttcgggag
540
gagagacgtc gcgcttgtgg tcccggatat gtggcgtgcg ggcagggtgga actgacagag
600
caagttgttg ggtatctgcg tcgcgacgaa ttcaccaatg atgtgtggta ctgctggcc
660
ctcgagatgc cc
672

```

<210> 1132

<211> 224

<212> PRT

<213> Homo sapiens

<400> 1132

```

Ala Leu Val Val Leu Met Ala Arg Glu Asn Pro Leu Asp Gln Tyr Leu
1      5      10      15
Phe Glu His Pro Glu Leu Leu Phe Ser Ser Ser Val Glu Ser Thr Val
20     25     30
Leu His Pro Asp Asn Pro Tyr Val Leu Gly Pro His Val Ala Ala Ala
35     40     45
Ala Gln Glu Ala Tyr Leu Ser Pro Ala Asp Glu Glu Phe Tyr Gly Ser
50     55     60
Ala Phe Ala Gly Ile Cys Lys Thr Leu Thr Gly Gln Asn Val Leu Arg
65     70     75     80
Arg Arg Gly Asn Arg Leu Phe Trp Thr Arg Pro Glu Arg Ala Val Asp
85     90     95
Ala Ile Asp Leu Arg Ser Ala Ala Gly Lys Gly Ile Asp Ile Ile Asp
100    105    110
Val Ser Thr Gly Arg Val Ile Gly Val Val Asp Glu Ala Ala Ala Asp
115    120    125
Arg Thr Val His Pro Gly Ala Val Tyr Leu His Gln Gly Asp Gln Trp

```

130		135		140
Leu Val Asp Glu Tyr	Asn Pro Val Glu His His	Ala Leu Val His Gln		
145	150	155	160	
Asp Leu Pro Gly Tyr	Trp Thr Gln Pro Gln Ser	Ala Ser Thr Val Arg		
	165	170	175	
Ile Leu Arg Glu Glu	Arg Arg Arg Ala Cys Gly	Pro Gly Tyr Val Ala		
	180	185	190	
Cys Gly Gln Val Glu	Leu Thr Glu Gln Val Val	Gly Tyr Leu Arg Arg		
	195	200	205	
Asp Glu Phe Thr Asn	Asp Val Trp Tyr Ser Leu	Ala Leu Glu Met Pro		
210	215	220		

<210> 1133

<211> 796

<212> DNA

<213> Homo sapiens

<400> 1133

```

acgcgtgaag ggggggtccag cgggtgtggc actcgatgac aagacagttt gagagcggct
60
tgtctccggg gacctggcgt aggtctcctc tgccttaacc cttggctttt gcacttcctc
120
tgtctgtcct ccatacaagc ttcttgcccc tagggaggac gggcttctta acaggggggag
180
ccggttcctg tcctaaccce actggcatct tacactctgg gagatagctt ccccttgaga
240
ggcgagttag ccacgtaagg ggaggtgggc gatggcttcc cttctgtctt gggttggggg
300
agtcaggtac agtatttttt cttttaaaagc atcattgatc acataataag gtttgtcata
360
gtccttaatc acagacctgt gaaatttgga gaattcacgg cacctaggat gggagtgage
420
ttctgattgt gagctgattt gggagctaac ctcaaggaaa ctctcttgc aagccccctg
480
ctgggtgtcg gggccttcgc cagggaacctc ccgggggactc tggacgctct ttgtctgccc
540
ttccttttcc ctcacctcgc tccccgtga gaaagtgggg ctcatgcagc tcagctcagt
600
gacagagggt ttattagggg tagctctggg acccatcttt tggtgatttc ttctctctct
660
ttctctaattg gaataattgt ttctgtctac acttctttat tttctcctct ctacagctgc
720
cttctaaaaa tgtgcttttc tgttcctgca gaactgaagc ttgcatggcc tttgttgtga
780
ctttcccttc acgcgt
796

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<210> 1134

<211> 147

<212> PRT

<213> Homo sapiens

<400> 1134

Met Gly Pro Arg Ala Thr Pro Asn Lys Pro Ser Val Thr Glu Leu Ser

```

      1           5           10           15
Cys Met Ser Pro Thr Phe Ser Arg Gly Ser Glu Val Arg Glu Lys Glu
      20           25           30
Gly Gln Thr Lys Ser Val Gln Ser Pro Arg Glu Val Pro Gly Glu Gly
      35           40           45
Pro Asp Thr Gln Gln Gly Ala Cys Lys Arg Ser Phe Leu Glu Val Ser
      50           55           60
Ser Gln Ile Ser Ser Gln Ser Glu Ala His Ser His Pro Arg Cys Arg
      65           70           75           80
Glu Phe Ser Lys Phe His Arg Ser Val Ile Lys Asp Tyr Asp Lys Pro
      85           90           95
Tyr Tyr Val Ile Asn Asp Ala Leu Lys Glu Lys Ile Leu Tyr Leu Thr
      100           105           110
Pro Pro Thr Gln Asp Arg Arg Glu Ala Ile Ala His Leu Pro Leu Arg
      115           120           125
Gly Ser Leu Ala Ser Gln Gly Glu Ala Ile Ser Gln Ser Val Arg Cys
      130           135           140
Gln Trp Gly
145

```

<210> 1135

<211> 376

<212> DNA

<213> Homo sapiens

<400> 1135

```

gatcaggcca cacaggacaa cttcgagaag ggctccatct tcccaccctt caccagcatc
60
agaaagatct ctgcgcacat cgctgcagcc gtggctgcaa aagcctacga gctcgggtctg
120
gcgaccgcgc tgccctcccc cagcgacctg gtgaaatatg cagagaactg catgtacact
180
cccgtctacc gcaactaccg gtagtgctgc ggggatcaat tttgcagtaa taaaaaatct
240
actatcaacg cggatggtac tctgttggtt atagtcctctg ctgctaacca cccttggttgc
300
tggtgctgct ggagaggcat tgtacctgtc catgcatata tgatatatat atgttgtaac
360
gttgtgaaag caaact
376

```

<210> 1136

<211> 67

<212> PRT

<213> Homo sapiens

<400> 1136

```

Asp Gln Ala Thr Gln Asp Asn Phe Glu Lys Gly Ser Ile Phe Pro Pro
      1           5           10           15
Phe Thr Ser Ile Arg Lys Ile Ser Ala His Ile Ala Ala Ala Val Ala
      20           25           30
Ala Lys Ala Tyr Glu Leu Gly Leu Ala Thr Arg Leu Pro Pro Pro Ser
      35           40           45
Asp Leu Val Lys Tyr Ala Glu Asn Cys Met Tyr Thr Pro Val Tyr Arg

```

50
Asn Tyr Arg
65

55

60

<210> 1137
<211> 357
<212> DNA
<213> Homo sapiens

<400> 1137
acgcgtcgct ggaacccgaa gatgaagcgc ttcattcttca ccgagcgcgaa cggatatctac
60
atcattgacc tgcaccagtc gctgacctac attgataagg cgtacgcctt cgtcaaggag
120
actgtcgcca agggcggcca gattcttttc gtcggcacga agaagcaggc ccaggagtcc
180
atcggtgagc aggccactcg cggtggcatg ccctatgtca accagcggtg gcttggggga
240
atgctcacta atttccagac catctcgaag cgcattgccc ggctcaagga gctcgaggcc
300
atggactttg acaaggtttc cggctccggt ctcaccaaga aggagctgct tatgctc
357

<210> 1138
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1138
Thr Arg Arg Trp Asn Pro Lys Met Lys Arg Phe Ile Phe Thr Glu Arg
1 5 10 15
Asn Gly Ile Tyr Ile Ile Asp Leu His Gln Ser Leu Thr Tyr Ile Asp
20 25 30
Lys Ala Tyr Ala Phe Val Lys Glu Thr Val Ala Lys Gly Gly Gln Ile
35 40 45
Leu Phe Val Gly Thr Lys Lys Gln Ala Gln Glu Ser Ile Val Glu Gln
50 55 60
Ala Thr Arg Val Gly Met Pro Tyr Val Asn Gln Arg Trp Leu Gly Gly
65 70 75 80
Met Leu Thr Asn Phe Gln Thr Ile Ser Lys Arg Ile Ala Arg Leu Lys
85 90 95
Glu Leu Glu Ala Met Asp Phe Asp Lys Val Ser Gly Ser Gly Leu Thr
100 105 110
Lys Lys Glu Leu Leu Met Leu
115

<210> 1139
<211> 456
<212> DNA
<213> Homo sapiens

<400> 1139
gtgcacaggc cgtctgaggc catgccgcgg acgatcgatc cgagtatggc ggcaccttca
60

ccaatcccgt aggaccgctc tcgtccagca tcgaccaagg cgctgttgag gcgttcggct
 120
 tcggtaatga actcgatgcg ctcaatatcc acgggggtag cgaaatcgta gatcttggcc
 180
 agactgaggc cttggaggag cgcggccgctc ggggggacgt ggcctgcggc cgggcgttcc
 240
 ttgcttctcaa ggacttcgctc gtcgcggctg acaaggaata cgtttgtgtg gtcgcctgca
 300
 atgcatgctc gagcgtggtg accatcgagg tgaaggacgg ttctggcata gaggtcatcg
 360
 tccacatcgg ccacagttag ttcgacgact cctgagtcga ctagatgacg cgccttctct
 420
 gccgcgtctt cgctgacgctc ggccaggacc gctagc
 456

<210> 1140
 <211> 122
 <212> PRT
 <213> Homo sapiens

<400> 1140
 Met Trp Thr Met Thr Ser Met Pro Lys Pro Ser Phe Thr Ser Met Val
 1 5 10 15
 Thr Thr Leu Glu His Ala Leu Gln Ala Thr Thr Gln Thr Tyr Ser Leu
 20 25 30
 Ser Ala Ala Thr Thr Lys Ser Leu Arg Ala Arg Asn Ala Arg Pro Gln
 35 40 45
 Ala Thr Ser Pro Arg Arg Pro Arg Ser Ser Lys Ala Ser Val Trp Pro
 50 55 60
 Arg Ser Thr Ile Ser Leu Pro Pro Trp Ile Leu Ser Ala Ser Ser Ser
 65 70 75 80
 Leu Pro Lys Pro Asn Ala Ser Thr Ala Pro Trp Ser Met Leu Asp Glu
 85 90 95
 Thr Gly Pro Thr Gly Leu Val Lys Val Pro Pro Tyr Ser Asp Arg Ser
 100 105 110
 Ser Ala Ala Trp Pro Gln Thr Thr Cys Ala
 115 120

<210> 1141
 <211> 354
 <212> DNA
 <213> Homo sapiens

<400> 1141
 ggcgccatgc tcggcgggct ggtgctgggt gtggccgaag cctttggcgc cgatatcttc
 60
 ggcgaccagt acaaggacgt ggtggcggtt ggctgttggt ttctggtgct gttgttccgt
 120
 ccgaccggca ttctggggccg tccggaggtt gagaaagtat gagcagatat cttaaactcg
 180
 cgtttttcag cgccctgttg gtgtggggccg tggcctttcc ggtactcggc ctcaagctga
 240
 gcattgtcgg gatcaaccac gaagtgcatt gcaccgggtcc cgtgaccttg accatcatcg
 300

ccctgtgctc ggtgccgatg ttctgcgcg tgctgtttac ccagcaagtc ggtg
354

<210> 1142
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1142
Gly Ala Met Leu Gly Gly Leu Val Leu Gly Val Ala Glu Ala Phe Gly
1 5 10 15
Ala Asp Ile Phe Gly Asp Gln Tyr Lys Asp Val Val Ala Phe Gly Leu
20 25 30
Leu Val Leu Val Leu Leu Phe Arg Pro Thr Gly Ile Leu Gly Arg Pro
35 40 45
Glu Val Glu Lys Val
50

<210> 1143
<211> 353
<212> DNA
<213> Homo sapiens

<400> 1143
acgcgttgca catccccag gaccatcaac cgcggcattg ccgcatagac ctggagatcc
60
catgcaacgt gaaatgaagt tcgaatcgat caaggcaaag gccaaaggcga tgctcatcgg
120
cgcagccgac gacacagcaa gcgcaggcgc gaccaaccga gggtaggtca acagcgccgc
180
attcgaaatc ctggcccacg tggccgtcaa tgcccaaacac tacgcgctct ccgagagacc
240
ggcgctggag gagttcgcca agagcttcca gccgcgcaac aaccaggact acgtggccgc
300
gatcgccaag aaggccgcga accacacat gcatcccggc aggcagtcga ttt
353

<210> 1144
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1144
Met His Gly Val Val Arg Gly Leu Leu Gly Asp Arg Gly His Val Val
1 5 10 15
Leu Val Val Ala Arg Leu Glu Ala Leu Gly Glu Leu Leu Gln Arg Arg
20 25 30
Ser Leu Gly Glu Arg Val Val Leu Gly Ile Asp Gly His Val Gly Gln
35 40 45
Asp Phe Glu Cys Gly Ala Val Glu Pro Pro Ser Val Gly Arg Ala Cys
50 55 60
Ala Cys Cys Val Val Gly Cys Ala Asp Glu His Arg Leu Gly Leu Cys
65 70 75 80
Leu Asp Arg Phe Glu Leu His Phe Thr Leu His Gly Ile Ser Arg Ser

Met Arg Gln Cys Arg Gly
100

85

90

95

<210> 1145
<211> 360
<212> DNA
<213> Homo sapiens

<400> 1145
gtcttcggcg ggctcggcct gttctattgc gtcatgaccc cgggtgactg gttctcggcc
60
catgaagtgg ccggcacctg ggtactcggg ctgtcggcgg cgatggctct gatgggtgttt
120
ttctacgtcc aggtcatcgc caagaagatc aatcctcgac cctccgacga gaaggacgcc
180
gaggtgatcg acggggctgg tccggtcggg ttcttcccgc cacagagtat ctggccgttc
240
tggtgcgcgc tcgttgctgc catcatgtgc ctcgccccga tcttcggctg gtggatctct
300
ctgctcgggc tgggcattgt tatctgggcc gcctcggggtt gggcttttga gtactaccgc
360

<210> 1146
<211> 120
<212> PRT
<213> Homo sapiens

<400> 1146
Val Phe Gly Gly Leu Gly Leu Phe Tyr Cys Val Met Thr Pro Val Tyr
1 5 10 15
Trp Phe Ser Ala His Glu Val Ala Gly Thr Trp Val Leu Gly Leu Ser
20 25 30
Ala Ala Met Ala Leu Met Val Phe Phe Tyr Val Gln Val Ile Ala Lys
35 40 45
Lys Ile Asn Pro Arg Pro Ser Asp Glu Lys Asp Ala Glu Val Ile Asp
50 55 60
Gly Ala Gly Pro Val Gly Phe Phe Pro Pro Gln Ser Ile Trp Pro Phe
65 70 75 80
Trp Cys Ala Leu Val Val Ala Ile Met Cys Leu Gly Pro Ile Phe Gly
85 90 95
Trp Trp Ile Ser Leu Leu Gly Leu Gly Ile Val Ile Trp Ala Ala Ser
100 105 110
Gly Trp Ala Phe Glu Tyr Tyr Arg
115 120

<210> 1147
<211> 409
<212> DNA
<213> Homo sapiens

<400> 1147
tgtacattgg ctatgcagtc tggcctcctg aaggttatga tagtagccaa aaatatagaa
60

gcaaaaaagg catccacctt cttcatcaat ccagaattga tcatgctcat gcctgtgggt
 120
 ggatcactat gtgctctcca aattgggagg ggaagtctac tctcctctct cctctctctc
 180
 ccaccttccc ctctctcttc tctcctttct attcccaggg cagtggaaca tgatgaggtt
 240
 cttttccctt catggatata ctctttctgc cctccacata aaggggcatt gatggatctt
 300
 caagaatggg atgcctttcc ctagaaaggc taaatattca tgaggctgaa tgtgaggatc
 360
 cagagtacac tgaaatataa ctgggtcatca gtacacatag aatctgatn
 409

<210> 1148
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1148
 Met Gln Ser Gly Leu Leu Lys Val Met Ile Val Ala Lys Asn Ile Glu
 1 5 10 15
 Ala Lys Lys Ala Ser Thr Phe Phe Ile Asn Pro Glu Leu Ile Met Leu
 20 25 30
 Met Pro Val Gly Gly Ser Leu Cys Ala Leu Gln Ile Gly Arg Gly Ser
 35 40 45
 Leu Leu Ser Ser Leu Leu Ser Leu Pro Pro Ser Pro Leu Ser Ser Leu
 50 55 60
 Leu Ser Ile Pro Arg Ala Val Glu His Asp Glu Val Leu Phe Pro Ser
 65 70 75 80
 Trp Ile Ser Ser Phe Cys Pro Pro His Lys Gly Ala Leu Met Asp Leu
 85 90 95
 Gln Glu Trp Asp Ala Phe Pro
 100

<210> 1149
 <211> 309
 <212> DNA
 <213> Homo sapiens

<400> 1149
 gtcgacttct gcatggaaaa acgcgatctg gtgattgagc acgttgcgga gatgtacggc
 60
 cgtgaggcgg tatcgcagat cattaccttc ggtaccatgg cggcgaaagc gggtattcgt
 120
 gacgtggggc gtgtactggg tcacccgtat ggcttcgtcg atcgcatctc caagctgggtg
 180
 ccgcccgatc cgggcatgac gctggaaaaa gcctttgccg ccgaaccgca gttgccggaa
 240
 atctacgagg ccgatgagga agtcaaagcg ctgatcgaca tggcgcgcaa gctgggaagg
 300
 gtgacgcgg
 309

<210> 1150

<211> 103
 <212> PRT
 <213> Homo sapiens

<400> 1150
 Val Asp Phe Cys Met Glu Lys Arg Asp Leu Val Ile Glu His Val Ala
 1 5 10 15
 Glu Met Tyr Gly Arg Glu Ala Val Ser Gln Ile Ile Thr Phe Gly Thr
 20 25 30
 Met Ala Ala Lys Ala Val Ile Arg Asp Val Gly Arg Val Leu Gly His
 35 40 45
 Pro Tyr Gly Phe Val Asp Arg Ile Ser Lys Leu Val Pro Pro Asp Pro
 50 55 60
 Gly Met Thr Leu Glu Lys Ala Phe Ala Ala Glu Pro Gln Leu Pro Glu
 65 70 75 80
 Ile Tyr Glu Ala Asp Glu Glu Val Lys Ala Leu Ile Asp Met Ala Arg
 85 90 95
 Lys Leu Gly Arg Val Thr Arg
 100

<210> 1151
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1151
 gcgcgcattt tttgcaaccc aagcgacgtc attatggccg agtcgccggc ttatgtcggg
 60
 gcgctcaata ccttcgcctc gtaccaaact gaggtcattc acgtcgacat ggacgacagc
 120
 ggggttggttc cggaatccct gcgtgagaaa gtgactgcag cgcgtaaga cggcaagtcg
 180
 gtgaagttcc ttacacggt tcctaactac tcgaaccggt cgggaatctc gcaatccacc
 240
 gagcgtcgcc gggagatcct agcgggtggct gacgagctgg atctgttggt ggttgaggac
 300
 aaccgtagc gggtactcaa cctcgatggt gatccactgc cgacgttgaa gtcgatggat
 360

<210> 1152
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1152
 Ala Arg Ile Phe Cys Asn Pro Ser Asp Val Ile Met Ala Glu Ser Pro
 1 5 10 15
 Ala Tyr Val Gly Ala Leu Asn Thr Phe Ala Ser Tyr Gln Thr Glu Val
 20 25 30
 Ile His Val Asp Met Asp Asp Ser Gly Leu Val Pro Glu Ser Leu Arg
 35 40 45
 Glu Lys Val Thr Ala Ala Arg Gln Asp Gly Lys Ser Val Lys Phe Leu
 50 55 60
 Tyr Thr Val Pro Asn Tyr Ser Asn Pro Ser Gly Ile Ser Gln Ser Thr

```

65          70          75          80
Glu Arg Arg Arg Glu Ile Leu Ala Val Ala Asp Glu Leu Asp Leu Leu
          85          90          95
Val Val Glu Asp Asn Pro Tyr Gly Leu Leu Asn Leu Asp Gly Asp Pro
          100          105          110
Leu Pro Thr Leu Lys Ser Met Asp
          115          120

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<210> 1153
 <211> 416
 <212> DNA
 <213> Homo sapiens

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<400> 1153
gcgtggattc gtcctggcgg cgctcgctacc gacctgccc agaccgggct cgaccagttg
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cgtgacctca tcaagcggat ggaaaagtac ctccccgaga tcggtcagtt ctgcaatgag
120
aatccgatct ttaaggcccc cactcagggc attgggttac ctgatctgtc tacctgtatg
180
gccctgggag ttactgggtc tgctctgcgc gctaccggcc tgccgtggga cctgcgcaag
240
accagccct attgcgatta cgacacgtat gacttcgacg tcgccacctg ggatacctgt
300
gactgttacg ggcgtttccg catccgcctg gaagagatgg accagtcggt gcgcattctc
360
aagcaatgcc tcaaacgcct cgaggacacc cagggtgacc gtaatatggt cgagga
416

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<210> 1154
 <211> 138
 <212> PRT
 <213> Homo sapiens

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<400> 1154
Ala Trp Ile Arg Pro Gly Gly Val Ala Thr Asp Leu Pro Glu Thr Gly
1      5      10      15
Leu Asp Gln Leu Arg Asp Leu Ile Lys Arg Met Glu Lys Tyr Leu Pro
20     25     30
Glu Ile Gly Gln Phe Cys Asn Glu Asn Pro Ile Phe Lys Ala Arg Thr
35     40     45
Gln Gly Ile Gly Tyr Ala Asp Leu Ser Thr Cys Met Ala Leu Gly Val
50     55     60
Thr Gly Pro Ala Leu Arg Ala Thr Gly Leu Pro Trp Asp Leu Arg Lys
65     70     75     80
Thr Gln Pro Tyr Cys Asp Tyr Asp Thr Tyr Asp Phe Asp Val Ala Thr
85     90     95
Trp Asp Thr Cys Asp Cys Tyr Gly Arg Phe Arg Ile Arg Leu Glu Glu
100    105    110
Met Asp Gln Ser Val Arg Ile Leu Lys Gln Cys Leu Lys Arg Leu Glu
115    120    125
Asp Thr Gln Gly Asp Arg Asn Met Val Glu
130    135

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<210> 1155
 <211> 339
 <212> DNA
 <213> Homo sapiens

<400> 1155
 cttaagttat tttggtcttt gcctctctcc tcaggttggtg aagattacag aaatctggga
 60
 tggcttatgg gacgcttctc agccctaagt aggaaaacag cagtgaaaat ggcaacaaaa
 120
 acatcacgca ggactggggg ttttggggaa acagctcact ttagagcagt gcagtgtaga
 180
 gctttccgctc ttctaccagg gtccaccttt aacactgttt atctgaaaat tttccccctg
 240
 gcttactcgc ttgcagctgc ccactttgca gaaagatggc gctctgatct ctacgctccc
 300
 tgttccttca gggactccat agtatTTTTT ttcacgcgt
 339

<210> 1156
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1156
 Met Gly Arg Phe Ser Ala Leu Ser Arg Lys Thr Ala Val Lys Met Ala
 1 5 10 15
 Thr Lys Thr Ser Arg Arg Thr Gly Gly Phe Gly Glu Thr Ala His Phe
 20 25 30
 Arg Ala Val Gln Cys Arg Ala Phe Arg Leu Leu Pro Gly Ser Thr Phe
 35 40 45
 Asn Thr Val Tyr Leu Lys Ile Phe Pro Leu Ala Tyr Ser Leu Ala Ala
 50 55 60
 Ala His Phe Ala Glu Arg Trp Arg Ser Asp Leu Tyr Ala Pro Cys Ser
 65 70 75 80
 Phe Arg Asp Ser Ile Val Phe Phe Phe Thr Arg
 85 90

<210> 1157
 <211> 426
 <212> DNA
 <213> Homo sapiens

<400> 1157
 nnacagcttc tctccgaccc ggcggcggtt gcacacgtcc ccgtctgagg agtattcgtg
 60
 ctggcaaaac tcgtgacccg acacctgagg gcctatcggt tgcacgttgc cgtcatcatc
 120
 gttatgcagg tttgcgcca aatcgcggtc ctgaccttgc caaccatcaa cgcagacatc
 180
 atcaacaagg gcgtcgtgac agcggatacc ggatatgtca ccaccactc cctcttcatg
 240
 ctggcggtcg ctttagggca ggccatctgc caggtcattg cggtttatct cgccgctcag
 300

gtggcgatgg gaatgggccc tgacgttcgc gacgccatct tcacccgcac ccttgacttc
 360
 tcggccccggg agatcaacaa attcggagca ccatcactca ttacccggac taccaacgac
 420
 gtccag
 426

<210> 1158
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 1158
 Val Leu Ala Lys Leu Val Thr Arg His Leu Arg Ala Tyr Arg Leu His
 1 5 10 15
 Val Ala Val Ile Ile Val Met Gln Val Cys Ala Gln Ile Ala Ala Leu
 20 25 30
 Thr Leu Pro Thr Ile Asn Ala Asp Ile Ile Asn Lys Gly Val Val Thr
 35 40 45
 Ala Asp Thr Gly Tyr Val Thr Thr His Ser Leu Phe Met Leu Ala Val
 50 55 60
 Ala Leu Gly Gln Ala Ile Cys Gln Val Ile Ala Val Tyr Leu Ala Ala
 65 70 75 80
 Gln Val Ala Met Gly Met Gly Arg Asp Val Arg Asp Ala Ile Phe Thr
 85 90 95
 Arg Thr Leu Asp Phe Ser Ala Arg Glu Ile Asn Lys Phe Gly Ala Pro
 100 105 110
 Ser Leu Ile Thr Arg Thr Thr Asn Asp Val Gln
 115 120

<210> 1159
 <211> 434
 <212> DNA
 <213> Homo sapiens

<400> 1159
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 ggacgaggca ggagcaggcc gggctctcgc catgggtcac tgtcgctct gccacgggaa
 120
 gttttcctcg agaagcctgc gcagcatctc cgagagggcg cctggagcga gcatggagag
 180
 gccatccgca gaggagcgcg tgctcgtagc ggacttccag cgctgcttg gtgtggctgt
 240
 ccgccaggac cccaccttgt ctccgtttgt ctgcaagagc tgccacgccc agttctacca
 300
 gtgccacagc cttctcaagt ccttcctgca gaggggtcaac gcctccccgg ctggtcgccc
 360
 gaagccttgt gcaaaggtcg gtgcccagcc cccaacaggg gcagaggagg gagcgtgtct
 420
 ggtggatctg atca
 434

<210> 1160

<211> 114
 <212> PRT
 <213> Homo sapiens

<400> 1160
 Met Gly His Cys Arg Leu Cys His Gly Lys Phe Ser Ser Arg Ser Leu
 1 5 10 15
 Arg Ser Ile Ser Glu Arg Ala Pro Gly Ala Ser Met Glu Arg Pro Ser
 20 25 30
 Ala Glu Glu Arg Val Leu Val Arg Asp Phe Gln Arg Leu Leu Gly Val
 35 40 45
 Ala Val Arg Gln Asp Pro Thr Leu Ser Pro Phe Val Cys Lys Ser Cys
 50 55 60
 His Ala Gln Phe Tyr Gln Cys His Ser Leu Leu Lys Ser Phe Leu Gln
 65 70 75 80
 Arg Val Asn Ala Ser Pro Ala Gly Arg Arg Lys Pro Cys Ala Lys Val
 85 90 95
 Gly Ala Gln Pro Pro Thr Gly Ala Glu Glu Gly Ala Cys Leu Val Asp
 100 105 110
 Leu Ile

<210> 1161
 <211> 355
 <212> DNA
 <213> Homo sapiens

<400> 1161
 ctgcacacac accaggccac gccacgagg acggccagtc agcatgcagc caatacaccc
 60
 acagagggat ggggagcagc cctcagtgcc agctccaaca ggcccactgc aggtcctgtc
 120
 actgcaccca aggagctgcc ttccatttca cctgacattt ccactaaggg cccagcgttt
 180
 atcattccag aagagcagca ggcagaacct tcacctccca agagctgcaa gtgcgctgtg
 240
 gcaggaaaag aagatctggc gtctgaagtc agctcctgct ctccaggaaa agagggacga
 300
 tgacatagga cttgagcaaa atgagagccc cgtgatggga gagaacacct gatca
 355

<210> 1162
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1162
 Met Gln Pro Ile His Pro Gln Arg Asp Gly Glu Gln Pro Ser Val Pro
 1 5 10 15
 Ala Pro Thr Gly Pro Leu Gln Val Leu Ser Leu His Pro Arg Ser Cys
 20 25 30
 Leu Pro Phe His Leu Thr Phe Pro Leu Arg Ala Gln Arg Leu Ser Phe
 35 40 45
 Gln Lys Ser Ser Arg Gln Asn Leu His Leu Pro Arg Ala Ala Ser Ala

50 55 60
 Leu Trp Gln Glu Lys Lys Ile Trp Arg Leu Lys Ser Ala Pro Ala Leu
 65 70 75 80
 Gln Glu Lys Arg Asp Asp Asp Ile Gly Leu Glu Gln Asn Glu Ser Pro
 85 90 95
 Val Met Gly Glu Asn Thr
 100

<210> 1163

<211> 466

<212> DNA

<213> Homo sapiens

<400> 1163

ngcgcgccag gaagcgggag gtcagctgta caccagggt aatagaactt ctaccctcag
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 aggagtcaaa gagaaggcag aactatggca ggaaagctcc ggaagtccca catccctgga
 120
 gtgagcatct ggcagctggt ggaggagatc cctgaaggct gcagcacgcc ggactttgag
 180
 cagaagcccg tcacctcggc tctgccagag gggaaaaatg ctgtctttcg ggctgtggtc
 240
 tgtggggagc ccaggcccga ggtgcgttgg cagaactcca aaggtgacct cagtgattcc
 300
 agcaagtaca agatctcctc cagccctggc agcaaggagc acgtgctgca gatcaacaag
 360
 ctgacaggcg aggacacgga tctgtaccac tgcacagcag taaatgcgta cggagaggcc
 420
 gcttgctcag tgagactcac cgtcatcgaa gttggctttc ggaaga
 466

<210> 1164

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1164

Met Ala Gly Lys Leu Arg Lys Ser His Ile Pro Gly Val Ser Ile Trp
 1 5 10 15
 Gln Leu Val Glu Ile Pro Glu Gly Cys Ser Thr Pro Asp Phe Glu
 20 25 30
 Gln Lys Pro Val Thr Ser Ala Leu Pro Glu Gly Lys Asn Ala Val Phe
 35 40 45
 Arg Ala Val Val Cys Gly Glu Pro Arg Pro Glu Val Arg Trp Gln Asn
 50 55 60
 Ser Lys Gly Asp Leu Ser Asp Ser Ser Lys Tyr Lys Ile Ser Ser Ser
 65 70 75 80
 Pro Gly Ser Lys Glu His Val Leu Gln Ile Asn Lys Leu Thr Gly Glu
 85 90 95
 Asp Thr Asp Leu Tyr His Cys Thr Ala Val Asn Ala Tyr Gly Glu Ala
 100 105 110
 Ala Cys Ser Val Arg Leu Thr Val Ile Glu Val Gly Phe Arg Lys
 115 120 125

<210> 1165
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 1165
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 60
 tgcttttagta aagtccttgt tgagccgcgt ctgctcaagc tcaacttgac nattatgtgt
 120
 ctgcacattc tgctgatgtc cacgttcgtg gccctgcccg gtcagttggc tgcagcagga
 180
 ttccccgccg ctgaacactg gaaagtgtat ctggtgacga tgctcatctc cttegtctcc
 240
 gttgtccctt tcattatcta tgcagaagtg aaacgccgca tgaagcgcgt attcctgacg
 300
 tgtgttgccg tgctgttgat tgccgaaatc gtactatggg gctccggtcc acacttctgg
 360
 gaactgggtca tcggcgtaga gcttttcttc ctgcgcttta atctcatgga agcc
 414

<210> 1166
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 1166
 Trp Val Val Pro Asp Thr Xaa Asn His Val Leu Asn Arg Ile Ser Gly
 1 5 10 15
 Met Val Lys Gly Cys Phe Ser Lys Val Leu Val Glu Pro Arg Leu Leu
 20 25 30
 Lys Leu Asn Leu Thr Ile Met Cys Leu His Ile Leu Leu Met Ser Thr
 35 40 45
 Phe Val Ala Leu Pro Gly Gln Leu Ala Ala Ala Gly Phe Pro Ala Ala
 50 55 60
 Glu His Trp Lys Val Tyr Leu Val Thr Met Leu Ile Ser Phe Val Ser
 65 70 75 80
 Val Val Pro Phe Ile Ile Tyr Ala Glu Val Lys Arg Arg Met Lys Arg
 85 90 95
 Val Phe Leu Thr Cys Val Ala Leu Leu Leu Ile Ala Glu Ile Val Leu
 100 105 110
 Trp Gly Ser Gly Pro His Phe Trp Glu Leu Val Ile Gly Val Gln Leu
 115 120 125
 Phe Phe Leu Ala Phe Asn Leu Met Glu Ala
 130 135

<210> 1167
 <211> 464
 <212> DNA
 <213> Homo sapiens

<400> 1167
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 60

ctgttgggac cggctggcta aggcctgggc accggtagcg gcctgggtgga taccctcatg
 120
 tagccgggtg acctgcctga ccatcttcgg caaaccagtg cgcagttgtg tggatgaactc
 180
 attgaccctt cgagacagtc gtgaggaacc gtcagcaagt tcgtcgatgc cgctcgatgc
 240
 gctcttgcca gagttcggat ccttgatcgc catcgccttg acggccaccc ccgaccacgc
 300
 ccgcacgccc agggcgtagc catcggtcat cgcgtcgcgg acgatgggta ccaggtcgtg
 360
 gcattcctgc gcggtgtggc ttgcacgca tcgacgcagg aagtcagcct cgccccggga
 420
 cagggcttcc ttactaagtt ccgcggtttt ctttcccgac gcgt
 464

<210> 1168

<211> 110

<212> PRT

<213> Homo sapiens

<400> 1168

Met	Thr	Asp	Gly	Tyr	Ala	Leu	Gly	Val	Arg	Ala	Gly	Ser	Gly	Val	Ala
1				5					10					15	
Val	Lys	Ala	Met	Ala	Ile	Lys	Asp	Pro	Asn	Ser	Gly	Lys	Ser	Ile	Asp
			20					25					30		
Asp	Gly	Ile	Asp	Glu	Leu	Ala	Asp	Gly	Ser	Ser	Arg	Leu	Ser	Arg	Gly
		35					40					45			
Val	Asn	Glu	Phe	Thr	Thr	Gln	Leu	Arg	Thr	Gly	Leu	Pro	Lys	Met	Val
	50					55					60				
Arg	Gln	Val	Thr	Arg	Leu	His	Glu	Gly	Ile	His	Gln	Ala	Ala	Thr	Gly
65					70				75					80	
Ala	Gln	Ala	Leu	Ala	Ser	Arg	Ser	Gln	Gln	Leu	Lys	Ala	Gly	Gly	Val
			85					90						95	
Lys	Leu	Ser	Ser	Gly	Ala	Ala	Thr	Leu	Ala	His	Gly	Val	Asp		
			100					105					110		

<210> 1169

<211> 486

<212> DNA

<213> Homo sapiens

<400> 1169

nacgcgtgaa gggagcagaa cggacaccag ttactagtgg ctctgggtcgg ggacagcctc
 60
 ctagagcctt tctggccaat gggaacagga atagcccgagg gctttctagc tgctatggac
 120
 tctgcctgga tgggtccgaag ttggtctcta ggaacgagcc ctttggaagt gctggcagag
 180
 agggaaagta ttacaggtt gctgcctcag accaccctg agaatgtgag taagaacttc
 240
 agccagtaca gtatcgaccc tgtcactcgg tatcccaata tcaacgtcaa cttcctccgg
 300
 ccaagccagg tgcgccattt atatgatact ggcgaaacaa aagatattca cctggaaatg
 360

gagagcctgg tgaattcccg aaccaccccc aaattgactc gcaatgagtc tgtagctcgt
 420
 tcaagcaaac tgctgggttg gtgccagagg cagacagatg gctatgcagg ggtaaactgtg
 480
 acagat
 486

<210> 1170
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 1170
 Arg Glu Gln Asn Gly His Gln Leu Leu Val Ala Leu Val Gly Asp Ser
 1 5 10 15
 Leu Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Ile Ala Arg Gly Phe
 20 25 30
 Leu Ala Ala Met Asp Ser Ala Trp Met Val Arg Ser Trp Ser Leu Gly
 35 40 45
 Thr Ser Pro Leu Glu Val Leu Ala Glu Arg Glu Ser Ile Tyr Arg Leu
 50 55 60
 Leu Pro Gln Thr Thr Pro Glu Asn Val Ser Lys Asn Phe Ser Gln Tyr
 65 70 75 80
 Ser Ile Asp Pro Val Thr Arg Tyr Pro Asn Ile Asn Val Asn Phe Leu
 85 90 95
 Arg Pro Ser Gln Val Arg His Leu Tyr Asp Thr Gly Glu Thr Lys Asp
 100 105 110
 Ile His Leu Glu Met Glu Ser Leu Val Asn Ser Arg Thr Thr Pro Lys
 115 120 125
 Leu Thr Arg Asn Glu Ser Val Ala Arg Ser Ser Lys Leu Leu Gly Trp
 130 135 140
 Cys Gln Arg Gln Thr Asp Gly Tyr Ala Gly Val Asn Val Thr Asp
 145 150 155

<210> 1171
 <211> 429
 <212> DNA
 <213> Homo sapiens

<400> 1171
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 60
 ggcagcgcca ggtgctggcg ctgcccagagg ccccgctgcca agtggggccc atagcagccg
 120
 actcgctaga ccctcccaaa acgcacacca cgcgcgacca ggaccgagag gcccgcacgg
 180
 ccctgctagg ccacaaacac tccactgtct ccagggtaaa agacaaacac agcctcgctt
 240
 gtccttccaa gagtacaacc tctgtctgat gaaaaacaaa cgacccagag aggaggcagc
 300
 tgccgggaca ctgcaggctg ggcccggcgc gcccttgag ggcagggtcaa aatcccggaa
 360
 caggcacagt gttcaggctg attgactgtc ccaggccagg gcggcctcaa ctgccagagc
 420

acctcctac
429

<210> 1172

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1172

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Met Gln Trp Glu Pro Arg Ala Gly Ser Ala Glu Ala Ala Pro Gly Ala
 1           5           10           15
Gly Ala Ala Arg Gly Pro Val Pro Ser Gly Ala His Ser Ser Arg Leu
          20          25          30
Ala Arg Pro Ser Gln Asn Ala His His Ala Arg Pro Gly Pro Arg Gly
          35          40          45
Pro His Gly Pro Ala Arg Pro Gln Thr Leu His Cys Leu Gln Gly Lys
          50          55          60
Arg Gln Thr Gln Pro Arg Leu Ser Leu Gln Glu Tyr Asn Leu Cys Leu
65          70          75          80
Met Lys Asn Lys Arg Pro Arg Glu Glu Ala Ala Ala Gly Thr Leu Gln
          85          90          95
Ala Gly Pro Ala Ala Pro Leu Glu Gly Arg Ser Lys Ser Arg Asn Arg
          100          105          110
His Ser Val Gln Ala Asp
          115

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<210> 1173

<211> 435

<212> DNA

<213> Homo sapiens

<400> 1173

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cgcgctcaatg acgacggcga gcattctgcc gagcaggtga tgcgagccac ccgcggtgct
60
ggacttggggg ccgaggccaa gcgtcgcatc atcttgggta cctatgcctt gtcggctggg
120
tactatgacg cctactacgg ctcggtcag aaagtccgta ccctcatcca acgcgacttc
180
gagaaagcat ggcagatgtg cgatgtgctc gtgtcaccgg ccacgccaac gactgccttc
240
cggctgggtg agcgtactgc tgacccgatg gcgatgtacc gtcctgatct atgcacggtc
300
ccggccaata tggccggaag tcccgcagga tctttcccga tcggtctatc agagaccgac
360
ggcatgccccg tcggcatgca ggtgatggcg ccaatcatgg cggacgatcg aatctaccga
420
gttggggccg ctcta
435

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<210> 1174

<211> 145

<212> PRT

<213> Homo sapiens

<400> 1174

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Arg Val Asn Asp Asp Gly Glu His Ser Ala Glu Gln Val Met Arg Ala
 1           5           10           15
Thr Arg Gly Ala Gly Leu Gly Ala Glu Ala Lys Arg Arg Ile Ile Leu
      20           25           30
Gly Thr Tyr Ala Leu Ser Ala Gly Tyr Tyr Asp Ala Tyr Tyr Gly Ser
      35           40           45
Ala Gln Lys Val Arg Thr Leu Ile Gln Arg Asp Phe Glu Lys Ala Trp
      50           55           60
Gln Met Cys Asp Val Leu Val Ser Pro Ala Thr Pro Thr Thr Ala Phe
65           70           75           80
Arg Leu Gly Glu Arg Thr Ala Asp Pro Met Ala Met Tyr Arg Ser Asp
      85           90           95
Leu Cys Thr Val Pro Ala Asn Met Ala Gly Ser Pro Ala Gly Ser Phe
      100          105          110
Pro Ile Gly Leu Ser Glu Thr Asp Gly Met Pro Val Gly Met Gln Val
      115          120          125
Met Ala Pro Ile Met Ala Asp Asp Arg Ile Tyr Arg Val Gly Ala Ala
      130          135          140
Leu
145

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<210> 1175

<211> 729

<212> DNA

<213> Homo sapiens

<400> 1175

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gatcgactg caatccaccc acatctactt gatatgaaaa ttggtcaagg caaatatgag
60
caggggttct ttccaaagtt acagtccgat gtcttggaac caggaccaac cagtaacaat
120
cgctgggtaa gtcggagtgc cactgcacag cgcaggaaaag gacgccttcg ccagcattct
180
gagcatgttg ggctggacaa cgacttgagg gagaaatata tgcaagaggc acgaagttaa
240
ggaaaaaacc tgaggcaacc caaactgtca gacctctctc ctgcagttat tgcacagacc
300
aactgtaaat tcgtagaagg cttattaaaa gaatgtagaa ataagacaaa gcgcatgttg
360
gtggagaaga tgggacatga agcgggtggaa cttggccatg gagaagcaaa catcacgggc
420
ctggaggaga acaccttgat cgccagcctt tgtgacctgc tggagaggat atggagccat
480
ggcttgagg tcaagcaggg gaagtcgggt ttgtggtcac atttaattcc ttttcaggac
540
agagaagaga accaagagcc ccttgcagaa tcaccagttg ccctcggacc agaaagaaaa
600
aaatctgact caggagttat gttgccaacg ctcagggtct ctcttattca ggacatgagg
660
catattcaaa acatgagtga gatcaagact gatgttggac gagctcgggc gtggataaga
720
ctgtctcta
729

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<210> 1176
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 1176
 Asp Arg Thr Ala Ile His Pro His Leu Leu Asp Met Lys Ile Gly Gln
 1 5 10 15
 Gly Lys Tyr Glu Gln Gly Phe Phe Pro Lys Leu Gln Ser Asp Val Leu
 20 25 30
 Ala Thr Gly Pro Thr Ser Asn Asn Arg Trp Val Ser Arg Ser Ala Thr
 35 40 45
 Ala Gln Arg Arg Lys Gly Arg Leu Arg Gln His Ser Glu His Val Gly
 50 55 60
 Leu Asp Asn Asp Leu Arg Glu Lys Tyr Met Gln Glu Ala Arg Ser Leu
 65 70 75 80
 Gly Lys Asn Leu Arg Gln Pro Lys Leu Ser Asp Leu Ser Pro Ala Val
 85 90 95
 Ile Ala Gln Thr Asn Cys Lys Phe Val Glu Gly Leu Leu Lys Glu Cys
 100 105 110
 Arg Asn Lys Thr Lys Arg Met Leu Val Glu Lys Met Gly His Glu Ala
 115 120 125
 Val Glu Leu Gly His Gly Glu Ala Asn Ile Thr Gly Leu Glu Glu Asn
 130 135 140
 Thr Leu Ile Ala Ser Leu Cys Asp Leu Leu Glu Arg Ile Trp Ser His
 145 150 155 160
 Gly Leu Gln Val Lys Gln Gly Lys Ser Val Leu Trp Ser His Leu Ile
 165 170 175
 Pro Phe Gln Asp Arg Glu Glu Asn Gln Glu Pro Leu Ala Glu Ser Pro
 180 185 190
 Val Ala Leu Gly Pro Glu Arg Lys Lys Ser Asp Ser Gly Val Met Leu
 195 200 205
 Pro Thr Leu Arg Val Ser Leu Ile Gln Asp Met Arg His Ile Gln Asn
 210 215 220
 Met Ser Glu Ile Lys Thr Asp Val Gly Arg Ala Arg Ala Trp Ile Arg
 225 230 235 240
 Leu Ser Leu

<210> 1177
 <211> 581
 <212> DNA
 <213> Homo sapiens

<400> 1177
 acgcgtgatg agttgcgcga gaccagcaac tgcagccgaa tacagttttc ttgtgtaccc
 60
 cgtcgcacag ctgcgagagg tgggcattgc cgagtgaggc aacgatgtct aaggcggaaa
 120
 gctcatcctc ggcagacggg aagactttgt cgtcggggat gttgtcaatg agagcgggga
 180
 cgtcgatctc ggtactgccc atggcgctcat gaaggatcgc gcgatacggg ggcagacccc
 240

cgatgagggc gtcgtcgaat ccagcgatga tcgatacctc tctcggtagc acgtccgtgg
 300
 ccaacaggtg gtcgacttgg gcggggggcta gccatgtaat tgttccgagc acatggaggg
 360
 tggctgccag gaggcggatg gccgggttctg gggcatcttt ggagatcttc agccggacat
 420
 cagtgggcag tccggccggg acttggcaga gggcctgggc gggatgggag cgctgggcga
 480
 cgacgaaacg ccccgacgcc gtaacgccgt gggcttggag atcgcaggtc cacttctctg
 540
 ggctttcacc ggcagagatc atggtgtgga ccaccattgt g
 581

<210> 1178
 <211> 192
 <212> PRT
 <213> Homo sapiens

<400> 1178
 Met Val Val His Thr Met Ile Ser Ala Gly Glu Ser Pro Glu Lys Trp
 1 5 10 15
 Thr Cys Asp Leu Gln Ala His Gly Val Thr Ala Ser Gly Arg Phe Val
 20 25 30
 Val Ala Gln Arg Ser His Pro Ala Gln Ala Leu Cys Gln Val Pro Ala
 35 40 45
 Gly Leu Pro Thr Asp Val Arg Leu Lys Ile Ser Lys Asp Ala Pro Glu
 50 55 60
 Pro Ala Ile Arg Leu Leu Ala Ala Thr Leu His Val Leu Gly Thr Ile
 65 70 75 80
 Thr Trp Leu Ala Pro Ala Gln Val Asp His Leu Leu Ala Thr Asp Val
 85 90 95
 Leu Pro Arg Glu Val Ser Ile Ile Ala Gly Phe Asp Asp Ala Leu Ile
 100 105 110
 Gly Val Val Ala Pro Tyr Arg Ala Ile Leu His Asp Ala Met Gly Ser
 115 120 125
 Thr Glu Ile Asp Val Pro Ala Leu Ile Asp Asn Ile Pro Asp Asp Lys
 130 135 140
 Val Phe Pro Ser Ala Glu Asp Glu Leu Ser Ala Leu Asp Ile Val Ala
 145 150 155 160
 Ser Leu Gly Asn Ala His Leu Ser Gln Leu Cys Asp Gly Val His Lys
 165 170 175
 Lys Thr Val Phe Gly Cys Ser Cys Trp Ser Arg Ala Thr His His Ala
 180 185 190

<210> 1179
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 1179
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 gattggggct tctggacatg ctgccacaag atgtctggaa actccagggg gcacctgccg
 120

agaccctgcc ctgggaacgg ccggaagaat cccaaaacat gagattccgg tgcagctgag
 180
 ccccgccaat tcattgtctc tttcagtcctc ttctgaaggc tgcatttggc aatgtgacct
 240
 tcgggggtggg gaaggcatca gaggaatata ggctatggga cgccagaggc agcgtcctgg
 300
 ggacaaagcc cacttcttcc catgcccagg gcttcctcat ggaccagca tgggtggacgt
 360
 ggccctcaga cgtccatggg tgggtggggga ggcacgtgct gtttggccct gtctctgctc
 420
 agagtctcat aggaagatgc atgggtccaca caacagttag tcggcagggga gtccaggctt
 480
 cccctcccaa ccagtgggtg tgagacgctt ggtttataac ccaagatccc ttgtccatt
 540
 ggtgcctcct gaatctccca cctcccgcgg cacctgcatg gcctctacct gacgcgt
 597

<210> 1180

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1180

Met	Gly	Arg	Gln	Arg	Gln	Arg	Pro	Gly	Asp	Lys	Ala	His	Phe	Phe	Pro
1			5					10					15		
Cys	Pro	Gly	Leu	Pro	His	Gly	Pro	Ser	Met	Val	Asp	Val	Ala	Leu	Arg
			20					25					30		
Arg	Pro	Trp	Val	Val	Gly	Glu	Ala	Arg	Ala	Val	Trp	Pro	Cys	Leu	Cys
			35				40					45			
Ser	Glu	Ser	His	Arg	Lys	Met	His	Gly	Pro	His	Asn	Ser	Glu	Ser	Ala
			50			55					60				
Gly	Ser	Pro	Gly	Phe	Pro	Ser	Gln	Pro	Val	Val	Leu	Arg	Arg	Leu	Val
65					70					75				80	
Tyr	Asn	Pro	Arg	Ser	Leu	Val	Pro	Leu	Val	Pro	Pro	Glu	Ser	Pro	Thr
				85				90						95	
Ser	Arg	Gly	Thr	Cys	Met	Ala	Ser	Thr							
			100					105							

<210> 1181

<211> 352

<212> DNA

<213> Homo sapiens

<400> 1181

gtcgactacc tcgatgtttc cccgcgtcag atgggtctccg tggctactgc catgattccg
 60
 ttctctgagc acgacgacgc taaccgtgcc ctgatgggtg cgaacatgca gcgtcaggct
 120
 gtgccgctgc tgcgttcgga ggctccgttc gtcgggtaccg gtatggagca gcgtgctgct
 180
 tacgacgccg gcgatgtcat tgtcgcttcg gccacagggtg tggctcgagac cgtgtcggca
 240
 ggcttcatca ccatcatgga cgatgagggc cagcgccaca cctacctgct gcgcaagttc
 300

gagcgcacca accagggcac ctgctacaac cagaagccac tggtgacgag gg
352

<210> 1182
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1182
Val Asp Tyr Leu Asp Val Ser Pro Arg Gln Met Val Ser Val Ala Thr
1 5 10 15
Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met
20 25 30
Gly Ala Asn Met Gln Arg Gln Ala Val Pro Leu Leu Arg Ser Glu Ala
35 40 45
Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly
50 55 60
Asp Val Ile Val Ala Ser Ala Thr Gly Val Val Glu Thr Val Ser Ala
65 70 75 80
Gly Phe Ile Thr Ile Met Asp Asp Glu Gly Gln Arg His Thr Tyr Leu
85 90 95
Leu Arg Lys Phe Glu Arg Thr Asn Gln Gly Thr Cys Tyr Asn Gln Lys
100 105 110
Pro Leu Leu Thr Arg
115

<210> 1183
<211> 432
<212> DNA
<213> Homo sapiens

<400> 1183
gaccccttctg ggcgctgggc caagcgcgtg gtgaggccgt cctctcctgc agaaccgccg
60
cctcttcgcc cctgcccgtt cacctgttct gtccctgtca cctcctccag gaagcctgcc
120
tgcccttctc catgctgatg ggcgtggccc ttgtccctgc agccatgcat tgacctcgt
180
ggctcctgga ggccaggcca cgtcctcctc ccctctgggt gaggtagagg cacagcctgg
240
gtgcgtgggg ccgtggcggc tccgaggcgc caccgctgtg tctctcatg agtgggtgcc
300
gtccaggtct gtccctgggt ggctgcgagg aggaggttgg cctcgcgcgg ccatgtgcgt
360
gacagtggag acatcgccag cctcctgctt gcacagctga cggcagcccc tctctctcca
420
gccatgtccc ca
432

<210> 1184
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1184

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Met Ala Gly Glu Arg Gly Ala Ala Val Ser Cys Ala Ser Arg Arg Leu
 1           5           10           15
Ala Met Ser Pro Leu Ser Arg Thr Trp Pro Arg Glu Ala Asn Leu Leu
      20           25           30
Leu Ala Ala Ser Pro Gly Gln Thr Trp Thr Ala Pro Thr His Glu Arg
    35           40           45
Thr Gln Arg Trp Arg Leu Gly Ala Ala Thr Ala Pro Arg Thr Gln Ala
 50           55           60
Val Pro Leu Thr His Pro Glu Gly Met Arg Thr Trp Pro Gly Leu Gln
65           70           75           80
Glu Pro Arg Arg Ser Met His Gly Cys Arg Asp Lys Gly His Ala His
      85           90           95
Gln His Gly Glu Gly Gln Ala Gly Phe Leu Glu Glu Val Ser Arg Thr
    100           105           110
Glu Gln Val Ser Gly Gln Gly Arg Arg Gly Arg Gly Ser Ala Gly Glu
 115           120           125
Asp Gly Leu Thr Thr Arg Leu Asp Gln Arg Pro Glu Gly
    130           135           140

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<210> 1185

<211> 423

<212> DNA

<213> Homo sapiens

<400> 1185

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accggtgaat ttggccttaa cagcgatgga actcctggcc catcttatga acctggcatg
60
gaattacgcg gcaaatatgt attgttgggt gaagggtgtac ggggctctct atctaaacaa
120
gtcatcaata aataccaatt atccgagggt catgaaccac aaaagttcgg ccttggttta
180
aaagaaatTTT gggaaataga cccagaaaaa cacaagaag gcagagtcag tcataccatg
240
ggctggccat taaatggcaa tgctggcggc ggttctttta tttatcatgc agaaaacaat
300
caagtcttta tcggctttgt ggtgcatctt aattacgcca acccttacct atccccttac
360
caagaatttc aacgctttta acaccatccg attatcgcg agctattaac tggcggtaaa
420
cgc
423

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<210> 1186

<211> 141

<212> PRT

<213> Homo sapiens

<400> 1186

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Thr Gly Glu Phe Gly Leu Asn Ser Asp Gly Thr Pro Gly Pro Ser Tyr
 1           5           10           15
Glu Pro Gly Met Glu Leu Arg Gly Lys Tyr Val Leu Leu Gly Glu Gly
      20           25           30
Val Arg Gly Ser Leu Ser Lys Gln Val Ile Asn Lys Tyr Gln Leu Ser

```

	35					40				45							
Glu	Gly	His	Glu	Pro	Gln	Lys	Phe	Gly	Leu	Gly	Leu	Lys	Glu	Ile	Trp		
	50					55					60						
Glu	Ile	Asp	Pro	Glu	Lys	His	Lys	Glu	Gly	Arg	Val	Ser	His	Thr	Met		
65					70					75					80		
Gly	Trp	Pro	Leu	Asn	Gly	Asn	Ala	Gly	Gly	Gly	Ser	Phe	Ile	Tyr	His		
				85					90					95			
Ala	Glu	Asn	Asn	Gln	Val	Phe	Ile	Gly	Phe	Val	Val	His	Leu	Asn	Tyr		
		100						105					110				
Ala	Asn	Pro	Tyr	Leu	Ser	Pro	Tyr	Gln	Glu	Phe	Gln	Arg	Phe	Lys	His		
	115						120					125					
His	Pro	Ile	Ile	Ala	Glu	Leu	Leu	Thr	Gly	Gly	Lys	Arg					
	130					135					140						

<210> 1187

<211> 387

<212> DNA

<213> Homo sapiens

<400> 1187

acgcgtgctg gtagttaa attgaatgct gatggtaatt tggtagacgaa ttcaggggct
60
aagggtccagg gctataatgc aatagatggc atagtcgggtg ggaacttaga agatatggta
120
gtacccactg ctggaatttc tcctcaagca acatcaagtg ttgatttaaa agtgaatctt
180
aattccgaag gtgaggatgt gccgccttat attcgagcgg actttgatcc agccaatcca
240
gatacttatg actataactca gacccaaacg gttgcggatg ggagtggtaa taatcattta
300
attagttatt actatgctaa aagtgatgta gcaaatacct atcagggttta tgccacggta
360
gatgggaagt cgactgatga taccggt
387

<210> 1188

<211> 129

<212> PRT

<213> Homo sapiens

<400> 1188

Thr	Arg	Ala	Gly	Glu	Phe	Lys	Leu	Asn	Ala	Asp	Gly	Asn	Leu	Val	Thr		
1				5				10					15				
Asn	Ser	Gly	Ala	Lys	Val	Gln	Gly	Tyr	Asn	Ala	Ile	Asp	Gly	Ile	Val		
		20					25					30					
Gly	Gly	Asn	Leu	Glu	Asp	Met	Val	Val	Pro	Thr	Ala	Arg	Ile	Ser	Pro		
	35					40				45							
Gln	Ala	Thr	Ser	Ser	Val	Asp	Leu	Lys	Val	Asn	Leu	Asn	Ser	Glu	Gly		
	50				55					60							
Glu	Asp	Val	Pro	Pro	Tyr	Ile	Arg	Ala	Asp	Phe	Asp	Pro	Ala	Asn	Pro		
65					70				75					80			
Asp	Thr	Tyr	Asp	Tyr	Thr	Gln	Thr	Gln	Thr	Val	Ala	Asp	Gly	Ser	Gly		
			85				90						95				
Asn	Asn	His	Leu	Ile	Ser	Tyr	Tyr	Tyr	Ala	Lys	Ser	Asp	Val	Ala	Asn		

	100		105		110										
Thr	Tyr	Gln	Val	Tyr	Ala	Thr	Val	Asp	Gly	Lys	Ser	Thr	Asp	Asp	Thr
	115		120										125		
Gly															

<210> 1189
 <211> 330
 <212> DNA
 <213> Homo sapiens

<400> 1189
 tcgatcgccg accgcccggg ccttgccccc ggcgatgatcg gtggcctggt ggccagcacc
 60
 ctgggtgctg gtttcattgg cggcatcggt gcagggttttc tggccggtta cagcgccaag
 120
 gccattgccc gctgggcacg gctgcccagc agcctggatg cgctcaaacc gattctgatc
 180
 atttcgctgc tggccagcct gttcactggg ttggtgatga tctacgtggt cggccagccg
 240
 gtggcggcca tgctcggagg cctgacacac tttctcgaca gcatgggtac caccaacgcc
 300
 attctcctgg gcntggtgct cggcgggctag
 330

<210> 1190
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 1190
 Ser Ile Ala Asp Arg Pro Gly Leu Ala Pro Gly Met Ile Gly Gly Leu
 1 5 10 15
 Leu Ala Ser Thr Leu Gly Ala Gly Phe Ile Gly Gly Ile Val Ala Gly
 20 25 30
 Phe Leu Ala Gly Tyr Ser Ala Lys Ala Ile Ala Arg Trp Ala Arg Leu
 35 40 45
 Pro Ser Ser Leu Asp Ala Leu Lys Pro Ile Leu Ile Ile Ser Leu Leu
 50 55 60
 Ala Ser Leu Phe Thr Gly Leu Val Met Ile Tyr Val Val Gly Gln Pro
 65 70 75 80
 Val Ala Ala Met Leu Gly Gly Leu Thr His Phe Leu Asp Ser Met Gly
 85 90 95
 Thr Thr Asn Ala Ile Leu Leu Gly Xaa Leu Leu Gly Gly
 100 105

<210> 1191
 <211> 351
 <212> DNA
 <213> Homo sapiens

<400> 1191
 cggccgacga tgtgcggtga gcaagagatt tggagagcca tgatgacgtc agcagacaaa
 60

gcagggacta acggacagac catgcagaca ccgccggtgg tgtcgccgca ggactgggag
 120
 gcagccccgtc agcaactgct cgtgaaggaa aaggcgcata cccgtgccccg cgacgcactc
 180
 gccgccgaac ggaggcgcac gccgtggatg gaagtgacaa aaacctacgc attcgaggcg
 240
 ccctcgggca aggccagtct gctcgatctg ttccagggcc ggaagcagct gatcctgtac
 300
 cgggccttct tcgagccggg cgtgttcggc tggcccgacc atgcctgccg c
 351

<210> 1192

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1192

Met	Cys	Gly	Glu	Gln	Glu	Ile	Trp	Arg	Ala	Met	Met	Thr	Ser	Ala	Asp
1			5						10					15	
Lys	Ala	Gly	Thr	Asn	Gly	Gln	Thr	Met	Gln	Thr	Pro	Pro	Val	Val	Ser
			20					25					30		
Pro	Gln	Asp	Trp	Glu	Ala	Ala	Arg	Gln	Gln	Leu	Leu	Val	Lys	Glu	Lys
		35					40					45			
Ala	His	Thr	Arg	Ala	Arg	Asp	Ala	Leu	Ala	Ala	Glu	Arg	Arg	Arg	Met
	50					55					60				
Pro	Trp	Met	Glu	Val	Thr	Lys	Thr	Tyr	Ala	Phe	Glu	Ala	Pro	Ser	Gly
65					70				75					80	
Lys	Ala	Ser	Leu	Leu	Asp	Leu	Phe	Gln	Gly	Arg	Lys	Gln	Leu	Ile	Leu
			85					90					95		
Tyr	Arg	Ala	Phe	Phe	Glu	Pro	Gly	Val	Phe	Gly	Trp	Pro	Asp	His	Ala
			100					105					110		

Cys Arg

<210> 1193

<211> 722

<212> DNA

<213> Homo sapiens

<400> 1193

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 cgacttagga cgcccagttt gtactcagtg tttgctcttt tatggcagag cctctgcact
 120
 cccagcctcc tggccccttc tgtacatgat ttctcttggt gccactccat gcatttttct
 180
 tggctcagga cttagtgggc ctccatggga cttggtacct ctacttggtc ccttctggaa
 240
 tctgtaactt tgtgttcccc accattcttt cctttatgaa ccgatggtgc aacagcatga
 300
 ctacctgaaa ttcttagtca ctcccagctg ctttagtgga gggaaaatgc ccacagcaca
 360
 ggaaatagtc ctgcccttcg agagaggcca ggggatggga gcgtgtccag agaagggcga
 420

tgggttgatg aaggggtggcc acagcgcccg ggaggaaggg gccagaacgc tctctgttct
 480
 gttccatgag gaggattatg ttggtgtgtg tagtcccctg gttcagagtt gtccagaaat
 540
 agtcagtgt aaggaacaat tttccaaaga tcaaaagagc tgtctcaaga tagcagtgcg
 600
 ttcccagccc ctacaggtgt atacagcaca aaggaggga cccctagtgt tggctgtcac
 660
 agaggggaagt ggacgtcctg tggtttgacc ccaccagatg gctttagaga tctgggcccg
 720
 ag
 722

<210> 1194
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1194
 Met Val Gln Gln His Asp Tyr Leu Lys Phe Leu Val Thr Pro Ser Cys
 1 5 10 15
 Phe Ser Gly Gly Lys Met Pro Thr Ala Gln Glu Ile Val Leu Pro Phe
 20 25 30
 Glu Arg Gly Gln Gly Met Gly Ala Cys Pro Glu Lys Gly Asp Gly Leu
 35 40 45
 Met Lys Gly Gly His Ser Ala Arg Glu Glu Gly Ala Arg Thr Leu Ser
 50 55 60
 Val Leu Phe His Glu Glu Asp Tyr Val Gly Val Cys Ser Pro Leu Val
 65 70 75 80
 Gln Ser Cys Pro Glu Ile Ala Gln Cys Lys Glu Gln Phe Ser Lys Asp
 85 90 95
 Gln Lys Ser Cys Leu Lys Ile Ala Val Arg Ser Gln Pro Leu Gln Val
 100 105 110
 Tyr Thr Ala Gln Arg Glu Gly Pro Ser Val Ala Val Thr Glu Gly
 115 120 125
 Ser Gly Arg Pro Val Val
 130

<210> 1195
 <211> 391
 <212> DNA
 <213> Homo sapiens

<400> 1195
 tctagagcat gatattccgc gggcgcggcc ggggtggactt tggttcgaga gtggaactaa
 60
 gtgagtaatg ggggcggcgc ggccagacgc gctcccagcc tcctggcgag agtgctgccc
 120
 ggtttcccg gggcacggga gtgtgtctag gaggggaggc caggatcctt cctcgagtcc
 180
 tgctctgaac aaaagaaaac gaggtgggtg gtgcttgaac ggccctgttt actctgcaga
 240
 tagccgaact ggtaggactc cggcgcgccc tatttatctt gattggctct gcctgaaggc
 300

aagcgttaat cccgtccaac ctgtatcact gcgaagagct cgttcgggag cgctttttgg
 360
 aaatgcagat tcttagcccc caccagatc t
 391

<210> 1196
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 1196
 Met Gly Ala Ala Arg Pro Asp Ala Leu Pro Ala Ser Trp Arg Glu Cys
 1 5 10 15
 Cys Pro Val Ser Arg Gly His Gly Ser Val Ser Arg Arg Gly Gly Gln
 20 25 30
 Asp Pro Ser Ser Ser Pro Val Leu Asn Lys Arg Lys Arg Gly Gly Trp
 35 40 45
 Cys Leu Asn Gly Pro Val Tyr Ser Ala Asp Ser Arg Thr Gly Arg Thr
 50 55 60
 Pro Ala Arg Pro Ile Tyr Leu Asp Trp Leu Cys Leu Lys Ala Ser Val
 65 70 75 80
 Asn Pro Val Gln Pro Val Ser Leu Arg Arg Ala Arg Ser Gly Ala Leu
 85 90 95
 Phe Gly Asn Ala Asp Ser
 100

<210> 1197
 <211> 386
 <212> DNA
 <213> Homo sapiens

<400> 1197
 acgcgtgatg atcatgaaaa tggtagagag cgtctagcag aagtcgcctc tgtgatgggc
 60
 tggcagcaag atgaaatcat cgtaaagta caaggggatg aaccctttct gcctgttgca
 120
 cttattcatg ccacgggttaa agcgttagcc gatgatgctg aatctgaaat ggccacgatt
 180
 gcctgtgcga ttgataacgt agcagagctg ttttaaccaa atgtagttaa agtcgtttgt
 240
 gatgaaaaaac agcgcgcctt gtatttcagt cgtgcgccta tgccatggga ccgtaatggg
 300
 tttatggaaa aaacagacga tcaagcgtaa ccagcggatt ttctgcgtt gcgtcatatt
 360
 ggtccgtatg tttaccgcac gacatn
 386

<210> 1198
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 1198
 Thr Arg Asp Asp His Glu Asn Gly Thr Glu Arg Leu Ala Glu Val Ala

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      1           5           10           15
Ser Val Met Gly Trp Gln Gln Asp Glu Ile Ile Val Asn Val Gln Gly
      20           25           30
Asp Glu Pro Phe Leu Pro Val Ala Leu Ile His Ala Thr Val Lys Ala
      35           40           45
Leu Ala Asp Asp Ala Glu Ser Glu Met Ala Thr Ile Ala Cys Ala Ile
      50           55           60
Asp Asn Val Ala Glu Leu Phe Asn Pro Asn Val Val Lys Val Val Cys
      65           70           75           80
Asp Glu Lys Gln Arg Ala Leu Tyr Phe Ser Arg Ala Pro Met Pro Trp
      85           90           95
Asp Arg Asn Gly Phe Met Glu Lys Thr Asp Asp Gln Ala Leu Pro Ala
      100           105           110
Asp Phe Pro Ala Leu Arg His Ile Gly Pro Tyr Val Tyr Arg Thr Thr
      115           120           125

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<210> 1199

<211> 318

<212> DNA

<213> Homo sapiens

<400> 1199

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acgcgttcag cgctcatgtac agccccgggc cgggtcaattt gatgggcctc aatgccgggc
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ttacgggcaa attgcgtcgc tccagcgggt tctacatcgg cgtgggggtgc gcgatgctgc
120
tgatggtcgg gctgggttggg ctcaccggcg aagcgatcat ctcccaggcg gcgctgccgt
180
atatttcttt gattggcggg gtgtacacgc tgtacctcgc ctaccaggtg ttcaccgcac
240
gtaccgaagt ggatgacgcc ccaagcgcg ctgccaagac cttgaccttc tggaatggcc
300
tggtgatcca gttgctcc
318

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<210> 1200

<211> 101

<212> PRT

<213> Homo sapiens

<400> 1200

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Met Tyr Ser Pro Gly Pro Val Asn Leu Met Gly Leu Asn Ala Gly Leu
      1           5           10           15
Thr Gly Lys Leu Arg Arg Ser Ser Gly Phe Tyr Ile Gly Val Gly Cys
      20           25           30
Ala Met Leu Leu Met Val Gly Leu Val Gly Leu Thr Gly Glu Ala Ile
      35           40           45
Ile Ser Gln Ala Ala Leu Pro Tyr Ile Ser Leu Ile Gly Gly Val Tyr
      50           55           60
Thr Leu Tyr Leu Ala Tyr Gln Val Phe Thr Ala Arg Thr Glu Val Asp
      65           70           75           80
Asp Ala Pro Ser Ala Pro Ala Lys Thr Leu Thr Phe Trp Asn Gly Leu
      85           90           95
Val Ile Gln Leu Leu

```

100

<210> 1201
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 1201
 gtcgacgcac aactccagct ggctcgctccc aacagcccga acatccccct ttatcgcgat
 60
 atgatacctca ccgtgctgcg catggccaag gatgaccgca accgttggaa tgcaaaaatc
 120
 acgctgcagg cgatccgcga gctggataac gccttccgcg tgctggaaca gttcaagggc
 180
 cgccgcaagg tcacggtggt ttggtcggcg cgcacgccgg tcgaaagccc gctgtacgcc
 240
 ttggcaaggg aagtcggcac gctgctggcg caatccgacc tgatggtgat caccggcggt
 300
 ggcggcggca tcatggccgc tgcccacgag ggcgcaaggt ctggaacaca gcctgggggt
 360

<210> 1202
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 1202
 Val Asp Ala Gln Leu Gln Leu Val Ala Pro Asn Ser Pro Asn Ile Pro
 1 5 10 15
 Leu Tyr Arg Asp Met Ile Leu Thr Val Leu Arg Met Ala Lys Asp Asp
 20 25 30
 Arg Asn Arg Trp Asn Ala Lys Ile Thr Leu Gln Ala Ile Arg Glu Leu
 35 40 45
 Asp Asn Ala Phe Arg Val Leu Glu Gln Phe Lys Gly Arg Arg Lys Val
 50 55 60
 Thr Val Phe Gly Ser Ala Arg Thr Pro Val Glu Ser Pro Leu Tyr Ala
 65 70 75 80
 Leu Ala Arg Glu Val Gly Thr Leu Leu Ala Gln Ser Asp Leu Met Val
 85 90 95
 Ile Thr Gly Gly Gly Gly Gly Ile Met Ala Ala Ala His Glu Gly Ala
 100 105 110
 Arg Ser Gly Thr Gln Pro Gly Gly
 115 120

<210> 1203
 <211> 477
 <212> DNA
 <213> Homo sapiens

<400> 1203
 ccggatatgg cagctcgact tcattcgacc agagttcttg gaacatttgg ctatcatgca
 60
 cctgagtatg caatgactgg acaacttagc tctaagagtg acgtttacag ttttggagtt
 120

ggtcttcttg agctcctgac tggaagaaag cctgtggatc ttccattacc aagaggacag
 180
 caaagtcttg tgacatgggc aactccacgg ctttgtgaag ataaagttag gcaatgcggt
 240
 gattcaagac ttggagtaga atatcctcct aaatccgttg caaagtttgc agctgttgct
 300
 gcactgtgtg tgcaatatga agctgacttt cgacccaaca tgagcatcgt ggtgaaggcg
 360
 cttcagcccc tgctgaatgc acgtgcatcc aacaaccctg gatgaatgaa tgaatgactg
 420
 ccgttgcttt tccctgacga gagtatctga atcagacaat catgtagcat tgaattc
 477

<210> 1204
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 1204
 Pro Asp Met Ala Ala Arg Leu His Ser Thr Arg Val Leu Gly Thr Phe
 1 5 10 15
 Gly Tyr His Ala Pro Glu Tyr Ala Met Thr Gly Gln Leu Ser Ser Lys
 20 25 30
 Ser Asp Val Tyr Ser Phe Gly Val Gly Leu Leu Glu Leu Leu Thr Gly
 35 40 45
 Arg Lys Pro Val Asp Leu Pro Leu Pro Arg Gly Gln Gln Ser Leu Val
 50 55 60
 Thr Trp Ala Thr Pro Arg Leu Cys Glu Asp Lys Val Arg Gln Cys Val
 65 70 75 80
 Asp Ser Arg Leu Gly Val Glu Tyr Pro Pro Lys Ser Val Ala Lys Phe
 85 90 95
 Ala Ala Val Ala Ala Leu Cys Val Gln Tyr Glu Ala Asp Phe Arg Pro
 100 105 110
 Asn Met Ser Ile Val Val Lys Ala Leu Gln Pro Leu Leu Asn Ala Arg
 115 120 125
 Ala Ser Asn Asn Pro Gly
 130

<210> 1205
 <211> 407
 <212> DNA
 <213> Homo sapiens

<400> 1205
 acgcgttgcc attgaagact ggcaattaca cgatttacac atcattgatg ctgcagttga
 60
 tgtgcacagg gaaacactag ctaccgtgca gcaggaaatg atgggagaaa tcagccatgg
 120
 taacaagaac caagccatcc tggacacaga cggccgggggt tgtgcgaacg gaacgttagt
 180
 ctatcaatgt gttgcggaac gattcaaggg atgctggccc ccccatcac ttgccaatc
 240
 aagatgtgga gggaaatctgt ctgcgcagaa cctggatctc gtggttgtag gacgttgctc
 300

ccttctcgct cggacgccgc tcatgctccg ccacgtcgct gagcgagtga caaggtatcc
360

tgggaccatg cgtatggttt caactgaagc gctggcgaat cgtaaan
407

<210> 1206

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1206

Met	Met	Gly	Glu	Ile	Ser	His	Gly	Asn	Lys	Asn	Gln	Ala	Ile	Leu	Asp
1				5					10					15	
Thr	Asp	Gly	Arg	Gly	Cys	Ala	Asn	Gly	Thr	Leu	Val	Tyr	Gln	Cys	Val
			20					25					30		
Ala	Glu	Arg	Phe	Lys	Gly	Cys	Trp	Pro	Pro	Pro	Ser	Leu	Ala	Gln	Ser
			35				40					45			
Arg	Cys	Gly	Gly	Asn	Leu	Ser	Ala	Gln	Asn	Leu	Asp	Leu	Val	Val	Val
	50				55					60					
Arg	Arg	Cys	Pro	Leu	Leu	Ala	Arg	Thr	Pro	Leu	Met	Leu	Arg	His	Val
65				70					75					80	
Ala	Glu	Arg	Val	Thr	Arg	Tyr	Pro	Gly	Thr	Met	Arg	Met	Val	Ser	Thr
			85					90						95	
Glu	Ala	Leu	Ala	Asn	Arg	Lys									
			100												

<210> 1207

<211> 292

<212> DNA

<213> Homo sapiens

<400> 1207

gctagcatgt cacttttttc ttcagtagat ggcactggag agacattgca ggatgaagag
60
gcttgcccttc attcctatgt gctttcccgt ccttgcttct ccagccatgt gtgggacaac
120
caggggtgct caccacctag tgagtttcag ggacactcca catgtcccag caagtcttat
180
cagcatctta gctggcttct caacaagact cagtggcacc cctgtggatg tctcccatca
240
agtttcatta gtgccccagg gggagactcc cagaaagttt cagcagcacc ac
292

<210> 1208

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1208

Met	Ser	Leu	Phe	Ser	Ser	Val	Asp	Gly	Thr	Gly	Glu	Thr	Leu	Gln	Asp
1				5					10					15	
Glu	Glu	Ala	Cys	Leu	His	Ser	Tyr	Val	Leu	Ser	Arg	Pro	Cys	Phe	Ser
			20					25					30		
Ser	His	Val	Trp	Asp	Asn	Gln	Gly	Cys	Ser	Pro	Pro	Ser	Glu	Phe	Gln

```

      35              40              45
Gly His Ser Thr Cys Pro Ser Lys Ser Tyr Gln His Leu Ser Trp Leu
  50              55              60
Leu Asn Lys Thr Gln Trp His Pro Cys Gly Cys Leu Pro Ser Ser Phe
  65              70              75              80
Ile Ser Ala Pro Gly Gly Asp Ser Gln Lys Val Ser Ala Ala Pro
      85              90              95

```

<210> 1209
 <211> 431
 <212> DNA
 <213> Homo sapiens

<400> 1209
 ttggttccta taatggcggg agcttacatt tttgctggta tcattatttt gttaatgcat
 60
 gccagtgaag ttattccggc aatatcaact attgtcgagt atgcctttac gccagcttct
 120
 gcgcagggtg gttttgctgg tgcaacggta tggatggcga ttcgttttgg tgttgcccgt
 180
 ggtgtatttt caaatgaggc aggtttaggt tcggcgccga tcgctcatgc cagtgcacaa
 240
 actaatgaac cggttcgcca agggttgggt gcgatggttag gtactttcct tgatacactt
 300
 attatttgta caggtttagt gattgttatt tctgggtgctt ggacagaagg attgtcgggt
 360
 gctgcgttaa catctgctgc atttaatctg gcgttacctg gttggggggg atacttagtc
 420
 gctatcagct g
 431

<210> 1210
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 1210
 Leu Val Pro Ile Met Ala Val Ala Tyr Ile Phe Ala Gly Ile Ile Ile
 1 5 10 15
 Leu Leu Met His Ala Ser Glu Val Ile Pro Ala Ile Ser Thr Ile Val
 20 25 30
 Glu Tyr Ala Phe Thr Pro Ala Ser Ala Gln Gly Gly Phe Ala Gly Ala
 35 40 45
 Thr Val Trp Met Ala Ile Arg Phe Gly Val Ala Arg Gly Val Phe Ser
 50 55 60
 Asn Glu Ala Gly Leu Gly Ser Ala Pro Ile Ala His Ala Ser Ala Gln
 65 70 75 80
 Thr Asn Glu Pro Val Arg Gln Gly Leu Val Ala Met Leu Gly Thr Phe
 85 90 95
 Leu Asp Thr Leu Ile Ile Cys Thr Gly Leu Val Ile Val Ile Ser Gly
 100 105 110
 Ala Trp Thr Glu Gly Leu Ser Gly Ala Ala Leu Thr Ser Ala Ala Phe
 115 120 125
 Asn Leu Ala Leu Pro Gly Trp Gly Gly Tyr Leu Val Ala Ile Ser

130

135

140

<210> 1211

<211> 480

<212> DNA

<213> Homo sapiens

<400> 1211

gaggagggac gagaggctgg tgagatggag tccagcaccc tgcaggagag cccaggggcc
60
agagccgaag ctgtgcttct ccatgagatg gatgaagatg atctggccaa tgccctgac
120
tggcctgaga ttcaacagga gctgaaaatc attgaatctg aggaggagct ctcatcgctg
180
ccacctcctg ctctgaagac cagcccaatt cagcctatc tcgagtcgag tctggggccc
240
tttattccct cagagcctcc tgggagcttg ccttgtggct ccttcctgc tccagtctcc
300
accctctgg aggtgtggac tagggatcca gccaatcaga gcacacaggg ggcttccaca
360
gcagccagca gagagaagcc ggaacctgag cagggcctgc acccagacct cgccagcctg
420
gctcctctgg aaatagttcc ttttgagaag gcctctccag aggctggagt gtgctcgaga
480

<210> 1212

<211> 160

<212> PRT

<213> Homo sapiens

<400> 1212

Glu	Glu	Gly	Arg	Glu	Ala	Gly	Glu	Met	Glu	Ser	Ser	Thr	Leu	Gln	Glu
1				5					10					15	
Ser	Pro	Arg	Ala	Arg	Ala	Glu	Ala	Val	Leu	Leu	His	Glu	Met	Asp	Glu
			20					25					30		
Asp	Asp	Leu	Ala	Asn	Ala	Leu	Ile	Trp	Pro	Glu	Ile	Gln	Gln	Glu	Leu
		35					40					45			
Lys	Ile	Ile	Glu	Ser	Glu	Glu	Glu	Leu	Ser	Ser	Leu	Pro	Pro	Pro	Ala
	50					55					60				
Leu	Lys	Thr	Ser	Pro	Ile	Gln	Pro	Ile	Leu	Glu	Ser	Ser	Leu	Gly	Pro
65					70					75				80	
Phe	Ile	Pro	Ser	Glu	Pro	Pro	Gly	Ser	Leu	Pro	Cys	Gly	Ser	Phe	Pro
			85					90					95		
Ala	Pro	Val	Ser	Thr	Pro	Leu	Glu	Val	Trp	Thr	Arg	Asp	Pro	Ala	Asn
			100					105					110		
Gln	Ser	Thr	Gln	Gly	Ala	Ser	Thr	Ala	Ala	Ser	Arg	Glu	Lys	Pro	Glu
		115					120					125			
Pro	Glu	Gln	Gly	Leu	His	Pro	Asp	Leu	Ala	Ser	Leu	Ala	Pro	Leu	Glu
	130					135					140				
Ile	Val	Pro	Phe	Glu	Lys	Ala	Ser	Pro	Glu	Ala	Gly	Val	Cys	Ser	Arg
145					150					155					160

<210> 1213

<211> 1141

<212> DNA

<213> Homo sapiens

<400> 1213

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nntcatgatg gcggcctggt gtgtgggtat gtccacgatg ggcgcgtcac gcgtgtcgcc
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cgtgatgctc aggggcgggg taccgggata gaggggccat cagggcggtg gagttacggc
120
tacaacgagg ctgggtcact catcagcgcg acggggcccc gcacacaaca taactggact
180
cacgacgcct atggccgggt caccagccac gccacatccg gaaccgacac caccttcgcc
240
tgggaccagg aaggccacct ggcgcgagacg tgtacgcgtg cacacgggca tgccactgcc
300
accagtatc gctatgacgc agcgggacgg cgcgctcagt cgaccagctc agacggccag
360
gaggagcggt actcctggga tggacggggg tggctgtctg acatcaccac cgacgccacg
420
accgtatcga ctcacgtcga tgcattgggg cgcgccagtc gtatcaccac taagggccag
480
cagggtacgag tggactggga cctcgtgacc ggagcccca cctcgattga tggtcgtcct
540
gtgcttcccc tgcccggagg acgcatcctc ggcgccacac ccatcggcga taccaaccta
600
tggcgtagag tcatgcccac cgacctgac aaccttacc agcccgccac ggccactatt
660
gaggggtgtcc ccgagacgat caggatggcc gggaacacgc tagtggttga tggtcacct
720
tgggtgggggc gcgcctctac gacccaacta ccaccacett ctgtgtcct gaccogttaa
780
ccccgcccgc cggcgcgcta tgggccaaca acccctacga ctacgccaac aacaaccccc
840
tcacctcac cgatcctctc gggaccacc cgcgcaccga cgaccaactg gcaactctca
900
cccaccccat cggcacactc gcacactacg tcgccaactc cgtcagcaca ctcgtgcac
960
acatcaccga tccgatcagc cactggtggg ccaccacaa agaccggatc ctctcccggg
1020
acttctgat cgggtgccggc ctcgatcgc gcggtatcgc gtagcgcca cgggcgtagg
1080
aggaccctc ctagccgcgg ccatttcggg gggactcatc tcaggcgggt ttccgctag
1140
c
1141

```

<210> 1214

<211> 259

<212> PRT

<213> Homo sapiens

<400> 1214

```

Xaa His Asp Gly Gly Leu Val Cys Gly Tyr Val His Asp Gly Arg Val
1           5           10          15
Thr Arg Val Ala Arg Asp Ala Gln Gly Arg Val Thr Gly Ile Glu Gly

```



```
<210> 1215
<211> 317
<212> DNA
<213> Homo sapiens
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```
<210> 1216
<211> 102
<212> PRT
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<213> Homo sapiens

<400> 1216

```

Met Tyr Cys Gly Glu Pro Thr Leu Phe Ser Thr Met Asn Ala Ser Thr
 1           5           10           15
Arg Pro Arg Asp Ser Asp Gly Ser Ser Pro Pro Lys Val Val Pro Arg
      20           25           30
Tyr Phe Phe His Ala Pro Thr Pro Ala Thr Ala Arg Thr Pro Pro Pro
      35           40           45
Arg Ser Gly Val Leu Pro Val Met Ala Gly Leu Thr Pro Gly Ala Val
      50           55           60
Pro Ile Lys Gly Lys Gln Val Gly Ile Pro Pro Asp Ala Gly Cys Arg
65           70           75           80
His Ala His Val Val His Pro Gln Val Asp Arg Ala His Arg Arg Leu
      85           90           95
Asp Leu Gln Arg Thr Arg
      100

```

<210> 1217

<211> 548

<212> DNA

<213> Homo sapiens

<400> 1217

```

nacgcgtggg ttgacgcgct attaaacgat aagagcaaaa aaacatttcc tcatttatta
60
cgttgtcggg tgaatgatgt ttctggtgat agtcagtgga tagagatgcg aggcagtgtg
120
acagggttggg acagccgtca tcgagctcag atggtgagag ggacattcga gcgtattaac
180
catcttattg acgctgaaaa tgaattaatt gcggcccggtg aagatgctca gcgacgagag
240
cttattttat cggcttttgc aaataatatt ccagaccctg tttggtctaa agatgaaagc
300
ggtcggttatt tggactgtaa ccatgcgttt tgtctgttta atggtttaga gcagagtgat
360
gttcaggggc aaaaagacag tgaattaaac ttagataata atggtcaata ttatcaagat
420
atgggcgggtg aggtattagc gcgagggggag atttttcatg aacattgttg gggtagcct
480
gcagatggaa gtgacaaccg cttgtttgaa gtatatcgag tccctatcaa agagcctacc
540
gtgaattc
548

```

<210> 1218

<211> 182

<212> PRT

<213> Homo sapiens

<400> 1218

```

Xaa Ala Trp Val Asp Ala Leu Leu Asn Asp Lys Ser Lys Lys Thr Phe
 1           5           10           15
Pro His Leu Leu Arg Cys Arg Val Asn Asp Val Ser Gly Asp Ser Gln

```

```

                20                25                30
Trp Ile Glu Met Arg Gly Ser Val Thr Gly Trp Asp Ser Arg His Arg
      35                40                45
Ala Gln Met Val Arg Gly Thr Phe Glu Arg Ile Asn His Leu Ile Asp
      50                55                60
Ala Glu Asn Glu Leu Ile Ala Ala Arg Glu Asp Ala Gln Arg Arg Glu
65                70                75                80
Leu Ile Leu Ser Ala Leu Leu Asn Asn Ile Pro Asp Pro Val Trp Ser
      85                90                95
Lys Asp Glu Ser Gly Arg Tyr Leu Asp Cys Asn His Ala Phe Cys Leu
      100                105                110
Phe Asn Gly Leu Glu Gln Ser Asp Val Gln Gly Gln Lys Asp Ser Glu
      115                120                125
Leu Asn Leu Asp Asn Asn Gly Gln Tyr Tyr Gln Asp Met Gly Gly Glu
      130                135                140
Val Leu Ala Arg Gly Glu Ile Phe His Glu His Cys Trp Gly Thr Pro
145                150                155                160
Ala Asp Gly Ser Asp Asn Arg Leu Phe Glu Val Tyr Arg Val Pro Ile
      165                170                175
Lys Glu Pro Thr Val Asn
      180

```

<210> 1219

<211> 308

<212> DNA

<213> Homo sapiens

<400> 1219

```

acgcgtgaag ggaggaatac agatggagaa atgggtccac caaaaaatga tgagggtacc
60
tccagagaaa attaccaaga ccattctggt agtattttcc agctccacag gcctttggaa
120
gttcccagac caccctccct cttttcaaac taaaacaggg atggctctta accaccaccc
180
aaaggcaagg ggggtcttaa aacccaaacc aagtggggca ggggccagcc tcttcaggag
240
ggcccaaccc tgcagcctct gccatttgg gaaagaccgt gagttggaat tatgggtcgg
300
tgggggggc
308

```

<210> 1220

<211> 95

<212> PRT

<213> Homo sapiens

<400> 1220

```

Met Glu Lys Trp Val His Gln Lys Met Met Arg Val Pro Pro Glu Lys
1                5                10                15
Ile Thr Lys Thr Ile Leu Leu Val Phe Ser Ser Ser Thr Gly Leu Trp
      20                25                30
Lys Phe Pro Asp His Pro Pro Ser Phe Gln Thr Lys Thr Gly Met Ala
      35                40                45
Leu Asn His His Pro Lys Ala Arg Gly Val Leu Lys Pro Lys Pro Ser

```

50		55		60											
Gly	Ala	Gly	Ala	Ser	Leu	Phe	Arg	Arg	Ala	Gln	Pro	Cys	Ser	Leu	Cys
65			70						75					80	
Pro	Phe	Gly	Lys	Asp	Arg	Glu	Leu	Glu	Leu	Trp	Val	Gly	Gly	Gly	
			85					90					95		

<210> 1221
 <211> 569
 <212> DNA
 <213> Homo sapiens

<400> 1221
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 60
 gcccgctccag gaaagctgca cctcagagaa gcagtttctt tccttacctg ggaagtttct
 120
 tctgtaacac gttaagcccc acaggtaagg cctgatcccc cctggacggc tcccctctcc
 180
 agtgttccca gtctggaggt antcttttct aagccatcct ctcagaatgt gatgggtacc
 240
 aggatgcaca cccggtggcc ctgtggtgtg aggcctcagc aaacacggtc agaagatgaa
 300
 cacacagaga cccgcccgtc ggaaggagag gagggagcgg atacggaggc ccacgtgcca
 360
 gaagggtccc ttgcagtggg gtgggttatgt gcctgcaatc ccagagtgtc ctcgaaggac
 420
 ctcagatcta acgagctcag ccggcagctg cacgtgggac cagccctctg agcttcactt
 480
 gttttctctt gtgccatcag aaaccaatac gaagataaaa tgggaaaaaa aaaaatccca
 540
 ttcacggcac agcctgccga gaaacgcgt
 569

<210> 1222
 <211> 91
 <212> PRT
 <213> Homo sapiens

<400> 1222
Met Asn Thr Gln Arg Pro Ala Arg Arg Lys Glu Arg Arg Glu Arg Ile
1 5 10 15
Arg Arg Pro Thr Cys Gln Lys Gly Pro Leu Gln Trp Cys Gly Tyr Val
20 25 30
Pro Ala Ile Pro Glu Cys Pro Arg Arg Thr Ser Asp Leu Thr Ser Ser
35 40 45
Ala Gly Ser Cys Thr Trp Asp Gln Pro Ser Glu Leu His Leu Phe Ser
50 55 60
Ser Val Pro Ser Glu Thr Asn Thr Lys Ile Lys Trp Glu Lys Lys Lys
65 70 75 80
Ser His Ser Arg His Ser Leu Pro Arg Asn Ala
85 90

<210> 1223
 <211> 450

<212> DNA

<213> Homo sapiens

<400> 1223

```

aagcttgctc aggctagtgc cgacgctgct gctctcaaac tcgtcgatgc ccaccggttg
60
ttgtgcgctc accgagaggg gccatacggg gtagacgagt ggtctcagcg catggttact
120
gtactttcag atgtgttgcc tgggtgttggc caaggccggt gggttctcgg cgaaactgca
180
atagtaacgc ataacctcgc acaattggga gtcaataacg gtgattgcgg ggtcatcggt
240
gaaacaaggc ccgtccccac gatagctcta ccgggacccg gtggagtccc cagacggttg
300
ccctgttccc tcatcccatc gctgcaaccc ttacaggcga tgacgattca caaagcgag
360
ggcagccaat tcacggacgt aacggtggtc ctgccaccac ccgactcgcc cctcctctct
420
cgtgagttgc tctataccgc catcacgcgt
450

```

<210> 1224

<211> 150

<212> PRT

<213> Homo sapiens

<400> 1224

```

Lys Leu Ala Gln Ala Ser Ala Asp Ala Ala Ala Leu Lys Leu Val Asp
 1           5           10           15
Ala His Arg Leu Leu Cys Ala His Arg Glu Gly Pro Tyr Gly Val Asp
          20           25           30
Glu Trp Ser Gln Arg Met Val Thr Val Leu Ser Asp Val Leu Pro Gly
          35           40           45
Val Gly Gln Gly Arg Trp Val Leu Gly Glu Thr Ala Ile Val Thr His
          50           55           60
Asn Leu Ala Gln Leu Gly Val Asn Asn Gly Asp Cys Gly Val Ile Val
65           70           75           80
Glu Thr Arg Pro Val Pro Thr Ile Ala Leu Pro Gly Pro Gly Gly Val
          85           90           95
Pro Arg Arg Leu Pro Cys Ser Leu Ile Pro Ser Leu Gln Pro Leu Gln
          100          105          110
Ala Met Thr Ile His Lys Ala Gln Gly Ser Gln Phe Thr Asp Val Thr
          115          120          125
Val Val Leu Pro Pro Pro Asp Ser Pro Leu Leu Ser Arg Glu Leu Leu
          130          135          140
Tyr Thr Ala Ile Thr Arg
145           150

```

<210> 1225

<211> 436

<212> DNA

<213> Homo sapiens

<400> 1225

ncccatcccc caccgaggat ggtgaacact gggatggcca cttgggagct caaagtgttg
 60
 tcagtgggag gacaaggtcc tcaattcctg gcacattggc ccagagaagt catgaaaacc
 120
 caaagcccc cgaaagtaag aagtagaaaa aaacccgacc ccgaccagat gaagggacct
 180
 gggaagtttt tggaaaagag actgctgaag tgtctccttg caggcatcac cgtgagctgg
 240
 ggctttgcac acagcatctt catggctttc cacaatgac ccagaactga tccagagaaa
 300
 cccagggatc agggggttgac ccgaccctgt catcatccca ttctacaaat gaggacactg
 360
 aggcctggtg aaaagggagg ggtggatgga accaggtggc ctggctctaa gaccagagg
 420
 ctggagtgtg ctcatg
 436

<210> 1226
 <211> 139
 <212> PRT
 <213> Homo sapiens

<400> 1226
 Met Val Asn Thr Gly Met Ala Thr Trp Glu Leu Lys Val Leu Ser Val
 1 5 10 15
 Gly Gly Gln Gly Pro Gln Phe Leu Ala His Trp Pro Arg Glu Val Met
 20 25 30
 Lys Thr Gln Ser Pro Pro Lys Val Arg Ser Arg Lys Lys Pro Asp Pro
 35 40 45
 Asp Gln Met Lys Gly Pro Gly Lys Phe Leu Glu Lys Arg Leu Leu Lys
 50 55 60
 Cys Leu Leu Ala Gly Ile Thr Val Ser Trp Gly Phe Ala His Ser Ile
 65 70 75 80
 Phe Met Ala Phe His Asn Asp Pro Arg Thr Asp Pro Glu Lys Pro Arg
 85 90 95
 Asp Gln Gly Leu Thr Arg Pro Cys His Pro Ile Leu Gln Met Arg
 100 105 110
 Thr Leu Arg Pro Gly Glu Lys Gly Gly Val Asp Gly Thr Arg Trp Pro
 115 120 125
 Gly Ser Lys Thr Gln Arg Leu Glu Cys Ala His
 130 135

<210> 1227
 <211> 756
 <212> DNA
 <213> Homo sapiens

<400> 1227
 gttgagttcc acgtgaaaca aaatgcactt tacaatagaa tgacgattcg tatcaaagat
 60
 aatgggtattg gaataccgat taacaaggta gataaaatct ttgatagatt ctaccgtgtc
 120
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 180

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<210> 1228

<211> 97

<212> PRT

<213> Homo sapiens

<400> 1228

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			20					25					30		
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		35				40					45				
Gly	Gly	Thr	Gly	Leu	Gly	Leu	Ala	Ile	Ser	Lys	Glu	Ile	Val	Glu	Ala
	50				55						60				
His	Asn	Gly	Arg	Ile	Trp	Ala	Asn	Ser	Val	Glu	Gly	Gln	Gly	Thr	Ser
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Glu

<210> 1229

<211> 377

<212> DNA

<213> Homo sapiens

<400> 1229

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<210> 1230
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Trp Asp Tyr Phe Ser Gln Leu Phe Ala Gln Val Thr Asn Pro Pro Leu
 50 55 60
 Asp Ala Ile Arg Glu Glu Leu Val Thr Ser Leu Thr Gly Thr Ile Gly
 65 70 75 80
 Pro Glu Ala Asn Leu Leu Glu Pro Gly Pro Glu Ser Cys Arg Gln Val
 85 90 95
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<210> 1231
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<210> 1232
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<213> Homo sapiens

<400> 1232

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Leu Ser Asn Ser Ser Asp Glu Ser Leu Arg Arg Val Glu Lys Leu Ala
      35           40           45
Gly Arg Ser Ala Gln Phe Tyr Gln Gly Asp Ile Leu Asp Ala Glu Cys
      50           55           60
Leu His Arg Ile Phe Glu Ala His Asp Ile Ser Ala Val Ile His Phe
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<210> 1233

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<212> DNA

<213> Homo sapiens

<400> 1233

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<210> 1234
 <211> 708
 <212> PRT
 <213> Homo sapiens

<400> 1234
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 35 40 45
 Val Gly Arg Asp Trp Asp Pro Ser Ser Thr Glu Gly Gly Ser Ser Pro
 50 55 60
 Leu Ile Cys Pro Asp Ser Ser Ala Arg Pro Arg Val Lys Ser Ser Tyr
 65 70 75 80
 Ser Met Glu Asn Ala Asn Lys Trp Ser Cys His Met Cys Thr Tyr Leu
 85 90 95
 Asn Trp Pro Arg Ala Ile Arg Cys Thr Gln Cys Leu Ser Gln Arg Arg
 100 105 110
 Thr Arg Ser Pro Thr Glu Ser Pro Gln Ser Ser Gly Ser Gly Ser Arg
 115 120 125
 Pro Val Ala Phe Ser Val Asp Pro Cys Glu Glu Tyr Asn Asp Arg Asn
 130 135 140
 Lys Leu Asn Thr Arg Thr Gln His Trp Thr Cys Ser Val Cys Thr Tyr

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Pro	Asn	Asn	Ile	Glu	Ala	Ile	Glu	Leu	Ala	Glu	Thr	Glu	Glu	Ala	Ser
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Arg	Phe	Gln	Arg	Gln	Asp	Met	Leu	Ala	Ile	Leu	Leu	Thr	Glu	Val	Ser
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Glu	Val	Leu	Asp	Arg	Asp	Val	Gln	Lys	Glu	Leu	Glu	Glu	Glu	Ser	Pro
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Trp	Lys	Asp	Trp	Glu	Ser	Trp	Tyr	Ser	Gln	Ser	Phe	Gly	Leu	His	Phe
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Tyr	Lys	Ser	Phe	Arg	Gly	Glu	Thr	Leu	Gly	Tyr	Thr	Arg	Phe	Gln	Gly
545					550					555					560
Val	Tyr	Leu	Pro	Leu	Leu	Trp	Glu	Gln	Ser	Phe	Cys	Trp	Lys	Ser	Pro
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Lys Leu Leu His Val His Phe Leu Ser Ala Gln Glu Leu Gly Asn Glu
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      645      650      655
Glu Gly Gly Val Leu Val Ala Met Gln Lys Ser Ser Arg Arg Arg Asn
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His Pro Leu Val Thr Gln Met Val Glu Lys Trp Leu Asp Arg Tyr Arg
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<210> 1235

<211> 383

<212> DNA

<213> Homo sapiens

<400> 1235

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<210> 1236

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1236

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Ile Gly Ile Leu Trp Gly Arg Tyr Asp Leu Leu Ala Glu Leu Pro Pro
35      40      45
Phe Leu Gly Gly Gly Glu Met Ile Glu Val Val Arg Met Glu Gly Ser
50      55      60
Thr Tyr Ala Glu Pro Pro His Arg Phe Glu Ala Gly Thr Pro Pro Ile

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65		70		75		80									
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Gly	Met	Gln	Ala	Ile	Ala	Glu	His	Glu	His	Glu	Leu	Ala	Ala	Arg	Met
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Leu	Glu	Asp	Tyr	Gln	Thr	Val	Lys	Gly	Val	Gln	Pro	Glu	Arg	Gly	
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<210> 1237

<211> 1608

<212> DNA

<213> Homo sapiens

<400> 1237

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1140
tactcctggg attcagtcac tgatgcatga attttatgat gtggcaaata ctgtgggaaa
1200

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tcctgggtca gtcctgaccc aatactgggc tcttttaaata gtatttgaac aatttcagtt
 1260
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 1320
 cattgaaaaa ccacaagtgc catttgatgc aatagaaaat aaaaaagctg cagttccaca
 1380
 aattaaaaaat gaaaataaag aaatacattg cagtgatgat gaaaacacac catgtcatat
 1440
 caagcagatc ttcacacatc cacatttgga actaaatcct gactttcatc caaagatcaa
 1500
 agattattac tgtgaagtcc catttgatgt ggtaacagtg acaattggag tggaaactcc
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<210> 1238
 <211> 458
 <212> PRT
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<400> 1238
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 Phe Pro Glu Leu Gln Leu Pro Val Ser Pro Ser Val Cys Leu Asp Gln
 35 40 45
 Gly Met Gln Leu Lys Pro Ser Thr Ser Ser His Leu Leu Lys Thr Val
 50 55 60
 Lys Pro Arg Val Trp Lys Pro Gly Asp Trp Ser Arg Glu Gln Leu Asn
 65 70 75 80
 Glu Thr Thr Val Leu Ala Pro His Glu Thr Ile Phe Arg Ala Lys Asp
 85 90 95
 Leu Ser Val Ile Leu Lys Ala Tyr Val Leu Val Thr Ser Leu Thr Pro
 100 105 110
 Leu Arg Ala Phe Ile His Ser Thr Gly Thr Val Trp Asn Pro Pro Lys
 115 120 125
 Lys Lys Arg Phe Thr Val Lys Leu Gln Thr Phe Phe Glu Thr Phe Leu
 130 135 140
 Arg Ala Ser Ser Pro Gln Gln Ala Phe Asp Ile Met Lys Glu Ala Ile
 145 150 155 160
 Gly Lys Leu Leu Leu Ala Ala Glu Val Phe Ser Glu Thr Ser Thr Leu
 165 170 175
 Gly Pro Lys Thr Phe His Arg Cys Arg Phe Cys Phe Gln Leu Leu Thr
 180 185 190
 Phe Asp Ile Gly Tyr Gly Ser Phe Met Tyr Pro Val Val Leu Gln Val
 195 200 205
 His Glu His Leu Asn Phe Gln Asp Tyr Asp Asn Met Asp Phe Glu Asp
 210 215 220
 Gln Asn Thr Glu Glu Phe Leu Leu Asn Asp Thr Phe Asn Phe Leu Phe
 225 230 235 240
 Pro Asn Glu Ser Ser Leu Ser Ile Phe Ser Glu Ile Phe Gln Arg Leu
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 Tyr Arg Ser Asp Val Phe Lys Gly Glu Asn Tyr Gln Lys Glu Leu Asn


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<212> DNA
<213> Homo sapiens
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<212> PRT
<213> Homo sapiens
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<400> 1240

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Ile Arg Thr Glu Leu Glu Met Gln Met Val Cys Asn Leu Arg Glu Phe
      35             40             45
Lys Glu Phe Ile Asp Asn Glu Met Ile Val Ile Leu Gly Gln Met Asp
      50             55             60
Ser Pro Thr Gln Ile Phe Glu His Val Phe Leu Gly Ser Glu Trp Asn
      65             70             75             80
Ala Ser Asn Leu Glu Asp Leu Gln Asn Arg Gly Val Arg Tyr Ile Leu
      85             90             95
Asn Val Thr Arg Glu Ile Asp Asn Phe Phe Pro Gly Val Phe Glu Tyr
      100            105            110
His Asn Ile Arg Val Tyr Asp Glu Glu Ala Thr Asp Leu Leu Ala Tyr
      115            120            125
Trp Asn Asp Thr Tyr Lys Phe Ile Ser Lys Ala Lys Lys His Gly Ser
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Lys Cys Leu Val His
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<210> 1241

<211> 489

<212> DNA

<213> Homo sapiens

<400> 1241

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120
taggaagatc aatgaggcgc gagtgtgtgt gtgtacgtgt gcgcgtgtgt gtgtgagaga
180
gagagaaaga aagaagaaag gtcccgattg caacgtgtca gatcttgcaa ctttcccccc
240
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300
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360
ggatttgtgt tgtgaggtcg gtggtgcggt cttttctttc tttctcgcg tgttttcccg
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480
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<210> 1242

<211> 127

<212> PRT

<213> Homo sapiens

<400> 1242

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Met Asn Asn Cys Glu Ala Ile Arg Leu His Ser Leu Arg Cys Ala Phe

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